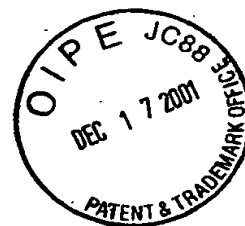


SEQUENCE LISTING



<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor

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<151> 1999-07-08

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Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile Phe Asp Gly Pro Glu
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Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly Ile Leu Asp Gly Trp
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gct cac tct gct gtg ctg gat caa gtg aaa caa ata gca ggt gaa aac 259
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Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr Asp Asn Val Val Asn
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 His Leu Leu Leu Val Ser Ile Leu Val Gly Ser Ile Ala Gly Ile Trp
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 Thr Cys Gly Gly Val Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro
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 Pro Lys Ile Lys Arg Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr
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 Gly Ile Lys Pro Leu His Leu Leu Leu Val Ser Ile Leu Val Gly Ser
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 Ile Ala Gly Ile Trp Val Ile Ser Gly Phe Thr Gly Pro Val Asp Ser
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 Arg Pro Val Asp Lys Val Ala Glu Ile Ser Thr Gln Gly Glu Thr Ser
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 Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn Leu Arg Ile His Val Gly
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 225 230 235 240
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Gln Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn Leu Arg Ile His Val
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Leu Asn Val Gly Cys His Ser Lys Ala Ala Glu Thr Leu Val His Lys
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 Met Ser Thr Gln Thr
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 Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile Phe Asp Gly Pro Glu
 10 15 20
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 Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly Ile Leu Asp Gly Trp
 25 30 35
 gct cac tct gct gtg ctg gat caa gtg aaa caa ata gca ggt gaa aac 259
 Ala His Ser Ala Val Leu Asp Gln Val Lys Gln Ile Ala Gly Glu Asn
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 Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr Asp Asn Val Val Asn
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 Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr Gly Ile Lys Pro Leu
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 His Leu Leu Leu Val Ser Ile Leu Val Gly Ser Ile Ala Gly Ile Trp
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Thr Cys Gly Gly Val Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro
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Pro Lys Ile Lys Arg Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr
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Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala	
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Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr				
	965	970	975	
gac aac tct att cgt gat ggt gcg aat gtg atg gag gat att cga gca				2976
Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala				
	980	985	990	
cag cag cgt ggt ttt gat gcg cgt aat gat aac tcc cgt gat gcg ctg				3024
Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu				
	995	1000	1005	
gtg ctt acc ggt ggg cgt aac att tct gta ctt gat gtt gat gcg ggt				3072
Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly				
	1010	1015	1020	
aaa ggt ttc ttt gat ccc atg atg act ggt atg gcg gcg aac cag ggt				3120
Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly				
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tct gtt cgc tat ttg ttg cct tct gcg aag gtg ggc gct gat ggc atg				3168
Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met				
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att acc cct ggt gat ccg gct gat cga gta cct gtt gca gcg cat cca				3216
Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro				
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gaa tca tgg gcg atg ggc ttt gac cca cat gac cgt cag aac atg act				3264
Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr				
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Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr				
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gcg atg ata cag ctg ggc ggt tgg aac ttt gaa gat ggc att att gtc				3360
Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val				
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tct gcc gat ttt gcg aat acc cat gtt att cgc gat acg gaa gat gag				3408
Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu				
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Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn				
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Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp				
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gca cgt gca gca ggg ctg gaa tca gag gtg gcg ttt ttc cga gac aac				3552
Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn				
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cct gat cta gag gtt gtc atg agt ccg ttt tct gcc att tct cgt ttt				3600
Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe				
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Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg	
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Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro	
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agc att tac gat gag aac ggt gag ctg aat aat cgt gtt aat cgt gca	4032
Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala	
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Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu	
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cat ttg cgc agt gat gag gat tta gcg gac ggt agt acc tct cga cat	4224
His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His	
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Glu Tyr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu	
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Leu Arg Phe Asp Gly Met Glu Asn His Met Ala Ser Val Ala Gln Cys	
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Pro Thr Pro Glu Ala Leu Arg Ser His Tyr Glu Gly Ser Gln Lys Ala	
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1765 1770 1775	
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Pro Ile Asp Ala Leu Tyr Arg Ala Glu Thr Leu Met Gly Pro Val Gly	
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Ala Thr Lys Asp Glu Trp Val Gln Gln Tyr Met Glu Met Tyr Ala Asp	
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1925	1930	1935	
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ccg cca gtt atg cct gtc aca cct ccg gca cag caa cct gtt tcg cct Pro Pro Val Met Pro Val Thr Pro Pro Ala Gln Gln Pro Val Ser Pro 2035 2040 2045			6144
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<210> 8

<211> 2149

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

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 20 25 30
 Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
 35 40 45
 Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
 50 55 60
 His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65 70 75 80
 Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
 85 90 95
 Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
 100 105 110
 Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
 115 120 125
 Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
 130 135 140
 Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
 145 150 155 160
 Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
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 Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
 180 185 190
 Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
 195 200 205
 Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
 210 215 220
 Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
 225 230 235 240
 Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
 245 250 255
 Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
 260 265 270
 Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
 275 280 285
 Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
 290 295 300

Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
 305 310 315 320
 Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
 325 330 335
 Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
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 Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
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 Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
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 Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
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 Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
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 Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
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 Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
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 Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
 450 455 460
 Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
 465 470 475 480
 Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
 485 490 495
 Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
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 Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
 515 520 525
 Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
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 Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
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 Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
 610 615 620
 Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys

625	630	635	640
Gln Asp Tyr Trp	Ala Met Leu Arg Gly	Glu Glu Thr Asp Leu Leu Asn	
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Pro Gly Val Asn Arg Asp Asp Tyr Met	Ala Ala Ile Arg Asp Gly Asp		
	660	665	670
His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val			
	675	680	685
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val			
	690	695	700
Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val			
	705	710	715
Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His			
	725	730	735
Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu			
	740	745	750
Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu			
	755	760	765
Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu			
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Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser			
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Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val			
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Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala			
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Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln			
	835	840	845
Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val			
	850	855	860
Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr			
	865	870	875
Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu			
	885	890	895
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val			
	900	905	910
Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly			
	915	920	925
Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg			
	930	935	940
Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp			
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			960

Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
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Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
980 985 990

Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
995 1000 1005

Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
1010 1015 1020

Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
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Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
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Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
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 Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
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 His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
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 Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
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Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile		
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Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu		
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Asn Glu His Tyr Ala Gln Ala Phe Ala Asn Arg Asp Gly Leu Val Thr		
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Leu Arg Phe Asp Gly Met Glu Asn His Met Ala Ser Val Ala Gln Cys		
1700	1705	1710
Phe Glu Thr Gly Ala Lys Gly Ser Pro Gly Lys Leu Lys Glu Tyr Ala		
1715	1720	1725
Thr Tyr Ile Gly Ala Asp Pro Ala Gln Gly Phe Lys Asp Val Gly Gln		
1730	1735	1740
Pro Thr Pro Glu Ala Leu Arg Ser His Tyr Glu Gly Ser Gln Lys Ala		
1745	1750	1755
Thr Ala Ile Lys Val Leu Phe Thr Gly Val Ala Gly Lys Lys Glu Gln		
1765	1770	1775
Glu Met Val Ala Leu Cys Arg Asn Leu Gly Leu Thr Lys Glu Ala Met		
1780	1785	1790
Ala Ala Ser Ala Pro Ala Gln Gln Ser Ile Leu Gln Ala Lys His Asp		
1795	1800	1805
Pro Ile Asp Ala Leu Tyr Arg Ala Glu Thr Leu Met Gly Pro Val Gly		
1810	1815	1820
Asp Leu Tyr Gln Gly Arg Lys Met Arg Arg Gly Glu Asn Glu Gln Gly		
1825	1830	1835
Arg Tyr Glu Trp Glu Val Val Arg Asp Glu Asn His Gln Pro Ile Gln		
1845	1850	1855
Ala Thr Lys Asp Glu Trp Val Gln Gln Tyr Met Glu Met Tyr Ala Asp		
1860	1865	1870
Asp Lys Gly Met Gly Val Ser Val Gly Val Asp Gln Val Glu Lys Ile		
1875	1880	1885
Ala Glu Glu Phe Ser Asp Glu Gln Gly Tyr Met Arg Val Leu Ser His		
1890	1895	1900
Asp Glu Leu Pro Thr Glu Ile Lys Pro Leu Ala Leu Asp Gln Leu Ala		
1905	1910	1915
Tyr Gly Asp Lys Lys Asn Arg Phe Asp Leu Leu Cys Glu Met Ala Lys		
1925	1930	1935

Gln Gln Val Asn Ile Tyr Asp Gly Asp Ala Tyr Asp Phe Ala Pro Arg
 1940 1945 1950
 Val Val Arg Ala Asn Met Lys Ala Met Glu Asp Ala Ala Arg Phe Gly
 1955 1960 1965
 Ile Pro Asp Val Glu Ile Gln Ser Ile Ser Ala Gln Gln Ser Leu Ala
 1970 1975 1980
 Ser Phe Glu Arg Val Pro Gln Arg Ser Gly Phe Arg Ile Glu Arg Arg
 1985 1990 1995 2000
 Val Pro Ala Glu Val Gly Thr Gly Ile Ala Ala Pro Ala Pro Leu Pro
 2005 2010 2015
 Asp Ala Gly Val Gln Gly Asn Tyr Val Gln Gln Gln Val Pro Ala Thr
 2020 2025 2030
 Pro Pro Val Met Pro Val Thr Pro Pro Ala Gln Gln Pro Val Ser Pro
 2035 2040 2045
 Ala Gln Thr Asp Phe Arg Gly Val Gly Gln Pro Leu Asp Gln Gly Gly
 2050 2055 2060
 Lys Ile Gly Asn Tyr Gly His Gln Gly Pro Ala Met Gly Ala Gln Gln
 2065 2070 2075 2080
 Pro Val Val Pro Gln Gln Gln Asn Ile Pro Pro Val His Asn Pro Val
 2085 2090 2095
 Pro Gln Asn Ser Val Pro Pro Thr Pro Val Val Pro Lys Pro Gly Thr
 2100 2105 2110
 Gly Asn Pro Phe Thr His Gly Gly Ala Asn Asn Gln Phe Met Gly Arg
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 Phe Asp Thr Ser Arg Tyr Asn Gln Gln Glu Pro Pro Gln Arg Gln Asp
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 Gly Gly Phe Glu Leu
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 Gly Phe Lys Asp Val Gly Gln Pro Thr Pro Glu Ala Leu Arg Ser His

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Tyr	Glu	Gly	Ser	Gln	Lys	Ala	Thr	Ala	Ile	Lys	Val	Leu	Phe	Thr	Gly															
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Val	Ala	Gly	Lys	Lys	Glu	Gln	Glu	Met	Val	Ala	Leu	Cys	Arg	Asn	Leu															
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Ile	Leu	Gln	Ala	Lys	His	Asp	Pro	Ile	Asp	Ala	Leu	Tyr	Arg	Ala	Glu															
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act	ctt	atg	gga	cca	gta	ggt	gat	ctc	tac	caa	ggt	cgc	aag	atg	cgt	336														
Thr	Leu	Met	Gly	Pro	Val	Gly	Asp	Leu	Tyr	Gln	Gly	Arg	Lys	Met	Arg															
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Arg	Gly	Glu	Asn	Glu	Gln	Gly	Arg	Tyr	Glu	Trp	Glu	Val	Val	Arg	Asp															
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Glu	Asn	His	Gln	Pro	Ile	Gln	Ala	Thr	Lys	Asp	Glu	Trp	Val	Gln	Gln															
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Tyr	Met	Glu	Met	Tyr	Ala	Asp	Asp	Lys	Gly	Met	Gly	Val	Ser	Val	Gly															
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Val	Asp	Gln	Val	Glu	Lys	Ile	Ala	Glu	Glu	Phe	Ser	Asp	Glu	Gln	Gly															
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Tyr	Met	Arg	Val	Leu	Ser	His	Asp	Glu	Leu	Pro	Thr	Glu	Ile	Lys	Pro															
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cta	gca	ctt	gat	cag	ctt	gcc	tat	ggc	gat	aag	aag	aac	cgc	ttt	gat	624														
Leu	Ala	Leu	Asp	Gln	Leu	Ala	Tyr	Gly	Asp	Lys	Lys	Asn	Arg	Phe	Asp															
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Leu	Leu	Cys	Glu	Met	Ala	Lys	Gln	Gln	Val	Asn	Ile	Tyr	Asp	Gly	Asp															
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Glu	Asp	Ala	Ala	Arg	Phe	Gly	Ile	Pro	Asp	Val	Glu	Ile	Gln	Ser	Ile															
245					250					255																				
tct	gca	cag	cag	tca	ttg	gcg	agc	ttt	gag	cga	gtc	cca	caa	cgt	tct	816														
Ser	Ala	Gln	Gln	Ser	Leu	Ala	Ser	Phe	Glu	Arg	Val	Pro	Gln	Arg	Ser															
260					265					270																				

ggt ttc cgt att gag cgt cgt gtg ccg gca gaa gta ggt aca ggg att 864
 Gly Phe Arg Ile Glu Arg Arg Val Pro Ala Glu Val Gly Thr Gly Ile
 275 280 285

gct gca cca gca ccg tta cct gat gca ggt gta cag ggg aat tat gtt 912
 Ala Ala Pro Ala Pro Leu Pro Asp Ala Gly Val Gln Gly Asn Tyr Val
 290 295 300

cag cag cag gtg cct gcg acc ccg cca gtt atg cct gtc aca cct ccg 960
 Gln Gln Gln Val Pro Ala Thr Pro Pro Val Met Pro Val Thr Pro Pro
 305 310 315 320

gca cag caa cct gtt tcg cct gct cag acg gac ttc cgg ggc gtt ggt 1008
 Ala Gln Gln Pro Val Ser Pro Ala Gln Thr Asp Phe Arg Gly Val Gly
 325 330 335

cag cca ctc gac cag ggc gga aaa atc ggg aat tat gga cat cag gga 1056
 Gln Pro Leu Asp Gln Gly Gly Lys Ile Gly Asn Tyr Gly His Gln Gly
 340 345 350

cct gca atg ggg gcg caa cag cca gtt gtg cct cag cag cag aat att 1104
 Pro Ala Met Gly Ala Gln Gln Pro Val Val Pro Gln Gln Gln Asn Ile
 355 360 365

ccg cct gtg cat aat ccg gta cca cag aat tct gtt ccg cct act ccg 1152
 Pro Pro Val His Asn Pro Val Pro Gln Asn Ser Val Pro Pro Thr Pro
 370 375 380

gtt gtg ccg aag cca ggt aca gga aac ccg ttt act cat ggt ggt gcg 1200
 Val Val Pro Lys Pro Gly Thr Gly Asn Pro Phe Thr His Gly Gly Ala
 385 390 395 400

aac aat cag ttt atg ggt cga ttt gat aca agc cgt tac aac caa cag 1248
 Asn Asn Gln Phe Met Gly Arg Phe Asp Thr Ser Arg Tyr Asn Gln Gln
 405 410 415

gaa cca cca caa cga cag gat ggc ggg ttt gag ctc taaataatgg 1294
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<211> 428

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

Tyr Glu Gly Ser Gln Lys Ala Thr Ala Ile Lys Val Leu Phe Thr Gly
 35 40 45

Val Ala Gly Lys Lys Glu Gln Glu Met Val Ala Leu Cys Arg Asn Leu
 50 55 60

Gly Leu Thr Lys Glu Ala Met Ala Ala Ser Ala Pro Ala Gln Gln Ser
 65 70 75 80
 Ile Leu Gln Ala Lys His Asp Pro Ile Asp Ala Leu Tyr Arg Ala Glu
 85 90 95
 Thr Leu Met Gly Pro Val Gly Asp Leu Tyr Gln Gly Arg Lys Met Arg
 100 105 110
 Arg Gly Glu Asn Glu Gln Gly Arg Tyr Glu Trp Glu Val Val Arg Asp
 115 120 125
 Glu Asn His Gln Pro Ile Gln Ala Thr Lys Asp Glu Trp Val Gln Gln
 130 135 140
 Tyr Met Glu Met Tyr Ala Asp Asp Lys Gly Met Gly Val Ser Val Gly
 145 150 155 160
 Val Asp Gln Val Glu Lys Ile Ala Glu Glu Phe Ser Asp Glu Gln Gly
 165 170 175
 Tyr Met Arg Val Leu Ser His Asp Glu Leu Pro Thr Glu Ile Lys Pro
 180 185 190
 Leu Ala Leu Asp Gln Leu Ala Tyr Gly Asp Lys Lys Asn Arg Phe Asp
 195 200 205
 Leu Leu Cys Glu Met Ala Lys Gln Gln Val Asn Ile Tyr Asp Gly Asp
 210 215 220
 Ala Tyr Asp Phe Ala Pro Arg Val Val Arg Ala Asn Met Lys Ala Met
 225 230 235 240
 Glu Asp Ala Ala Arg Phe Gly Ile Pro Asp Val Glu Ile Gln Ser Ile
 245 250 255
 Ser Ala Gln Gln Ser Leu Ala Ser Phe Glu Arg Val Pro Gln Arg Ser
 260 265 270
 Gly Phe Arg Ile Glu Arg Arg Val Pro Ala Glu Val Gly Thr Gly Ile
 275 280 285
 Ala Ala Pro Ala Pro Leu Pro Asp Ala Gly Val Gln Gly Asn Tyr Val
 290 295 300
 Gln Gln Gln Val Pro Ala Thr Pro Pro Val Met Pro Val Thr Pro Pro
 305 310 315 320
 Ala Gln Gln Pro Val Ser Pro Ala Gln Thr Asp Phe Arg Gly Val Gly
 325 330 335
 Gln Pro Leu Asp Gln Gly Gly Lys Ile Gly Asn Tyr Gly His Gln Gly
 340 345 350
 Pro Ala Met Gly Ala Gln Gln Pro Val Val Pro Gln Gln Gln Asn Ile
 355 360 365
 Pro Pro Val His Asn Pro Val Pro Gln Asn Ser Val Pro Pro Thr Pro
 370 375 380

Val Val Pro Lys Pro Gly Thr Gly Asn Pro Phe Thr His Gly Gly Ala
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Asn Asn Gln Phe Met Gly Arg Phe Asp Thr Ser Arg Tyr Asn Gln Gln
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Glu Pro Pro Gln Arg Gln Asp Gly Gly Phe Glu Leu
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<223> FRXA01542

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gct gtg cgt atc tat agg caa gca gaa gcc ttg atg aaa cag cgc gca 96
Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
20 25 30

gca aac aat aag ggc tta gac ctc aat gat gaa gcg acc tat ggc gcc 144
Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
35 40 45

atc atg ttt gcg tct ttc gat gat gcc ttc gcc gct gat gcc gaa gct 192
Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
50 55 60

cat ggc tgt gta cac cga cca cag ttc gcg aag gta act agg cga aat 240
His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
65 70 75 80

att ctt aat tca ccg caa tac acg gcg att aag tca tct tat gac gcg 288
Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
85 90 95

ctg gtg cag cag gat ctc gtg gcc caa cag cag cag gca caa gcg cta 336
Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
100 105 110

cag caa gct gct tat gag caa gag cag gca gct att ttc cag gca cgt 384
Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
115 120 125

gat caa gca aca ttc cag gct gaa caa acg ctc gcg caa gag tcc gtt 432
Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
130 135 140

cgc caa tca gag ggt gtg ggt tta cct gtc att gat ccg atg gag agc 480
Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145 150 155 160

tat ttc cgg gag tac gcc ttc tat gaa ggt gtc gag atg ttt ggt acc	528
Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr	
165 170 175	
tgg ggt acg cac gtt gat gct ggt gtg tcg cag ttt agc acc tct gat	576
Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp	
180 185 190	
ggc cgt gcg atc cga gcg ctt gtt gat gag cat ctc gca acc tat gaa	624
Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu	
195 200 205	
cca gta gag cag cgg ggg agt act cag gca ttc ttc gcc tct gtc aat	672
Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn	
210 215 220	
gct gcc ttt gct gag gtg gca cct cac gca gca ccc atg ttt agt gcg	720
Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala	
225 230 235 240	
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Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His	
245 250 255	
cgt ttc gac aag atg gtc ggc act gca att gga cct aat ggt ttg cct	816
Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro	
260 265 270	
gag gga cct gat ctg ggt ggt cgt cgt tta cct att tcg cct tat gat	864
Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp	
275 280 285	
cca cgc tgg tca gac cgc gaa gta gtc cgt gtg cac ggt acc aag ctg	912
Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu	
290 295 300	
cta tca ctg tcc gaa gag agt gtt ggc atg atc agg gac ctt gat cta	960
Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu	
305 310 315 320	
gca acg atc cac cta caa gat aat gat gtt tac gag ggc act cat cga	1008
Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg	
325 330 335	
gaa gac gac act aaa ggc ggt gtg cga ccg ttg act caa tgg gtc aat	1056
Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn	
340 345 350	
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Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg	
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Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala	
370 375 380	
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Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser	
385 390 395 400	
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Gln	Lys	Ile	Asp	Pro	Asn	Lys	Val	Met	Ser	Asp	Glu	Gly	Ile	Ala	Arg			
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Ser	Glu	Ala	Ile	Leu	Thr	Tyr	Leu	Ser	Asp	Glu	Gly	Val	Asp	Phe	Arg			
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atc	gag	cca	gat	cgt	gag	ccg	gga	cag	ctt	aaa	gtg	cgt	att	gag	ggc		1344	
Ile	Glu	Pro	Asp	Arg	Glu	Pro	Gly	Gln	Leu	Lys	Val	Arg	Ile	Glu	Gly			
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acc	cgt	att	gat	att	cgt	ctc	act	gat	act	cgc	gcc	aat	gaa	cag	tgg		1392	
Thr	Arg	Ile	Asp	Ile	Arg	Leu	Thr	Asp	Thr	Arg	Ala	Asn	Glu	Gln	Trp			
	450					455					460							
gtg	ggt	cgt	gtc	tat	gat	tct	ggc	act	gtg	att	aag	tat	tcc	gcc	gaa		1440	
Val	Gly	Arg	Val	Tyr	Asp	Ser	Gly	Thr	Val	Ile	Lys	Tyr	Ser	Ala	Glu			
465					470				475						480			
caa	aca	gcg	gaa	gaa	cgt	cta	cga	gct	cgt	gag	cgc	atg	gag	aac	ggt		1488	
Gln	Thr	Ala	Glu	Glu	Arg	Leu	Arg	Ala	Arg	Glu	Arg	Met	Glu	Asn	Gly			
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gat	gga	acg	tgg	aca	ccg	gct	act	gat	tat	gaa	cca	agc	cca	act	gaa		1536	
Asp	Gly	Thr	Trp	Thr	Pro	Ala	Thr	Asp	Tyr	Glu	Pro	Ser	Pro	Thr	Glu			
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gtt	gtc	gat	ctc	gtg	aaa	ttt	gct	ctc	ggt	cga	gag	gtt	gag	cga	cag		1584	
Val	Val	Asp	Leu	Val	Lys	Phe	Ala	Leu	Gly	Arg	Glu	Val	Glu	Arg	Gln			
		515					520					525						
gat	ggc	aaa	ggt	ctt	gtt	ggt	gtg	cct	aat	gct	cga	cac	cca	cgt	gct		1632	
Asp	Gly	Lys	Gly	Leu	Val	Gly	Val	Pro	Asn	Ala	Arg	His	Pro	Arg	Ala			
	530					535					540							
tta	gag	cag	gca	cag	gat	gca	tat	ttc	act	aag	aat	cgt	tcc	gca	ttc		1680	
Leu	Glu	Gln	Ala	Gln	Asp	Ala	Tyr	Phe	Thr	Lys	Asn	Arg	Ser	Ala	Phe			
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Met	Val	Arg	Glu	Gly	Leu	Ser	Ile	Val	Gln	Asp	Ala	Arg	Asp	Arg	Ser			
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Ala	Gly	Pro	Gly	Lys	Trp	Phe	Asp	Asn	Glu	Ala	Lys	Ala	Ser	Glu	Trp			
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ctt	ggt	aac	aat	atc	gcc	ctt	act	cgt	gcg	cgt	gtg	gcc	gaa	gag	ctc		1824	
Leu	Gly	Asn	Asn	Ile	Ala	Leu	Thr	Arg	Ala	Arg	Val	Ala	Glu	Glu	Leu			
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ggc	gtt	gaa	gaa	ctg	att	gcg	ctt	tct	gca	cag	tac	gcc	gat	gat	cct		1872	
Gly	Val	Glu	Glu	Leu	Ile	Ala	Leu	Ser	Ala	Gln	Tyr	Ala	Asp	Asp	Pro			
	610					615					620							
gac	ttc	atg	ccg	gct	ttt	gct	ggt	gag	gat	gag	ctc	atg	gcg	ata	aag		1920	
Asp	Phe	Met	Pro	Ala	Phe	Ala	Gly	Glu	Asp	Glu	Leu	Met	Ala	Ile	Lys			
	625				630					635					640			
cag	gac	tat	tgg	gcg	atg	ctg	cga	ggt	gag	gaa	acc	gat	ctg	ctt	aac		1968	
Gln	Asp	Tyr	Trp	Ala	Met	Leu	Arg	Gly	Glu	Glu	Thr	Asp	Leu	Leu	Asn			

645	650	655	
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cat gag cag att gct gcg atg acc tca gca atg aat gct gtg acc gtg His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val 675 680 685			2064
gag gat cgt gtg cgt cag cac gcg gcc ctt gtt ctt gat gat tat gtc Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val 690 695 700			2112
ggc acg gtg gag cct gat cct gtt acc ggc ttg cgt ttt aat ccg gtg Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val 705 710 715 720			2160
aca gtt gct cag cac atg ccg agt gct aaa tcc ctg tgg tca aac cat Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His 725 730 735			2208
gac gat att att gcc gcg ttg cga gcg act tcg att act ggc gat gaa Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu 740 745 750			2256
ctg cgc ggt gac gaa ttc tat aac gat gtt att aat caa cag ttg ctc Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu 755 760 765			2304
aaa ttt aat cct gag acc gcg cag aaa atg gtt aat aac cct gat ctt Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu 770 775 780			2352
gac ccg cag ttg gct cga ttt ggc act gtc att gcc gag act att tcc Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser 785 790 795 800			2400
cgc aat ggt gct gat gtg gtc gat att gct gtt gac gat aac ggt gtg Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val 805 810 815			2448
gtg cgg tgg acc gca cag cga cgt gtt ggt gcg aag gat agt cgt gca Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala 820 825 830			2496
gta gat agt aag ggg cag gtt cgc ggt gaa cgc acc cgt cat gtg cag Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln 835 840 845			2544
ggt gag ata ggt cag att ttt act cgc ggt gag cat ggt gaa att gtc Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val 850 855 860			2592
acc aaa ttt aat ggt ggc gag aac tat atg ttt gcc cct ggc tac acc Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr 865 870 875 880			2640
gcg tct gtg gta cca caa aag cct ggt gag aca aag agt tta gaa gag Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu 885 890 895			2688

cgt acc aag ctc aaa ggc tat gag cag gtg atg tca gag gcg ttg gtg	2736
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val	
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tac cgt gtg cga gaa gat ttg atg ttc act gag cga tcc cga gtg ggt	2784
Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly	
915 920 925	
gct aca acc agc atc aac agt gca tat aag cga ctg tat gac aat cgc	2832
Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg	
930 935 940	
ttc cct gtg gac ttc ttc gag cgc agc gcc gaa gaa ggt ttg agc gat	2880
Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp	
945 950 955 960	
gag tgg cgt gct gcg ttg ctt gag act gcg agt ttg cgt gtg cgc tac	2928
Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr	
965 970 975	
gac aac tct att cgt gat ggt gcg aat gtg atg gag gat att cga gca	2976
Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala	
980 985 990	
cag cag cgt ggt ttt gat gcg cgt aat gat aac tcc cgt gat gcg ctg	3024
Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu	
995 1000 1005	
gtg ctt acc ggt ggg cgt aac att tct gta ctt gat gtt gat gcg ggt	3072
Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly	
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Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly	
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Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met	
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Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro	
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Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr	
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Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr	
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Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val	
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tct gcc gat ttt gcg aat acc cat gtt att cgc gat acg gaa gat gag	3408
Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu	
1125 1130 1135	

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aag ggt gtg acc gct ctt gtt gtt gat cca gcg atg agt gat gct gat Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp 1155 1160 1165	3504
gca cgt gca gca ggg ctg gaa tca gag gtg gcg ttt ttc cga gac aac Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn 1170 1175 1180	3552
cct gat cta gag gtt gtc atg agt ccg ttt tct gcc att tct cgt ttt Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe 1185 1190 1195 1200	3600
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ttc agg aat aat gat ggt tct act cgt gtt caa cca ggt gcc tct ggt Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly 1220 1225 1230	3696
gat ctc aac ttc atc gtc acg cat atg gct gtt gat gcg aaa acc aat Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn 1235 1240 1245	3744
gtc tat gat gaa gaa gct gtt cgt gag ggc caa gga cgt aaa gcg tct Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser 1250 1255 1260	3792
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tat ctt cgc gtc acg ggg ctt gat gtc acc ccg tat ggt gag ttg cgc Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg 1300 1305 1310	3936
gag ggg ttc agc gag tcc aat gag cag cgc aat atc atc gag atg cca Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro 1315 1320 1325	3984
agc att tac gat gag aac ggt gag ctg aat aat cgt gtt aat cgt gca Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala 1330 1335 1340	4032
cag gtg cgc gaa gct ttt gtt gag cag atc agt cgc gct ggt ggt gtt Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val 1345 1350 1355 1360	4080
atg gag att cct ttc cag tta cag ttg cgc aat ggt gca cag cta gaa Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu 1365 1370 1375	4128
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Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro	
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His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His	
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Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu	
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gca gaa gag caa gcc aag att gac gca ttg cgc cag gag gaa gcg cag	4320
Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln	
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cac ggc acg ttg cct cgt gct gcg gaa aag cga ctg agc gag tca cag	4368
His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln	
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Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly	
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Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val	
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Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala	
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Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn	
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Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met	
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Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg	
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Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser	
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Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val	
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Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr	
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Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp	
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Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln	

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Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile			
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Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile			
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Ser Arg Glu Glu Leu Leu Val Asn Arg Ala His Met Asp Asp Leu			
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Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
35 40 45

Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
50 55 60

His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
65 70 75 80

Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
85 90 95

Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
100 105 110

Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
115 120 125

Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
130 135 140

Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145 150 155 160

Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
165 170 175

Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
180 185 190

Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
 195 200 205
 Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
 210 215 220
 Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
 225 230 235 240
 Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
 245 250 255
 Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
 260 265 270
 Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
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 Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
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 Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
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 Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
 325 330 335
 Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
 340 345 350
 Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
 355 360 365
 Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
 370 375 380
 Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
 385 390 395 400
 Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
 405 410 415
 Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
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 Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
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 Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
 450 455 460
 Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
 465 470 475 480
 Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
 485 490 495
 Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
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 Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln

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Asp Gly Lys Gly Leu Val	Gly Val Pro Asn Ala	Arg His Pro Arg Ala	530	535	540									
Leu Glu Gln Ala Gln Asp	Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe		545	550	555							560		
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Ala Gly Pro Gly Lys Trp Phe Asp	Asn Glu Ala Lys Ala Ser Glu Trp		580		585							590		
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Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr	Ala Asp Asp Pro		610		615							620		
Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys			625		630							640		
Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn			645		650							655		
Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp			660		665							670		
His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val			675		680							685		
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val			690		695							700		
Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val			705		710							720		
Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His			725		730							735		
Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu			740		745							750		
Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu			755		760							765		
Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu			770		775							780		
Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser			785		790							800		
Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val			805		810							815		
Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala			820		825							830		
Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln			835		840							845		

Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
 850 855 860
 Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
 865 870 875 880
 Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
 885 890 895
 Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
 900 905 910
 Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
 915 920 925
 Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
 930 935 940
 Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
 945 950 955 960
 Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
 965 970 975
 Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
 980 985 990
 Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
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 Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
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 Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
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 Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
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 Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
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 Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
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 Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
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 Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
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 Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
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Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
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Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
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Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
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Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
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Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
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Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
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Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
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Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
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Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
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Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
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Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
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Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
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Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
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Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
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His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
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Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
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Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425 1430 1435 1440

His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
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Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
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Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
1475 1480 1485

Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala

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Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn		
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Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met		
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Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg		
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Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser		
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Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val		
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Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr		
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Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp		
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Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln		
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Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile		
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Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile		
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 Val Val Thr Val Ala
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 cag gca gtc gta gag gcg gag att agt ctt gct gca caa gca agt gag 211

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Gln	Val	Arg	Glu	Gln	Ala	Glu	Ala	Pro	Asp	Val	Asn	Glu	Gln	Val	Glu		
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Glu	Val	Ser	Val	Glu	Val	Ser	Ser	Val	Gln	Ser	Leu	Thr	Gln	Pro	Lys		
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Thr	Leu	Gly	Gln	Leu	His	Asp	Pro	Arg	Lys	Asn	Val	Met	Ser	Ser	Ser		
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Glu	Ser	Glu	Glu	Pro	Glu	Thr	Leu	Arg	Asp	Val	Leu	Pro	Arg	Arg	Lys		
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cag	cgc	agc	att	ttt	ggt	gaa	tca	gct	ccg	tct	gat	ttt	gat	gac	ctc	547	
Gln	Arg	Ser	Ile	Phe	Gly	Glu	Ser	Ala	Pro	Ser	Asp	Phe	Asp	Asp	Leu		
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Ser	Asp	Val	Glu	Glu	Phe	Asp	Thr	Ser	His	Trp	Val	Arg	Ala	Gly	Gln		
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Asp	Asp	Arg	Ser	Asp	Asp	Asp	Arg	Leu	Ala	Asp	Glu	Ala	Gly	Val	Pro		
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Val	Asp	Glu	Gln	Leu	His	Met	Arg	Glu	Val	His	Ala	Gln	Ser	Phe	Asp		
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Pro	Ile	Asp	Val	Ala	Lys	Lys	Glu	Arg	Lys	Ala	Ala	Glu	Lys	Lys	Tyr		
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Ala	Lys	Pro	Pro	Lys	Ser	Asp	Asn	Pro	Tyr	Leu	Ala	Arg	Asp	Ala	Lys		
		230			235					240					245		
gat	gca	gct	gct	cgt	aag	cgg	aag	atc	aat	gca	gct	cat	gat	aat	ttt	883	
Asp	Ala	Ala	Ala	Arg	Lys	Arg	Lys	Ile	Asn	Ala	Ala	His	Asp	Asn	Phe		
				250					255					260			
gcc	caa	gag	atg	gca	cag	gct	gcg	atg	gga	cca	ctg	cgc	aaa	ggg	gtc	931	
Ala	Gln	Glu	Met	Ala	Gln	Ala	Ala	Met	Gly	Pro	Leu	Arg	Lys	Gly	Val		

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Asn	Thr	Gln	Thr	Val	Met	Ala	Ala	Cys	Thr	Thr	Ala	Ala	Val	Met	Trp					
280						285					290									
tgc	atg	agc	cca	cgt	atg	acc	ggt	gtg	aac	gtg	gat	atg	aag	cgc	aag	1027				
Cys	Met	Ser	Pro	Arg	Met	Thr	Gly	Val	Asn	Val	Asp	Met	Lys	Arg	Lys					
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ttt	aac	aag	gat	ctg	gaa	cag	gct	aaa	gac	act	aag	ttg	tcg	aag	tat	1075				
Phe	Asn	Lys	Asp	Leu	Glu	Gln	Ala	Lys	Asp	Thr	Lys	Leu	Ser	Lys	Tyr					
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Val	Ser	Lys	Asp	Phe	Trp	Lys	Ser	Lys	Leu	Thr	Arg	Asp	Lys	Thr	Glu					
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Lys	Glu	Ala	Lys	Ser	Leu	Ser	Asp	Ala	Phe	Met	Gln	Gln	Lys	Thr	Ala					
345						350					355									
atc	atc	agc	aac	cgt	gaa	cga	atc	ccc	atg	agt	gtt	gct	tct	gcc	gcg	1219				
Ile	Ile	Ser	Asn	Arg	Glu	Arg	Ile	Pro	Met	Ser	Val	Ala	Ser	Ala	Ala					
360						365					370									
cag	acc	gtg	gtt	cgg	ttg	tct	gat	caa	gcg	tat	gag	gcg	atg	cgt	gaa	1267				
Gln	Thr	Val	Val	Arg	Leu	Ser	Asp	Gln	Ala	Tyr	Glu	Ala	Met	Arg	Glu					
375						380					385									
gta	gat	acg	gat	ggt	caa	gcg	ata	gtg	gat	gcg	aag	gat	gtc	tct	gca	1315				
Val	Asp	Thr	Asp	Gly	Gln	Ala	Ile	Val	Asp	Ala	Lys	Asp	Val	Ser	Ala					
390						395					400					405				
cag	gtg	gca	gaa	gat	att	gac	atg	gtg	gtc	aag	cag	ggt	gaa	gag	cat	1363				
Gln	Val	Ala	Glu	Asp	Ile	Asp	Met	Val	Val	Lys	Gln	Gly	Glu	Glu	His					
410						415					420									
ggc	ctg	aag	tcg	aag	gat	att	tat	ggc	gct	gcc	cgc	gat	att	gtg	ggt	1411				
Gly	Leu	Lys	Ser	Lys	Asp	Ile	Tyr	Gly	Ala	Ala	Arg	Asp	Ile	Val	Gly					
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cgt	cgc	atg	gag	cgc	gat	cca	ggc	tat	gct	gcc	cgg	ttt	aat	gag	acg	1459				
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gct	ttt	ggc	acc	gtg	cgc	ctg	ggt	gaa	caa	cga	cgt	ggc	atg	gtg	att	1507				
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455						460					465									
tca	aag	acc	ccg	aca	tgg	caa	ttc	cct	gat	ggt	gca	ggt	ttg	agt	aaa	1555				
Ser	Lys	Thr	Pro	Thr	Trp	Gln	Phe	Pro	Asp	Gly	Ala	Gly	Leu	Ser	Lys					
470						475					480					485				
aac	gcc	ggc	tgg	ttt	agt	gtt	cgt	gag	ccg	atg	ggt	aat	gcg	cag	aac	1603				
Asn	Ala	Gly	Trp	Phe	Ser	Val	Arg	Glu	Pro	Met	Gly	Asn	Ala	Gln	Asn					
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Phe	Ala	Asp	Asn	Leu	Ala	Ala	Thr	Leu	Ala	Thr	Glu	Met	Arg	Val	Ala					
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 Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala Ser Ala Lys Lys
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 Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala Ser Arg Val Arg
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 Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile Lys Val Leu Gln
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 Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln Val Lys Glu Val
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 Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val Met Gln Arg Asp His
 600 605 610

cca gcg att ctg gat aag ttt gtg cgc aaa cat ggg cag aca ttt ggg 1987
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 Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met Glu Lys Asp Thr
 630 635 640 645

agc agc gag tac act gat gct atg gtt cga cct caa gaa aat cgt gga 2083
 Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln Glu Asn Arg Gly
 650 655 660

tca ggt cga gaa ctg gca gct cgt cgt cgt gta caa gca gcg caa atc 2131
 Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln Ala Ala Gln Ile
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aat cag gca gca cag ctg gat atg aat gtt cat gat ttc cgt gaa tcg 2179
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 680 685 690

aat ctg cca gag gaa cga ccc gcg aat cct tat gaa gcg tat gtt cgt 2227
 Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu Ala Tyr Val Arg
 695 700 705

gag act gaa gcg aaa acc aat gat ccg cag tac ggt tat taatagaaaa 2276
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<213> Corynebacterium glutamicum

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 Asn Glu Gln Val Glu Glu Val Ser Val Glu Val Ser Ser Val Gln Ser
 50 55 60
 Leu Thr Gln Pro Lys Thr Leu Gly Gln Leu His Asp Pro Arg Lys Asn
 65 70 75 80
 Val Met Ser Ser Ser Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln
 85 90 95
 Pro Val Ala Tyr Gly Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val
 100 105 110
 Leu Pro Arg Arg Lys Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu
 115 120 125
 Val Ala Asp Gly Glu Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser
 130 135 140
 Asp Phe Asp Asp Leu Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp
 145 150 155 160
 Val Arg Ala Gly Gln Asp Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp
 165 170 175
 Glu Ala Gly Val Pro Arg Ser Gly Ala Gln Asp Val Ala Asp Asn Glu
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 Ala Asn Leu Ser Gly Val Asp Glu Gln Leu His Met Arg Glu Val His
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 Ala Gln Ser Phe Asp Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala
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 Ala Glu Lys Lys Tyr Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu
 225 230 235 240
 Ala Arg Asp Ala Lys Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala
 245 250 255
 Ala His Asp Asn Phe Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro
 260 265 270
 Leu Arg Lys Gly Val Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr
 275 280 285
 Ala Ala Val Met Trp Cys Met Ser Pro Arg Met Thr Gly Val Asn Val
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 Asp Met Lys Arg Lys Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr
 305 310 315 320

Lys Leu Ser Lys Tyr Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr
 325 330 335
 Arg Asp Lys Thr Glu Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met
 340 345 350
 Gln Gln Lys Thr Ala Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser
 355 360 365
 Val Ala Ser Ala Ala Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr
 370 375 380
 Glu Ala Met Arg Glu Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala
 385 390 395 400
 Lys Asp Val Ser Ala Gln Val Ala Glu Asp Ile Asp Met Val Val Lys
 405 410 415
 Gln Gly Glu Glu His Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala
 420 425 430
 Arg Asp Ile Val Gly Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala
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 Arg Phe Asn Glu Thr Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg
 450 455 460
 Arg Gly Met Val Ile Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly
 465 470 475 480
 Ala Gly Leu Ser Lys Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met
 485 490 495
 Gly Asn Ala Gln Asn Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr
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 Glu Met Arg Val Ala Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp
 515 520 525
 Val Val Ala Gly Phe Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu
 530 535 540
 Ala Ser Ala Lys Lys Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser
 545 550 555 560
 Ala Ser Arg Val Arg Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala
 565 570 575
 Ile Lys Val Leu Gln Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu
 580 585 590
 Gln Val Lys Glu Val Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val
 595 600 605
 Met Gln Arg Asp His Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His
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 Gly Gln Thr Phe Gly Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr
 625 630 635 640
 Met Glu Lys Asp Thr Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro

645	650	655
Gln Glu Asn Arg Gly Ser Gly Arg	Glu Leu Ala Ala Arg Arg Arg Val	
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Gln Ala Ala Gln Ile Asn Gln Ala Ala	Gln Leu Asp Met Asn Val His	
675	680	685
Asp Phe Arg Glu Ser Asn Leu Pro Glu Glu Arg	Pro Ala Asn Pro Tyr	
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Glu Ala Tyr Val Arg Glu Thr Glu Ala Lys Thr	Asn Asp Pro Gln Tyr	
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Gly Tyr		

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 Met Ser Ser Ser Asp
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 ttg gct tct att att ggt gta gag caa cag cct gtt gct tat ggt gag 163
 Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro Val Ala Tyr Gly Glu
 10 15 20
 tct gag gaa cca gaa aca ctg cgt gat gtg ttg cct cgg cga aag ctt 211
 Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu Pro Arg Arg Lys Leu
 25 30 35
 cac cca tct gag ata aca ccg agt tat gag gtt gct gat ggt gaa cag 259
 His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val Ala Asp Gly Glu Gln
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 cgc agc att ttt ggt gaa tca gct ccg tct gat ttt gat gac ctc agt 307
 Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp Phe Asp Asp Leu Ser
 55 60 65
 gat gtc gaa gaa ttt gat acc agt cat tgg gtg cgt gct gga caa gat 355
 Asp Val Glu Glu Phe Asp Thr Ser His Trp Val Arg Ala Gly Gln Asp
 70 75 80 85
 gat cgt agt gat gat gat cga ctc gct gat gag gct ggt gta ccg cct 403
 Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp Glu Ala Gly Val Pro Pro
 90 95 100
 agt ggc gca caa gat gta gct gat aat gag gct aat ctt tct ggt gtg 451
 Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala Asn Leu Ser Gly Val

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caa gag atg gca cag gct gcg atg gga cca ctg cgc aaa ggg gtc aac Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu Arg Lys Gly Val Asn 185 190 195			691
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tcc aaa gat ttt tgg aag tca aag ctg acg cgc gat aag acg gag aag Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg Asp Lys Thr Glu Lys 250 255 260			883
gaa gcg aag tcg ctc tct gat gcg ttc atg cag cag aaa aca gcg atc Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln Gln Lys Thr Ala Ile 265 270 275			931
atc agc aac cgt gaa cga atc ccc atg agt gtt gct tct gcc gcg cag Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val Ala Ser Ala Ala Gln 280 285 290			979
acc gtg gtt cgg ttg tct gat caa gcg tat gag gcg atg cgt gaa gta Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu Ala Met Arg Glu Val 295 300 305			1027
gat acg gat ggt caa gcg ata gtg gat gcg aag gat gtc tct gca cag Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys Asp Val Ser Ala Gln 310 315 320 325			1075
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Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg Gly Met Val Ile Ser	
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aag acc ccg aca tgg caa ttc cct gat ggt gca ggt ttg agt aaa aac	1315
Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala Gly Leu Ser Lys Asn	
390 395 400 405	
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Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly Asn Ala Gln Asn Phe	
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Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu Met Arg Val Ala Gly	
425 430 435	
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Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val Val Ala Gly Phe Met	
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Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala Ser Ala Lys Lys Leu	
455 460 465	
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Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala Ser Arg Val Arg Gln	
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Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile Lys Val Leu Gln Asp	
490 495 500	
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Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln Val Lys Glu Val Gln	
505 510 515	
gta tgg gcg atg gat cag gct gag aag gtg atg cag cgt gat cat cca	1699
Val Trp Ala Met Asp Gln Ala Glu Lys Val Met Gln Arg Asp His Pro	
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Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly Gln Thr Phe Gly Gln	
535 540 545	
gat gcg gac gct ttt gtt aaa tcc ata act atg gaa aaa gac acg agc	1795
Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met Glu Lys Asp Thr Ser	
550 555 560 565	
agc gag tac act gat gct atg gtt cga cct caa gaa aat cgt gga tca	1843
Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln Glu Asn Arg Gly Ser	
570 575 580	
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 600 605 610

ctg cca gag gaa cga ccc gcg aat cct tat gaa gcg tat gtt cgt gag 1987
 Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu Ala Tyr Val Arg Glu
 615 620 625

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 630 635 640

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Pro Arg Arg Lys Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val
 35 40 45

Ala Asp Gly Glu Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp
 50 55 60

Phe Asp Asp Leu Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp Val
 65 70 75 80

Arg Ala Gly Gln Asp Asp Arg Ser Asp Asp Arg Leu Ala Asp Glu
 85 90 95

Ala Gly Val Pro Pro Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala
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Asn Leu Ser Gly Val Asp Glu Gln Leu His Met Arg Glu Val His Ala
 115 120 125

Gln Ser Phe Asp Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala
 130 135 140

Glu Lys Lys Tyr Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala
 145 150 155 160

Arg Asp Ala Lys Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala
 165 170 175

His Asp Asn Phe Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu
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Arg Lys Gly Val Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala
 195 200 205

Ala Val Met Trp Cys Met Ser Pro Arg Met Thr Gly Val Asn Val Asp

210	215	220
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Asp Lys Thr Glu Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln 260 265 270		
Gln Lys Thr Ala Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val 275 280 285		
Ala Ser Ala Ala Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu 290 295 300		
Ala Met Arg Glu Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys 305 310 315 320		
Asp Val Ser Ala Gln Val Ala Glu Asp Ile Asp Met Val Val Lys Gln 325 330 335		
Gly Glu Glu His Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg 340 345 350		
Asp Ile Val Gly Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg 355 360 365		
Phe Asn Glu Thr Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg 370 375 380		
Gly Met Val Ile Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala 385 390 395 400		
Gly Leu Ser Lys Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly 405 410 415		
Asn Ala Gln Asn Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu 420 425 430		
Met Arg Val Ala Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val 435 440 445		
Val Ala Gly Phe Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala 450 455 460		
Ser Ala Lys Lys Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala 465 470 475 480		
Ser Arg Val Arg Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile 485 490 495		
Lys Val Leu Gln Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln 500 505 510		
Val Lys Glu Val Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val Met 515 520 525		
Gln Arg Asp His Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly 530 535 540		

Gln Thr Phe Gly Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met
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Glu Lys Asp Thr Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln
 565 570 575

Glu Asn Arg Gly Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln
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Ala Ala Gln Ile Asn Gln Ala Ala Gln Leu Asp Met Asn Val His Asp
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Tyr

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 Met Ala Gln Arg Lys
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 Leu Ala Ser Val Ile Gly Ala Ala Leu Ala Ala Ser Ala Val Leu Val
 10 15 20

gga tta atg aca ccc gca aca gca caa agt agt ggc agc tca tca aca 211
 Gly Leu Met Thr Pro Ala Thr Ala Gln Ser Ser Gly Ser Ser Ser Thr
 25 30 35

gac atc act cga gca ctc acc tca agt ggt ggt gtg gct gat agc cgt 259
 Asp Ile Thr Arg Ala Leu Thr Ser Ser Gly Gly Val Ala Asp Ser Arg
 40 45 50

gct cct gaa ggt ggc gca aag gtc gtt gtt ttc ggt gac tcc cac acc 307
 Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe Gly Asp Ser His Thr
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tct ggc acc aat gct cca ttc cgt acc gat gag cgt ggc tgc ctc aag 355
 Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp Glu Arg Gly Cys Leu Lys
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 Val Ala Asp Ser Arg Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe
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 Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp Glu
 65 70 75 80
 Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln Ser
 85 90 95
 Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser Gly
 100 105 110
 Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg His
 115 120 125
 Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe Val
 130 135 140
 Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu Leu
 145 150 155 160
 Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly Asp
 165 170 175
 Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr Ala
 180 185 190
 Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr
 195 200 205
 Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr Thr
 210 215 220
 Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro Leu
 225 230 235 240
 Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu Asp
 245 250 255
 Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val Asp
 260 265 270
 Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro Trp
 275 280 285

Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro Trp
 290 295 300

His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg Asp
 305 310 315 320

Arg Val Asn Ala

<210> 19

<211> 806

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(783)

<223> FRXA01422

<400> 19

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 Phe Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp
 1 5 10 15

gag cgt ggc tgc ctc aag ggt gca aac aac tgg gca gat cag ctg cag 96
 Glu Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln
 20 25 30

tct cag ctg gga ctt ggc gcg gga gac ctc att gat gtc tcc tgc tcc 144
 Ser Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser
 35 40 45

ggt gca tcg atc aac tct gat gga ttc cac ttc tct gat gaa gtc cgc 192
 Gly Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg
 50 55 60

cat gct gaa gct cgt ggc gca atc ggc cca aac acc acc gat att ttt 240
 His Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe
 65 70 75 80

gtt cag ttg ggc aag aat gat cag tgg ggc ctt tcc aat gtg aac ctt 288
 Val Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu
 85 90 95

ctg cag tct gtt cag acc tgc ttg act gat gtg ttc gct ggt tgt ggc 336
 Leu Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly
 100 105 110

gat gct gcg gtt gct gct ggc aag atg cag gat cca aat gca gtt act 384
 Asp Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr
 115 120 125

gct gaa aac tat gca gag cgc atg aag cca gtc att gac tac ttg aag 432
 Ala Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys
 130 135 140

tac tac gca cca aac gca gag atc acc ttg gtt ggt tac cag gaa tac 480
 Tyr Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr
 145 150 155 160

acc gct cgc agc gga agt cag gta tgt gtt cgc ctt ggt gga acc cca 528
 Thr Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro
 165 170 175

ctg gtg aaa aat gat gca cct gcg ctg gtt tcg ttc atg aac aag ttg 576
 Leu Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu
 180 185 190

gac atg gcg att gat ggt gct gct gga atc ctc ggc gtc agc cac gtt 624
 Asp Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val
 195 200 205

gat ctg cgt agc gcg act gaa ggg cac gac agc tgc tcc aac gat cct 672
 Asp Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro
 210 215 220

tgg gtc aac ggt gtc ttt gat gca cgt gca gaa atc gtc ggc ggt ccg 720
 Trp Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro
 225 230 235 240

tgg cac cca tct gtt aag gga gac tcg gtt act gca ggg atc ctg cga 768
 Trp His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg
 245 250 255

gat cga gta aac gcc taaagatgac gtcgaaaagc att 806
 Asp Arg Val Asn Ala
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<210> 20

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

Phe Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp
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Glu Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln
 20 25 30

Ser Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser
 35 40 45

Gly Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg
 50 55 60

His Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe
 65 70 75 80

Val Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu
 85 90 95

Leu Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly
 100 105 110

Asp Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr
 115 120 125

Ala Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys
 130 135 140

Tyr Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr
 145 150 155 160
 Thr Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro
 165 170 175
 Leu Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu
 180 185 190
 Asp Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val
 195 200 205
 Asp Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro
 210 215 220
 Trp Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro
 225 230 235 240
 Trp His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg
 245 250 255
 Asp Arg Val Asn Ala
 260

<210> 21
 <211> 771
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(748)
 <223> RXN01403

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 tagagtttgc ggccgatcgc ggtattcagg aattcagcca ttg gtg cgc ggt cgg 115
 Leu Val Arg Gly Arg
 1 5
 ggc tat ttc aat gcg gtg gat att tat gag acc tcc acg caa cct gac 163
 Gly Tyr Phe Asn Ala Val Asp Ile Tyr Glu Thr Ser Thr Gln Pro Asp
 10 15 20
 cag gaa ttt cct ttc gat ttt gac act ttt tca gcc gac ccc acg ccg 211
 Gln Glu Phe Pro Phe Asp Phe Asp Thr Phe Ser Ala Asp Pro Thr Pro
 25 30 35
 ttt caa ctc tct gcg gtg cgt gcc gat acc ggc gag acc gtt ttt tgg 259
 Phe Gln Leu Ser Ala Val Arg Ala Asp Thr Gly Glu Thr Val Phe Trp
 40 45 50
 ggc agg gaa gac acc ccg gat ttg agc gct ctg atg aag cgg gtt cgc 307
 Gly Arg Glu Asp Thr Pro Asp Leu Ser Ala Leu Met Lys Arg Val Arg
 55 60 65
 gcg tcg tcg acc atg cct ggt ttc atg ccg atc acc tac atc gac ggc 355
 Ala Ser Ser Thr Met Pro Gly Phe Met Pro Ile Thr Tyr Ile Asp Gly

70	75	80	85	
cat cca tat gtc gat ggc gcg gtc ggg gag acc ggc ggt ttg atg cta				403
His Pro Tyr Val Asp Gly Ala Val Gly Glu Thr Gly Gly Leu Met Leu				
	90	95	100	
cag ccg gcc atc gat gcg ggc ttc acc cgc ttt ttc gtt atc gcc tcc				451
Gln Pro Ala Ile Asp Ala Gly Phe Thr Arg Phe Phe Val Ile Ala Ser				
	105	110	115	
cgt ccg cgc gat tat tgg cgc aag gag atc ggg cgc ccg ggt ttc atc				499
Arg Pro Arg Asp Tyr Trp Arg Lys Glu Ile Gly Arg Pro Gly Phe Ile				
	120	125	130	
aaa gct gct tta cga cgt ttc ccc aca atc gcc gac ctc acc atc gcg				547
Lys Ala Ala Leu Arg Arg Phe Pro Thr Ile Ala Asp Leu Thr Ile Ala				
	135	140	145	
cgt cct gca ctg tat aac tcg gta aag caa cag atc ctc gac cta gag				595
Arg Pro Ala Leu Tyr Asn Ser Val Lys Gln Gln Ile Leu Asp Leu Glu				
	150	155	160	165
aaa caa ggc agc gcc tat gtg ttc ttt gcg gac aac atg aac atc cag				643
Lys Gln Gly Ser Ala Tyr Val Phe Phe Ala Asp Asn Met Asn Ile Gln				
	170	175	180	
aac acg gaa atc aat ctg aag aaa ctc cgt gca tct ttc gat gca ggc				691
Asn Thr Glu Ile Asn Leu Lys Lys Leu Arg Ala Ser Phe Asp Ala Gly				
	185	190	195	
atg cag cag acc cgc aaa gat tgg ccg gag atc atg agc ttc ctg aac				739
Met Gln Gln Thr Arg Lys Asp Trp Pro Glu Ile Met Ser Phe Leu Asn				
	200	205	210	
caa acc aga taatgaaggt ttttagtcca act				771
Gln Thr Arg				
	215			

<210> 22

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

Leu	Val	Arg	Gly	Arg	Gly	Tyr	Phe	Asn	Ala	Val	Asp	Ile	Tyr	Glu	Thr
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Ser	Thr	Gln	Pro	Asp	Gln	Glu	Phe	Pro	Phe	Asp	Phe	Asp	Thr	Phe	Ser
		20						25					30		

Ala	Asp	Pro	Thr	Pro	Phe	Gln	Leu	Ser	Ala	Val	Arg	Ala	Asp	Thr	Gly
		35					40					45			

Glu	Thr	Val	Phe	Trp	Gly	Arg	Glu	Asp	Thr	Pro	Asp	Leu	Ser	Ala	Leu
	50					55					60				

Met	Lys	Arg	Val	Arg	Ala	Ser	Ser	Thr	Met	Pro	Gly	Phe	Met	Pro	Ile
65					70					75					80

Thr	Tyr	Ile	Asp	Gly	His	Pro	Tyr	Val	Asp	Gly	Ala	Val	Gly	Glu	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85										90					95				
Gly	Gly	Leu	Met	Leu	Gln	Pro	Ala	Ile	Asp	Ala	Gly	Phe	Thr	Arg	Phe				
			100					105					110						
Phe	Val	Ile	Ala	Ser	Arg	Pro	Arg	Asp	Tyr	Trp	Arg	Lys	Glu	Ile	Gly				
		115					120					125							
Arg	Pro	Gly	Phe	Ile	Lys	Ala	Ala	Leu	Arg	Arg	Phe	Pro	Thr	Ile	Ala				
	130					135					140								
Asp	Leu	Thr	Ile	Ala	Arg	Pro	Ala	Leu	Tyr	Asn	Ser	Val	Lys	Gln	Gln				
145					150					155					160				
Ile	Leu	Asp	Leu	Glu	Lys	Gln	Gly	Ser	Ala	Tyr	Val	Phe	Phe	Ala	Asp				
			165					170						175					
Asn	Met	Asn	Ile	Gln	Asn	Thr	Glu	Ile	Asn	Leu	Lys	Lys	Leu	Arg	Ala				
		180						185					190						
Ser	Phe	Asp	Ala	Gly	Met	Gln	Gln	Thr	Arg	Lys	Asp	Trp	Pro	Glu	Ile				
	195					200						205							
Met	Ser	Phe	Leu	Asn	Gln	Thr	Arg												
	210					215													

<210> 23

<211> 437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(414)

<223> FRXA01403

<400> 23

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Pro	Ile	Thr	Tyr	Ile	Asp	Gly	His	Pro	Tyr	Val	Asp	Gly	Ala	Val	Gly	
1				5				10						15		
gag	acc	ggc	ggt	ttg	atg	cta	cag	ccg	gcc	atc	gat	gcg	ggc	ttc	acc	96
Glu	Thr	Gly	Gly	Leu	Met	Leu	Gln	Pro	Ala	Ile	Asp	Ala	Gly	Phe	Thr	
		20						25				30				
cgc	ttt	ttc	gtt	atc	gcc	tcc	cgt	ccg	cgc	gat	tat	tgg	cgc	aag	gag	144
Arg	Phe	Phe	Val	Ile	Ala	Ser	Arg	Pro	Arg	Asp	Tyr	Trp	Arg	Lys	Glu	
		35					40					45				
atc	ggg	cgc	ccg	ggt	ttc	atc	aaa	gct	gct	tta	cga	cgt	ttc	ccc	aca	192
Ile	Gly	Arg	Pro	Gly	Phe	Ile	Lys	Ala	Ala	Leu	Arg	Arg	Phe	Pro	Thr	
	50					55				60						
atc	gcc	gac	ctc	acc	atc	gcg	cgt	cct	gca	ctg	tat	aac	tcg	gta	aag	240
Ile	Ala	Asp	Leu	Thr	Ile	Ala	Arg	Pro	Ala	Leu	Tyr	Asn	Ser	Val	Lys	
	65				70					75				80		
caa	cag	atc	ctc	gac	cta	gag	aaa	caa	ggc	agc	gcc	tat	gtg	ttc	ttt	288
Gln	Gln	Ile	Leu	Asp	Leu	Glu	Lys	Gln	Gly	Ser	Ala	Tyr	Val	Phe	Phe	
			85					90						95		

gcg gac aac atg aac atc cag aac acg gaa atc aat ctg aag aaa ctc 336
Ala Asp Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu
100 105 110

cgt gca tct ttc gat gca ggc atg cag cag acc cgc aaa gat tgg ccg 384
Arg Ala Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro
115 120 125

gag atc atg agc ttc ctg aac caa acc aga taatgaaggt ttttagtcca 434
Glu Ile Met Ser Phe Leu Asn Gln Thr Arg
130 135

act 437

<210> 24
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 24
Pro Ile Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly
1 5 10 15

Glu Thr Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr
20 25 30

Arg Phe Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu
35 40 45

Ile Gly Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr
50 55 60

Ile Ala Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys
65 70 75 80

Gln Gln Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe
85 90 95

Ala Asp Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu
100 105 110

Arg Ala Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro
115 120 125

Glu Ile Met Ser Phe Leu Asn Gln Thr Arg
130 135

<210> 25
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101) .. (466)
<223> RXN01326

<400> 25

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gcaaacatct ttttaacgctt ttggcccgtta ttatggtggc atg gct ttc ccc gtg 115
Met Ala Phe Pro Val
1 5

aca gaa gac aaa atc ctg gca gct gag gaa acc ctt ggc agg cgc ctc 163
Thr Glu Asp Lys Ile Leu Ala Ala Glu Glu Thr Leu Gly Arg Arg Leu
10 15 20

ccc gaa act ttg cgc gaa cga cta ctt caa aac aat ggt ggc gaa gtc 211
Pro Glu Thr Leu Arg Glu Arg Leu Leu Gln Asn Asn Gly Gly Glu Val
25 30 35

atc gac aat gaa aac aac gac tgg att ctc cat cca gtt cgt gat gac 259
Ile Asp Asn Glu Asn Asn Asp Trp Ile Leu His Pro Val Arg Asp Asp
40 45 50

agc gac cga aaa agg ctt gtc cga act gcc aac gac atc atc cgc gag 307
Ser Asp Arg Lys Arg Leu Val Arg Thr Ala Asn Asp Ile Ile Arg Glu
55 60 65

acc gaa tct gca cgt gaa tgg gac aat ttc ccc gaa aat gcg atc gca 355
Thr Glu Ser Ala Arg Glu Trp Asp Asn Phe Pro Glu Asn Ala Ile Ala
70 75 80 85

att gca aat gac gga acg ggc gac tta ata att ctg ctt ccc gac gat 403
Ile Ala Asn Asp Gly Thr Gly Asp Leu Ile Ile Leu Leu Pro Asp Asp
90 95 100

gat gct ttc tac atc tgg tcg cac gaa gat gaa ccc ctg atc gaa act 451
Asp Ala Phe Tyr Ile Trp Ser His Glu Asp Glu Pro Leu Ile Glu Thr
105 110 115

gaa ctt gag gat gcc taaaacagct ggacagaatt cga 489
Glu Leu Glu Asp Ala
120

<210> 26

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

Met Ala Phe Pro Val Thr Glu Asp Lys Ile Leu Ala Ala Glu Glu Thr
1 5 10 15

Leu Gly Arg Arg Leu Pro Glu Thr Leu Arg Glu Arg Leu Leu Gln Asn
20 25 30

Asn Gly Gly Glu Val Ile Asp Asn Glu Asn Asn Asp Trp Ile Leu His
35 40 45

Pro Val Arg Asp Asp Ser Asp Arg Lys Arg Leu Val Arg Thr Ala Asn
50 55 60

Asp Ile Ile Arg Glu Thr Glu Ser Ala Arg Glu Trp Asp Asn Phe Pro
65 70 75 80

Glu Asn Ala Ile Ala Ile Ala Asn Asp Gly Thr Gly Asp Leu Ile Ile

85	90	95	
Leu Leu Pro Asp Asp Asp Ala Phe Tyr Ile Trp Ser His Glu Asp Glu			
100	105	110	
Pro Leu Ile Glu Thr Glu Leu Glu Asp Ala			
115	120		
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<211> 361			
<212> DNA			
<213> Corynebacterium glutamicum			
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<222> (45)..(338)			
<223> FRXA01326			
<400> 27			
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		Leu Arg Glu Arg	
		1	
cta ctt caa aac aat ggt ggc gaa gtc atc gac aat gaa aac aac gac			104
Leu Leu Gln Asn Asn Gly Gly Glu Val Ile Asp Asn Glu Asn Asn Asp			
5	10	15	20
tgg att ctc cat cca gtt cgt gat gac agc gac cga aaa agg ctt gtc			152
Trp Ile Leu His Pro Val Arg Asp Asp Ser Asp Arg Lys Arg Leu Val			
25	30	35	
cga act gcc aac gac atc atc cgc gag acc gaa tct gca cgt gaa tgg			200
Arg Thr Ala Asn Asp Ile Ile Arg Glu Thr Glu Ser Ala Arg Glu Trp			
40	45	50	
gac aat ttc ccc gaa aat gcg atc gca att gca aat gac gga acg ggc			248
Asp Asn Phe Pro Glu Asn Ala Ile Ala Ile Ala Asn Asp Gly Thr Gly			
55	60	65	
gac tta ata att ctg ctt ccc gac gat gat gct ttc tac atc tgg tcg			296
Asp Leu Ile Ile Leu Leu Pro Asp Asp Asp Ala Phe Tyr Ile Trp Ser			
70	75	80	
cac gaa gat gaa ccc ctg atc gaa act gaa ctt gag gat gcc			338
His Glu Asp Glu Pro Leu Ile Glu Thr Glu Leu Glu Asp Ala			
85	90	95	
taaaacagct ggacagaatt cga			361

<210> 28
 <211> 98
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 28
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 1 5 10 15
 Glu Asn Asn Asp Trp Ile Leu His Pro Val Arg Asp Asp Ser Asp Arg

	20		25		30
Lys Arg Leu Val Arg Thr Ala Asn Asp Ile Ile Arg Glu Thr Glu Ser					
	35		40		45
Ala Arg Glu Trp Asp Asn Phe Pro Glu Asn Ala Ile Ala Ile Ala Asn					
	50		55		60
Asp Gly Thr Gly Asp Leu Ile Ile Leu Leu Pro Asp Asp Asp Ala Phe					
	65		70		75
Tyr Ile Trp Ser His Glu Asp Glu Pro Leu Ile Glu Thr Glu Leu Glu					
		85		90	95

Asp Ala

<210> 29
 <211> 648
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(625)
 <223> RXN01301

<400> 29
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cgcggtgcggg acgtgttcat ttctgtatag gaaaactacc ttg atc gtt gat acc 115
 Leu Ile Val Asp Thr
 1 5

cag ttt gag aag atc cct gct cac gac gtc gtg ggc atc cgg gta atc 163
 Gln Phe Glu Lys Ile Pro Ala His Asp Val Val Gly Ile Arg Val Ile
 10 15 20

ctt tcc tct gag gat ctc cct gag ctc ttt aaa cgc ggc tac gcg gaa 211
 Leu Ser Ser Glu Asp Leu Pro Glu Leu Phe Lys Arg Gly Tyr Ala Glu
 25 30 35

gta aag aaa ttc ctc cgc cta gaa ggc atc gaa cct aaa ggt cct gcc 259
 Val Lys Lys Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala
 40 45 50

cgc gcc tac tac ttt ggc gat gtc tct gac acc gta gac atc ctg att 307
 Arg Ala Tyr Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile
 55 60 65

ggt ttc ccc gtc agc ccc gcg caa gca gaa tcc ctg cgc cgc ggc gca 355
 Gly Phe Pro Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala
 70 75 80 85

ttg agc caa tcc ggt ggc gac atc gat gac gtt gtc ctc cac cac ttc 403
 Leu Ser Gln Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe
 90 95 100

cgc gac atg aaa acc atg cac agc cgc cac tcc ggc ccc ttc gat gga 451
 Arg Asp Met Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly

105	110	115	
gtc gag cgc gtc tgg gac gaa atc ctc gat gaa gtc gaa gac ctc gga			499
Val Glu Arg Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly			
120	125	130	
tgc act ctg cca tcc agc agc atc ggt tgg gaa gaa tac atc gag ggc			547
Cys Thr Leu Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly			
135	140	145	
cca gcc acc gct gat acc tgc gac caa ctg gcc tct gaa gtt tat gtt			595
Pro Ala Thr Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val			
150	155	160	165
cag gtg tgc caa gca ccg gtg aag tct gca taaagattca cccggaattt			645
Gln Val Cys Gln Ala Pro Val Lys Ser Ala			
170	175		
ccc			648
<210> 30			
<211> 175			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 30			
Leu Ile Val Asp Thr Gln Phe Glu Lys Ile Pro Ala His Asp Val Val			
1	5	10	15
Gly Ile Arg Val Ile Leu Ser Ser Glu Asp Leu Pro Glu Leu Phe Lys			
20	25	30	
Arg Gly Tyr Ala Glu Val Lys Lys Phe Leu Arg Leu Glu Gly Ile Glu			
35	40	45	
Pro Lys Gly Pro Ala Arg Ala Tyr Tyr Phe Gly Asp Val Ser Asp Thr			
50	55	60	
Val Asp Ile Leu Ile Gly Phe Pro Val Ser Pro Ala Gln Ala Glu Ser			
65	70	75	80
Leu Arg Arg Gly Ala Leu Ser Gln Ser Gly Gly Asp Ile Asp Asp Val			
85	90	95	
Val Leu His His Phe Arg Asp Met Lys Thr Met His Ser Arg His Ser			
100	105	110	
Gly Pro Phe Asp Gly Val Glu Arg Val Trp Asp Glu Ile Leu Asp Glu			
115	120	125	
Val Glu Asp Leu Gly Cys Thr Leu Pro Ser Ser Ser Ile Gly Trp Glu			
130	135	140	
Glu Tyr Ile Glu Gly Pro Ala Thr Ala Asp Thr Cys Asp Gln Leu Ala			
145	150	155	160
Ser Glu Val Tyr Val Gln Val Cys Gln Ala Pro Val Lys Ser Ala			
165	170	175	

<210> 31
 <211> 428
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(405)
 <223> FRXA01301

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 Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala Arg Ala Tyr
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 tac ttt ggc gat gtc tct gac acc gta gac atc ctg att ggt ttc ccc 96
 Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile Gly Phe Pro
 20 25 30
 gtc agc ccc gcg caa gca gaa tcc ctg cgc cgc ggc gca ttg agc caa 144
 Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala Leu Ser Gln
 35 40 45
 tcc ggt ggc gac atc gat gac gtt gtc ctc cac cac ttc cgc gac atg 192
 Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe Arg Asp Met
 50 55 60
 aaa acc atg cac agc cgc cac tcc ggc ccc ttc gat gga gtc gag cgc 240
 Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly Val Glu Arg
 65 70 75 80
 gtc tgg gac gaa atc ctc gat gaa gtc gaa gac ctc gga tgc act ctg 288
 Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly Cys Thr Leu
 85 90 95
 cca tcc agc agc atc ggt tgg gaa gaa tac atc gag ggc cca gcc acc 336
 Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly Pro Ala Thr
 100 105 110
 gct gat acc tgc gac caa ctg gcc tct gaa gtt tat gtt cag gtg tgc 384
 Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val Gln Val Cys
 115 120 125
 caa gca ccg gtg aag tct gca taaagattca cccggaattt ccc 428
 Gln Ala Pro Val Lys Ser Ala
 130 135

<210> 32
 <211> 135
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 32
 Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala Arg Ala Tyr
 1 5 10 15
 Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile Gly Phe Pro
 20 25 30
 Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala Leu Ser Gln

35	40	45
Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe Arg Asp Met		
50	55	60
Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly Val Glu Arg		
65	70	75
Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly Cys Thr Leu		
85	90	95
Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly Pro Ala Thr		
100	105	110
Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val Gln Val Cys		
115	120	125
Gln Ala Pro Val Lys Ser Ala		
130	135	

<210> 33
 <211> 567
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(544)
 <223> RXN01276

<400> 33
 tgcgtaaaac cctcatcacc atgctcgcgga ccaccgcgat cgccttttcc gccatctcac 60
 cagtgcaggc gcaaaccgtg gacacagaca ctgacgcctc gtg tca tct gag ctg 115
 Val Ser Ser Glu Leu
 1 5
 agc agc ggc aca agc tca gga agt tca gag gat tcc gaa gat tct gac 163
 Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp Ser Glu Asp Ser Asp
 10 15 20
 atc tcc aac cgg gac atc atc ttc ggc atc gca gct atc gct gca gtc 211
 Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala Ala Ile Ala Ala Val
 25 30 35
 ggc gga ctt atc gca agt ggt gtg cac tgg gca gta caa cag cgc atg 259
 Gly Gly Leu Ile Ala Ser Gly Val His Trp Ala Val Gln Gln Arg Met
 40 45 50
 atc cca aat ccc ctc cca gga atc att cca aat ccc cct gca ctg gca 307
 Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn Pro Pro Ala Leu Ala
 55 60 65
 cct cag gcg cct gcc cca gca cct gct ccc gct cct gcc cct cag gca 355
 Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Gln Ala
 70 75 80 85
 gtc gcg ccc cag gtt gtc gct ccc cag gtt gtc gcg cct gct cca gcc 403
 Val Ala Pro Gln Val Val Ala Pro Gln Val Val Ala Pro Ala Pro Ala
 90 95 100

cca gta cag acc aac cgc acc tac aaa aac tgc acc gaa gta tgg aac 451
 Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys Thr Glu Val Trp Asn
 105 110 115

gtc ctg gga agg tcc atc cgc caa agc gat cca ggc tac ggc aca cac 499
 Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro Gly Tyr Gly Thr His
 120 125 130

ctc gac cgc gac cgc gac ggc atc ggc tgc gaa tca cgc cct agg 544
 Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu Ser Arg Pro Arg
 135 140 145

tagtttgggt tttggggatc ttc 567

<210> 34
 <211> 148
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 34
 Val Ser Ser Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp
 1 5 10 15

Ser Glu Asp Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala
 20 25 30

Ala Ile Ala Ala Val Gly Gly Leu Ile Ala Ser Gly Val His Trp Ala
 35 40 45

Val Gln Gln Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn
 50 55 60

Pro Pro Ala Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala
 65 70 75 80

Pro Ala Pro Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln Val Val
 85 90 95

Ala Pro Ala Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys
 100 105 110

Thr Glu Val Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro
 115 120 125

Gly Tyr Gly Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu
 130 135 140

Ser Arg Pro Arg
 145

<210> 35
 <211> 669
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(646)

<223> FRXA01276

<400> 35

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aatagtaata attttgacag ctogtgcaaa gatgattggc atg cgt aaa acc ctc 115
                               Met Arg Lys Thr Leu
                               1                               5

atc acc atg ctc gcg acc acc gcg atc gcc ttt tcc gcc atc tca cca 163
Ile Thr Met Leu Ala Thr Thr Ala Ile Ala Phe Ser Ala Ile Ser Pro
                               10                               15                               20

gtg cag gcg caa acc gtg gac aca gac act gac gcc tcc gtg tca tct 211
Val Gln Ala Gln Thr Val Asp Thr Asp Thr Asp Ala Ser Val Ser Ser
                               25                               30                               35

gag ctg agc agc ggc aca agc tca gga agt tca gag gat tcc gaa gat 259
Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp Ser Glu Asp
                               40                               45                               50

tct gac atc tcc aac cgg gac atc atc ttc ggc atc gca gct atc gct 307
Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala Ala Ile Ala
                               55                               60                               65

gca gtc ggc gga ctt atc gca ggt ggt gtg cac tgg gca gta caa cag 355
Ala Val Gly Gly Leu Ile Ala Gly Gly Val His Trp Ala Val Gln Gln
                               70                               75                               80                               85

cgc atg atc cca aat ccc ctc cca gga atc att cca aat ccc cct gca 403
Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn Pro Pro Ala
                               90                               95                               100

ctg gca cct cag gcg cct gcc cca gca cct gct ccc gct cct gcc cct 451
Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
                               105                               110                               115

cag gca gtc gcg ccc cag gtt gtc gct ccc cag gtt gtc gcg cct gct 499
Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln Val Val Ala Pro Ala
                               120                               125                               130

cca gcc cca gta cag acc aac cgc acc tac aaa aac tgc acc gaa gta 547
Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys Thr Glu Val
                               135                               140                               145

tgg aac gtc ctg gga agg tcc atc cgc caa agc gat cca ggc tac ggc 595
Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro Gly Tyr Gly
                               150                               155                               160                               165

aca cac ctc gac cgc gac cgc gac ggc atc ggc tgc gaa tca cgc cct 643
Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu Ser Arg Pro
                               170                               175                               180

agg tagtttgggt tttggggatc ttc 669
Arg

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<210> 36

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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Met Arg Lys Thr Leu Ile Thr Met Leu Ala Thr Thr Ala Ile Ala Phe
 1           5           10           15

Ser Ala Ile Ser Pro Val Gln Ala Gln Thr Val Asp Thr Asp Thr Asp
          20           25           30

Ala Ser Val Ser Ser Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser
          35           40           45

Glu Asp Ser Glu Asp Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly
 50           55           60

Ile Ala Ala Ile Ala Ala Val Gly Gly Leu Ile Ala Gly Gly Val His
 65           70           75           80

Trp Ala Val Gln Gln Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile
          85           90           95

Pro Asn Pro Pro Ala Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala
100           105           110

Pro Ala Pro Ala Pro Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln
115           120           125

Val Val Ala Pro Ala Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys
130           135           140

Asn Cys Thr Glu Val Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser
145           150           155           160

Asp Pro Gly Tyr Gly Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly
          165           170           175

Cys Glu Ser Arg Pro Arg
          180

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<210> 37

<211> 366

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(343)

<223> RXN01231

<400> 37

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ccaggcatcg agcacttcac ccccctatga cgccttgcaa atg ctg ggc tac acc 115
                                     Met Leu Gly Tyr Thr
                                     1           5

ttc gtc atc ttt atc ctg gcg ccg ttt ctc atc ctc acc gga ata gcg 163
Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile Leu Thr Gly Ile Ala
          10           15           20

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atg gcc ccg gcc atc cgg tcc cgc ttc ccg tgg tac gtc aaa ctc ttc 211
Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp Tyr Val Lys Leu Phe
                25                      30                      35

ggc ggc cac cag ggt gca cgt tcc ctg cac ttc atc gcc atg gtg ttg 259
Gly Gly His Gln Gly Ala Arg Ser Leu His Phe Ile Ala Met Val Leu
                40                      45                      50

atg acg ggc ttt gtc atc atg cac gtc ggc ctg gtt ttt tgg tcc atg 307
Met Thr Gly Phe Val Ile Met His Val Gly Leu Val Phe Trp Ser Met
                55                      60                      65

gcg act aca aca tgg tcc aca tgg tct tcg gcg ata tgaacactga 353
Ala Thr Thr Thr Trp Ser Thr Trp Ser Ser Ala Ile
                70                      75                      80

ccgtgcggcg cag 366

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<210> 38
<211> 81
<212> PRT
<213> Corynebacterium glutamicum

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<400> 38
Met Leu Gly Tyr Thr Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile
 1                5                10                15

Leu Thr Gly Ile Ala Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp
                20                25                30

Tyr Val Lys Leu Phe Gly Gly His Gln Gly Ala Arg Ser Leu His Phe
                35                40                45

Ile Ala Met Val Leu Met Thr Gly Phe Val Ile Met His Val Gly Leu
                50                55                60

Val Phe Trp Ser Met Ala Thr Thr Thr Trp Ser Thr Trp Ser Ser Ala
 65                70                75                80

Ile

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<210> 39
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(604)
<223> FRXA01231

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<221> misc_feature
<222> 84, 399, 506, 541, 542, 544
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<222> 62
<223> Xaa = Cys, Gly, Arg, or Ser

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<223> Xaa = Ser, Arg, Asn, or His

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<223> Xaa = Ser

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<221> VARIANT

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<223> Xaa = Ile, Leu, or Phe

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<223> Xaa = Gly

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<221> VARIANT

<222> 136

<223> Xaa = Ser, Pro, Thr, or Ala

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<221> VARIANT

<222> 137

<223> Xaa = Gln or His

<220>

<221> VARIANT

<222> 147

<223> Xaa = Asp or Glu

<220>

<221> VARIANT

<222> 148

<223> Xaa = Tyr, His, Gln, Asn, Lys, Asp, Glu, or

<223> STOP codon

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cctgggacgt cttccccgag gcgtgggang acattgaagg tttacctggg ctttcgtgcc 60

ccaggcatcg agcacttcac ccccctatga cgccttgcaa atg ctg ggc tac acc 115
Met Leu Gly Tyr Thr
1 5

ttc gtc atc ttt atc ctg gcg ccg ttt ctc atc ctc acc gga ata gcg 163
Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile Leu Thr Gly Ile Ala
10 15 20

atg gcc ccg gcc atc cgg tcc cgc ttc ccg tgg tac gtc aaa ctc ttc 211
Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp Tyr Val Lys Leu Phe
25 30 35

ggc ggc cac cag ggt gca cgt tcc ctg cac ttc atc gcc atg gtg ttg 259
Gly Gly His Gln Gly Ala Arg Ser Leu His Phe Ile Ala Met Val Leu
40 45 50

atg acg ggc ttt gtc atc atg cac ngc cgg cct ggt ttt ttg gtc cat 307
 Met Thr Gly Phe Val Ile Met His Xaa Arg Pro Gly Phe Leu Val His
 55 60 65
 ggc gac tac aac atg gtc cac atg gtc ttc ggc gat atg aac act gac 355
 Gly Asp Tyr Asn Met Val His Met Val Phe Gly Asp Met Asn Thr Asp
 70 75 80 85
 cgt gcg gcg cag gcc tac atc atc gtg atc acc acc atc gtc ant ggt 403
 Arg Ala Ala Gln Ala Tyr Ile Ile Val Ile Thr Thr Ile Val Xaa Gly
 90 95 100
 ggt gtt ktt ctg rat cgk gct cag tat att kgt mrc tgg ctk acc grg 451
 Gly Val Xaa Leu Xaa Xaa Ala Gln Tyr Ile Xaa Xaa Trp Xaa Thr Xaa
 105 110 115
 mcc gcg ccm wgc ggt tya ccg cca gcw tca tck gag wtm ggw cgc aaa 499
 Xaa Ala Xaa Xaa Gly Xaa Pro Pro Xaa Ser Xaa Glu Xaa Xaa Arg Lys
 120 125 130
 atc ttt nct caw ccg gct gcg tcc ccg gat gag cag gca gan nan cac 547
 Ile Phe Xaa Xaa Pro Ala Ala Ser Pro Asp Glu Gln Ala Xaa Xaa His
 135 140 145
 cta cac gga caa gga cat ctc gca gtt cca ctg gac caa tgg cct gcc 595
 Leu His Gly Gln Gly His Leu Ala Val Pro Leu Asp Gln Trp Pro Ala
 150 155 160 165
 gcc gac cga tgatgaatcc cccgagtggg tgc 627
 Ala Asp Arg

<210> 40
 <211> 168
 <212> PRT
 <213> Corynebacterium glutamicum

<220>
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 <222> 62
 <223> Xaa = Cys, Gly, Arg, or Ser

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 <223> Xaa = Ile, Thr, Asn, or Ser

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<223> Xaa = Ser

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<223> Xaa = Ile, Leu, or Phe

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<223> Xaa = Gly

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<223> Xaa = Ser, Pro, Thr, or Ala

<220>

<221> VARIANT

<222> 137

<223> Xaa = Gln or His

<220>

<221> VARIANT

<222> 147

<223> Xaa = Asp or Glu

<220>

<221> VARIANT

<222> 148

<223> Xaa = Tyr, His, Gln, Asn, Lys, Asp, Glu, or

<223> STOP codon

<400> 40

Met	Leu	Gly	Tyr	Thr	Phe	Val	Ile	Phe	Ile	Leu	Ala	Pro	Phe	Leu	Ile
1				5					10					15	

Leu	Thr	Gly	Ile	Ala	Met	Ala	Pro	Ala	Ile	Arg	Ser	Arg	Phe	Pro	Trp
			20					25					30		

Tyr	Val	Lys	Leu	Phe	Gly	Gly	His	Gln	Gly	Ala	Arg	Ser	Leu	His	Phe
		35					40					45			

Ile	Ala	Met	Val	Leu	Met	Thr	Gly	Phe	Val	Ile	Met	His	Xaa	Arg	Pro
	50					55					60				

Gly	Phe	Leu	Val	His	Gly	Asp	Tyr	Asn	Met	Val	His	Met	Val	Phe	Gly
65					70					75					80

Asp	Met	Asn	Thr	Asp	Arg	Ala	Ala	Gln	Ala	Tyr	Ile	Ile	Val	Ile	Thr
				85					90					95	

Thr	Ile	Val	Xaa	Gly	Gly	Val	Xaa	Leu	Xaa	Xaa	Ala	Gln	Tyr	Ile	Xaa
			100					105					110		

Xaa	Trp	Xaa	Thr	Xaa	Xaa	Ala	Xaa	Xaa	Gly	Xaa	Pro	Pro	Xaa	Ser	Xaa
		115					120					125			

Glu	Xaa	Xaa	Arg	Lys	Ile	Phe	Xaa	Xaa	Pro	Ala	Ala	Ser	Pro	Asp	Glu
	130					135					140				

Gln	Ala	Xaa	Xaa	His	Leu	His	Gly	Gln	Gly	His	Leu	Ala	Val	Pro	Leu
145					150					155					160

Asp	Gln	Trp	Pro	Ala	Ala	Asp	Arg
						165	

<210> 41

<211> 954

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(931)

<223> RXN01210

<400> 41

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ttcgtgcaa aaccgcccac cttggaatcc gtattcatgg acatcgccctc actcgagaac 60

acctcgctgc aaaccgccta gaatcttttaa ggagaccaca atg acc acg tca cac 115
                                         Met Thr Thr Ser His
                                         1                               5

acc gcc cgc ggg ctg caa cat gca acc ccg gag cgc cgc aag act tca 163
Thr Ala Arg Gly Leu Gln His Ala Thr Pro Glu Arg Arg Lys Thr Ser
                               10                               15                               20

ttt ttc aaa acc tct ctg ttt aag gcc gaa tgg ctc cag ttc cgc aga 211
Phe Phe Lys Thr Ser Leu Phe Lys Ala Glu Trp Leu Gln Phe Arg Arg
                               25                               30                               35

aat aaa acc ctg ttg ttc atg gcc acc gta ttc cca gtc gga atc cct 259
Asn Lys Thr Leu Leu Phe Met Ala Thr Val Phe Pro Val Gly Ile Pro
                               40                               45                               50

ttg ttg ctc ttt ctc atc gga aat ggt ggg gca gca gag tcc gcg aac 307
Leu Leu Leu Phe Leu Ile Gly Asn Gly Gly Ala Ala Glu Ser Ala Asn
                               55                               60                               65

tcc ttc gac tac ttc gtc atg tac acc ctg cta ttt gtg cag ttc tac 355
Ser Phe Asp Tyr Phe Val Met Tyr Thr Leu Leu Phe Val Gln Phe Tyr
                               70                               75                               80                               85

acg gtg ctg tcc atg gca acc acc cgc cgt gat gaa cgt gtg ctg aaa 403
Thr Val Leu Ser Met Ala Thr Thr Arg Arg Asp Glu Arg Val Leu Lys
                               90                               95                               100

agg ctg cgc acg gga gaa gcc cgc gac atc gat atc atc ggt gcc atc 451
Arg Leu Arg Thr Gly Glu Ala Arg Asp Ile Asp Ile Ile Gly Ala Ile
                               105                               110                               115

tgt ttc ccc ggc gcg ctc ctc aca ctg atc ttc acc gtg gtg atc att 499
Cys Phe Pro Gly Ala Leu Leu Thr Leu Ile Phe Thr Val Val Ile Ile
                               120                               125                               130

cca ttg ctc atg gtt ttg gga gct ccc gcg ccc atc aac ctt gtg ccc 547
Pro Leu Leu Met Val Leu Gly Ala Pro Ala Pro Ile Asn Leu Val Pro
                               135                               140                               145

att gtg ttt gcc gta ctg atc gga cta ctt ctt tgt agt gct ctt gcc 595
Ile Val Phe Ala Val Leu Ile Gly Leu Leu Leu Cys Ser Ala Leu Ala
                               150                               155                               160                               165

ttg atg acc agc ggt ttc acc cga aac gcc gaa gcc gca cag atg acc 643
Leu Met Thr Ser Gly Phe Thr Arg Asn Ala Glu Ala Ala Gln Met Thr
                               170                               175                               180

tcc atg ccc gtg ttc atg ctt gcg atg ggt gga ctt gga tca atc cgc 691
Ser Met Pro Val Phe Met Leu Ala Met Gly Gly Leu Gly Ser Ile Arg
                               185                               190                               195

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ttc gta ttc ggc gac agc att gtg gct gat atc ttg gcc tac acc cca 739
 Phe Val Phe Gly Asp Ser Ile Val Ala Asp Ile Leu Ala Tyr Thr Pro
 200 205 210
 ttc gcc gcg atc agt gac ctt gtc caa atc ggc tgg gct ggc gcc acc 787
 Phe Ala Ala Ile Ser Asp Leu Val Gln Ile Gly Trp Ala Gly Ala Thr
 215 220 225
 ttc gcc gac agc gtt ggt gga gta gag gca gca aac ttc gct gga att 835
 Phe Ala Asp Ser Val Gly Gly Val Glu Ala Ala Asn Phe Ala Gly Ile
 230 235 240 245
 ttc caa gac atg ctc ata cca ctt gga att ctg gca gcg tgg aca gct 883
 Phe Gln Asp Met Leu Ile Pro Leu Gly Ile Leu Ala Ala Trp Thr Ala
 250 255 260
 gca gcg gtg tgg gcg gcg aac cgc tac atg cgc tgg gac tcg tac cgc 931
 Ala Ala Val Trp Ala Ala Asn Arg Tyr Met Arg Trp Asp Ser Tyr Arg
 265 270 275
 taagcctgca gccgacggga tta 954

<210> 42
 <211> 277
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 42
 Met Thr Thr Ser His Thr Ala Arg Gly Leu Gln His Ala Thr Pro Glu
 1 5 10 15
 Arg Arg Lys Thr Ser Phe Phe Lys Thr Ser Leu Phe Lys Ala Glu Trp
 20 25 30
 Leu Gln Phe Arg Arg Asn Lys Thr Leu Leu Phe Met Ala Thr Val Phe
 35 40 45
 Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly Gly Ala
 50 55 60
 Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr Leu Leu
 65 70 75 80
 Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg Arg Asp
 85 90 95
 Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp Ile Asp
 100 105 110
 Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu Ile Phe
 115 120 125
 Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro Ala Pro
 130 135 140
 Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu Leu Leu
 145 150 155 160
 Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn Ala Glu

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gta	ttc	cca	gtc	gga	atc	cct	ttg	ttg	ctc	ttt	ctc	atc	gga	aat	ggt	48	
Val	Phe	Pro	Val	Gly	Ile	Pro	Leu	Leu	Leu	Phe	Leu	Ile	Gly	Asn	Gly		
1				5					10					15			
ggg	gca	gca	gag	tcc	gcg	aac	tcc	ttc	gac	tac	ttc	gtc	atg	tac	acc	96	
Gly	Ala	Ala	Glu	Ser	Ala	Asn	Ser	Phe	Asp	Tyr	Phe	Val	Met	Tyr	Thr		
			20					25					30				
ctg	cta	ttt	gtg	cag	ttc	tac	acg	gtg	ctg	tcc	atg	gca	acc	acc	cgc	144	
Leu	Leu	Phe	Val	Gln	Phe	Tyr	Thr	Val	Leu	Ser	Met	Ala	Thr	Thr	Arg		
		35					40					45					
cgt	gat	gaa	cgt	gtg	ctg	aaa	agg	ctg	cgc	acg	gga	gaa	gcc	cgc	gac	192	
Arg	Asp	Glu	Arg	Val	Leu	Lys	Arg	Leu	Arg	Thr	Gly	Glu	Ala	Arg	Asp		
	50					55					60						
atc	gat	atc	atc	ggt	gcc	atc	tgt	ttc	ccc	ggc	gcg	ctc	ctc	aca	ctg	240	
Ile	Asp	Ile	Ile	Gly	Ala	Ile	Cys	Phe	Pro	Gly	Ala	Leu	Leu	Thr	Leu		
65					70					75					80		
atc	ttc	acc	gtg	gtg	atc	att	cca	ttg	ctc	atg	gtt	ttg	gga	gct	ccc	288	
Ile	Phe	Thr	Val	Val	Ile	Ile	Pro	Leu	Leu	Met	Val	Leu	Gly	Ala	Pro		
				85					90					95			
gcg	ccc	atc	aac	ctt	gtg	ccc	att	gtg	ttt	gcc	gta	ctg	atc	gga	cta	336	
Ala	Pro	Ile	Asn	Leu	Val	Pro	Ile	Val	Phe	Ala	Val	Leu	Ile	Gly	Leu		

100	105	110	
ctt ctt tgt agt gct ctt gcc ttg atg acc agc ggt ttc acc cga aac			384
Leu Leu Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn			
115	120	125	
gcc gaa gcc gca cag atg acc tcc atg ccc gtg ttc atg ctt gcg atg			432
Ala Glu Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met			
130	135	140	
ggt gga ctt gga tca atc cgc ttc gta ttc ggc gac agc att gtg gct			480
Gly Gly Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala			
145	150	155	160
gat atc ttg gcc tac acc cca ttc gcc gcg atc agt gac ctt gtc caa			528
Asp Ile Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln			
165	170	175	
atc ggc tgg gct ggc gcc acc ttc gcc gac agc gtt ggt gga gta gag			576
Ile Gly Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu			
180	185	190	
gca gca aac ttc gct gga att ttc caa gac atg ctc ata cca ctt gga			624
Ala Ala Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly			
195	200	205	
att ctg gca gcg tgg aca gct gca gcg gtg tgg gcg gcg aac cgc tac			672
Ile Leu Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr			
210	215	220	
atg cgc tgg gac tcg tac cgc taagcctgca gccgacggga tta			716
Met Arg Trp Asp Ser Tyr Arg			
225	230		

<210> 44

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Val Phe Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly	
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Gly Ala Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr	
20 25 30	

Leu Leu Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg	
35 40 45	

Arg Asp Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp	
50 55 60	

Ile Asp Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu	
65 70 75 80	

Ile Phe Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro	
85 90 95	

Ala Pro Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu	
100 105 110	

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attgtcatat tgggcgaata aaccggtagg attccccttc						gtg	agc	gcc	gaa	aat	115					
						Val	Ser	Ala	Glu	Asn						
						1				5						
acc gag aac aca gat tcc cca ttt gaa atc tcc gag ttt gat gat cac																163
Thr	Glu	Asn	Thr	Asp	Ser	Pro	Phe	Glu	Ile	Ser	Glu	Phe	Asp	Asp	His	
				10					15					20		
cga cgc ccc ctc cag cgg gcc ctc aaa ttc ggt tcc atc gcc cta att																211
Arg	Arg	Pro	Leu	Gln	Arg	Ala	Leu	Lys	Phe	Gly	Ser	Ile	Ala	Leu	Ile	
				25					30					35		
gtc ttc acc ctg atc tcc cta gcg atc tgg ggt gca act cgt ggc gta																259
Val	Phe	Thr	Leu	Ile	Ser	Leu	Ala	Ile	Trp	Gly	Ala	Thr	Arg	Gly	Val	
				40					45					50		
ccc ggc gta tca gca gtt gtt atc ggc gca gca gtt ggc gca ggc ttt																307
Pro	Gly	Val	Ser	Ala	Val	Val	Ile	Gly	Ala	Ala	Val	Gly	Ala	Gly	Phe	
				55					60					65		
gtc ctc tta acg gct ctc agc gtc ctg ttt aca act aat tcc aac gtc																355
Val	Leu	Leu	Thr	Ala	Leu	Ser	Val	Leu	Phe	Thr	Thr	Asn	Ser	Asn	Val	

70 75 80 85 400
 acc acc acc ggt gcg gtg gtg ctc ggt ggc tgg ctg ctg aag atc
 Thr Thr Thr Gly Ala Val Val Leu Gly Gly Trp Leu Leu Lys Ile
 90 95 100

<210> 46
 <211> 100
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 46
 Val Ser Ala Glu Asn Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser
 1 5 10 15
 Glu Phe Asp Asp His Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly
 20 25 30
 Ser Ile Ala Leu Ile Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly
 35 40 45
 Ala Thr Arg Gly Val Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala
 50 55 60
 Val Gly Ala Gly Phe Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr
 65 70 75 80
 Thr Asn Ser Asn Val Thr Thr Thr Gly Ala Val Val Leu Gly Gly Trp
 85 90 95
 Leu Leu Lys Ile
 100

<210> 47
 <211> 361
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> FRXA01206

<400> 47
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 Val Ser Ala Glu Asn
 1 5
 acc gag aac aca gat tcc cca ttt gaa atc tcc gag ttt gat gat cac 163
 Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser Glu Phe Asp Asp His
 10 15 20
 cga cgc ccc ctc cag cgg gcc ctc aaa ttc ggt tcc atc gcc cta att 211
 Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly Ser Ile Ala Leu Ile
 25 30 35
 gtc ttc acc ctg atc tcc cta gcg atc tgg ggt gca act cgt ggc gta 259

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<400> 49
aaagattttac tgcgtacaac tctaaccaac aatattggca atggggttggt ccatcttagc 60
gctttacctg tgaactctgc agagcggtac gcttaagcta atg aat ccc gaa ttt      115
                                         Met Asn Pro Glu Phe
                                           1           5
att cac ggc gca acc gaa att gaa acc aca aac agg ggc ctt cgc ccg      163
Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn Arg Gly Leu Arg Pro
                10                      15                          20
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cat cga ctc agc aaa gaa ata gta gaa cgc tac tgt gat ccc cag ttt	211
His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr Cys Asp Pro Gln Phe	
25 30 35	
agc gcg atg gaa cgc caa cca tcg ggc gtg cgc gtt gtg tgt cgc acc	259
Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg Val Val Cys Arg Thr	
40 45 50	
acc gcc acc tcc gtc acg ctg acc acg tat tcc acg cgg gtg gtg tac	307
Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser Thr Arg Val Val Tyr	
55 60 65	
ctc gat tcc ggc cgg ccg ggc ggc aag att gat gtg ctt atc gac ggc	355
Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp Val Leu Ile Asp Gly	
70 75 80 85	
gcc ccc aca tct tcc acg cca act tcc ggg ggc gag acc acg gaa gtc	403
Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly Glu Thr Thr Glu Val	
90 95 100	
aat ttc atc acc ggc gcc acg gaa cgg cgc ctg aaa gat ccg cag gtg	451
Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu Lys Asp Pro Gln Val	
105 110 115	
ctc aca gtg gat gga ctt tca gag cag gaa aag gtg gtg gag ttc tgg	499
Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys Val Val Glu Phe Trp	
120 125 130	
ctg cct cac aat gaa gaa att gaa gtg atc tcc ctt aaa gcc aac gca	547
Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser Leu Lys Ala Asn Ala	
135 140 145	
gct tta aac act gtc gaa gac acc cgt ccc gtg tgg atc aat tac ggc	595
Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val Trp Ile Asn Tyr Gly	
150 155 160 165	
agc tcc att agc cac ggt tcg gtt gcc act gcc cca acc aaa att tgg	643
Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala Pro Thr Lys Ile Trp	
170 175 180	
cca gcc att gtt gcc cag tcc aaa aac tac aac ctg cgt aac ttc ggt	691
Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn Leu Arg Asn Phe Gly	
185 190 195	
ttt ggt ggc agc gcc atg ttg gat cct ttt atg gcg agg cta atc agg	739
Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met Ala Arg Leu Ile Arg	
200 205 210	
gat act cca gct gat ctg atc acc ttg gaa att ggc atc aat att gtc	787
Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile Gly Ile Asn Ile Val	
215 220 225	
aat ggt gat gtg atg cgt cgc cgc gga cta gag gct gct gtg gat ggg	835
Asn Gly Asp Val Met Arg Arg Arg Gly Leu Glu Ala Ala Val Asp Gly	
230 235 240 245	
ttc atc aat acc atc cgc gat ggc cac ccc acc acg ccg atc aag att	883
Phe Ile Asn Thr Ile Arg Asp Gly His Pro Thr Thr Pro Ile Lys Ile	
250 255 260	

gtg tcg ccg ttc tac tgc ccc att cat gag aaa act cca gga ccc ggc 931
Val Ser Pro Phe Tyr Cys Pro Ile His Glu Lys Thr Pro Gly Pro Gly
265 270 275

gcg ttt gat acc tca tcg ttt ggc agt ggt cag att agg ttc atc gcc 979
Ala Phe Asp Thr Ser Ser Phe Gly Ser Gly Gln Ile Arg Phe Ile Ala
280 285 290

act ggt gaa cct gat gag cat ggt cga ctg acg ctg gag atg gtg cgt 1027
Thr Gly Glu Pro Asp Glu His Gly Arg Leu Thr Leu Glu Met Val Arg
295 300 305

gag gtg ttg gag ggg ttc gtc gaa aag caa aaa gac ccg cac ctg acc 1075
Glu Val Leu Glu Gly Phe Val Glu Lys Gln Lys Asp Pro His Leu Thr
310 315 320 325

tac gtc gat ggt gcg agc ctt tat cag gcc agc gat gcg ccg ttg ctg 1123
Tyr Val Asp Gly Ala Ser Leu Tyr Gln Ala Ser Asp Ala Pro Leu Leu
330 335 340

gat aat ttg cac cca gac gag gcg tcg cac gcc tta att gcg cag cgt 1171
Asp Asn Leu His Pro Asp Glu Ala Ser His Ala Leu Ile Ala Gln Arg
345 350 355

ttg ctt aag caa ctt tgaaatcggc ttcggtgatt tcg 1209
Leu Leu Lys Gln Leu
360

<210> 50

<211> 362

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met Asn Pro Glu Phe Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn
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Arg Gly Leu Arg Pro His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr
20 25 30

Cys Asp Pro Gln Phe Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg
35 40 45

Val Val Cys Arg Thr Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser
50 55 60

Thr Arg Val Val Tyr Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp
65 70 75 80

Val Leu Ile Asp Gly Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly
85 90 95

Glu Thr Thr Glu Val Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu
100 105 110

Lys Asp Pro Gln Val Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys
115 120 125

Val Val Glu Phe Trp Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser
130 135 140

Leu Lys Ala Asn Ala Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val
 145 150 155 160

Trp Ile Asn Tyr Gly Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala
 165 170 175

Pro Thr Lys Ile Trp Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn
 180 185 190

Leu Arg Asn Phe Gly Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met
 195 200 205

Ala Arg Leu Ile Arg Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile
 210 215 220

Gly Ile Asn Ile Val Asn Gly Asp Val Met Arg Arg Arg Gly Leu Glu
 225 230 235 240

Ala Ala Val Asp Gly Phe Ile Asn Thr Ile Arg Asp Gly His Pro Thr
 245 250 255

Thr Pro Ile Lys Ile Val Ser Pro Phe Tyr Cys Pro Ile His Glu Lys
 260 265 270

Thr Pro Gly Pro Gly Ala Phe Asp Thr Ser Ser Phe Gly Ser Gly Gln
 275 280 285

Ile Arg Phe Ile Ala Thr Gly Glu Pro Asp Glu His Gly Arg Leu Thr
 290 295 300

Leu Glu Met Val Arg Glu Val Leu Glu Gly Phe Val Glu Lys Gln Lys
 305 310 315 320

Asp Pro His Leu Thr Tyr Val Asp Gly Ala Ser Leu Tyr Gln Ala Ser
 325 330 335

Asp Ala Pro Leu Leu Asp Asn Leu His Pro Asp Glu Ala Ser His Ala
 340 345 350

Leu Ile Ala Gln Arg Leu Leu Lys Gln Leu
 355 360

<210> 51

<211> 778

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(778)

<223> FRXA01121

<400> 51

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gctttacctg tgaactctgc agagcggtac gcttaagcta atg aat ccc gaa ttt 115
 Met Asn Pro Glu Phe
 1 5

att cac ggc gca acc gaa att gaa acc aca aac agg ggc ctt cgc ccg 163
 Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn Arg Gly Leu Arg Pro
 10 15 20

cat cga ctc agc aaa gaa ata gta gaa cgc tac tgt gat ccc cag ttt 211
 His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr Cys Asp Pro Gln Phe
 25 30 35

agc gcg atg gaa cgc caa cca tcg ggc gtg cgc gtt gtg tgt cgc acc 259
 Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg Val Val Cys Arg Thr
 40 45 50

acc gcc acc tcc gtc acg ctg acc acg tat tcc acg cgg gtg gtg tac 307
 Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser Thr Arg Val Val Tyr
 55 60 65

ctc gat tcc ggc cgg ccg ggc ggc aag att gat gtg ctt atc gac ggc 355
 Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp Val Leu Ile Asp Gly
 70 75 80 85

gcc ccc aca tct tcc acg cca act tcc ggg ggc gag acc acg gaa gtc 403
 Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly Glu Thr Thr Glu Val
 90 95 100

aat ttc atc acc ggc gcc acg gaa cgg cgc ctg aaa gat ccg cag gtg 451
 Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu Lys Asp Pro Gln Val
 105 110 115

ctc aca gtg gat gga ctt tca gag cag gaa aag gtg gtg gag ttc tgg 499
 Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys Val Val Glu Phe Trp
 120 125 130

ctg cct cac aat gaa gaa att gaa gtg atc tcc ctt aaa gcc aac gca 547
 Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser Leu Lys Ala Asn Ala
 135 140 145

gct tta aac act gtc gaa gac acc cgt ccc gtg tgg atc aat tac ggc 595
 Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val Trp Ile Asn Tyr Gly
 150 155 160 165

agc tcc att agc cac ggt tcg gtt gcc act gcc cca acc aaa att tgg 643
 Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala Pro Thr Lys Ile Trp
 170 175 180

cca gcc att gtt gcc cag tcc aaa aac tac aac ctg cgt aac ttc ggt 691
 Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn Leu Arg Asn Phe Gly
 185 190 195

ttt ggt ggc agc gcc atg ttg gat cct ttt atg gcg agg cta atc agg 739
 Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met Ala Arg Leu Ile Arg
 200 205 210

gat act cca gct gat ctg atc acc ttg gaa att ggc atc 778
 Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile Gly Ile
 215 220 225

<210> 52

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Met Asn Pro Glu Phe Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn
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Arg Gly Leu Arg Pro His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr
 20 25 30

Cys Asp Pro Gln Phe Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg
 35 40 45

Val Val Cys Arg Thr Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser
 50 55 60

Thr Arg Val Val Tyr Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp
 65 70 75 80

Val Leu Ile Asp Gly Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly
 85 90 95

Glu Thr Thr Glu Val Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu
 100 105 110

Lys Asp Pro Gln Val Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys
 115 120 125

Val Val Glu Phe Trp Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser
 130 135 140

Leu Lys Ala Asn Ala Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val
 145 150 155 160

Trp Ile Asn Tyr Gly Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala
 165 170 175

Pro Thr Lys Ile Trp Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn
 180 185 190

Leu Arg Asn Phe Gly Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met
 195 200 205

Ala Arg Leu Ile Arg Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile
 210 215 220

Gly Ile
 225

<210> 53

<211> 902

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(879)

<223> RXN01085

<400> 53

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 Arg Lys Arg Gly Glu Gly Leu Asp Pro Asn Ser Pro Glu Ala Ile Glu

1	5	10	15	
cag gcg aag aag aaa ggg gaa cgg aag gct cgt aat gag cgt tgc cgc				96
Gln Ala Lys Lys Lys Gly Glu Arg Lys Ala Arg Asn Glu Arg Cys Arg				
	20	25	30	
aaa aac ttc aaa ggt ggt ggc acc aaa gat ctt aag cag act gat cgg				144
Lys Asn Phe Lys Gly Gly Gly Thr Lys Asp Leu Lys Gln Thr Asp Arg				
	35	40	45	
acc ttt gat cag ctg cga aaa cag cgg gtg acg gat aaa gcc cgc aac				192
Thr Phe Asp Gln Leu Arg Lys Gln Arg Val Thr Asp Lys Ala Arg Asn				
	50	55	60	
cgt gac gta cac aat gag cag caa ctg gca cgc ggt gaa atc gga gaa				240
Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile Gly Glu				
	65	70	75	80
atg cgc tca ccg atg tgg gtt gag gtg ggt gct gcg att ctg ggc gtg				288
Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu Gly Val				
	85	90		95
ttt gtc ctg gtt gtg atg tgg ctg gcc tgg ggc ggt atc ggg ctg ctg				336
Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly Leu Leu				
	100	105	110	
atc cag acc atg atg aat act ggc tca cct aat gac aaa gag ctt ttt				384
Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu Leu Phe				
	115	120	125	
gat gag ctt ggt gtg aga ccc tat tat gtt gct gtc gaa cag caa atc				432
Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln Gln Ile				
	130	135	140	
ggc acc agt agt gct cac acc acg tgc tac caa ccg ctt gat gaa ttt				480
Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp Glu Phe				
	145	150	155	160
ggc aat aat ttt ggc gac tgt acg cgt agc gtg cct aaa gag cca gtg				528
Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu Pro Val				
	165	170	175	
tgg tac gcc gat tat gta gct agt gtg ttc gca gaa cat ggc ttt gat				576
Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly Phe Asp				
	180	185	190	
gca cca gaa cct att gat aat tgc gtg ggt agc tgg ctg tta ttt ggt				624
Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu Phe Gly				
	195	200	205	
cat gtg ggc att att cgg gtg acg ttt gtg att gcg gtt gca gcg ggt				672
His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala Ala Gly				
	210	215	220	
gtg tat gcg atg tca cgc gca gca atg atg cgt cag cta gaa aca caa				720
Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu Thr Gln				
	225	230	235	240
aac gtc gct gtg gac acc acc gat att aac cag cac acc aat gac gca				768
Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn Asp Ala				
	245	250	255	

cgt ttg gcg att ccg cag gag att gtg cgc gat ttg agt ctg ttc ccc 816
 Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu Phe Pro
 260 265 270

 gat gtc ggt gca cac ttc acc agt cca gcc ctc aag cat gat ttc cca 864
 Asp Val Gly Ala His Phe Thr Ser Pro Ala Leu Lys His Asp Phe Pro
 275 280 285

 tgt gat gct gtc gaa taagggttt gaaaaaggtg gat 902
 Cys Asp Ala Val Glu
 290

<210> 54
 <211> 293
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 54
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 Gln Ala Lys Lys Lys Gly Glu Arg Lys Ala Arg Asn Glu Arg Cys Arg
 20 25 30

 Lys Asn Phe Lys Gly Gly Gly Thr Lys Asp Leu Lys Gln Thr Asp Arg
 35 40 45

 Thr Phe Asp Gln Leu Arg Lys Gln Arg Val Thr Asp Lys Ala Arg Asn
 50 55 60

 Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile Gly Glu
 65 70 75 80

 Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu Gly Val
 85 90 95

 Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly Leu Leu
 100 105 110

 Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu Leu Phe
 115 120 125

 Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln Gln Ile
 130 135 140

 Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp Glu Phe
 145 150 155 160

 Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu Pro Val
 165 170 175

 Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly Phe Asp
 180 185 190

 Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu Phe Gly
 195 200 205

 His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala Ala Gly
 210 215 220

Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu Thr Gln
 225 230 235 240

Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn Asp Ala
 245 250 255

Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu Phe Pro
 260 265 270

Asp Val Gly Ala His Phe Thr Ser Pro Ala Leu Lys His Asp Phe Pro
 275 280 285

Cys Asp Ala Val Glu
 290

<210> 55
 <211> 1057
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1057)
 <223> FRXA01085

<400> 55
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gcagactgat cggaccctttg atcagctgcg aaaacagcgg gtg acg gat aaa gcc 115
 Val Thr Asp Lys Ala
 1 5

cgc aac cgt gac gta cac aat gag cag caa ctg gca cgc ggt gaa atc 163
 Arg Asn Arg Asp Val His Asn Glu Gln Leu Ala Arg Gly Glu Ile
 10 15 20

gga gaa atg cgc tca ccg atg tgg gtt gag gtg ggt gct gcg att ctg 211
 Gly Glu Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu
 25 30 35

ggc gtg ttt gtc ctg gtt gtg atg tgg ctg gcc tgg ggc ggt atc ggg 259
 Gly Val Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly
 40 45 50

ctg ctg atc cag acc atg atg aat act ggc tca cct aat gac aaa gag 307
 Leu Leu Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu
 55 60 65

ctt ttt gat gag ctt ggt gtg aga ccc tat tat gtt gct gtc gaa cag 355
 Leu Phe Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln
 70 75 80 85

caa atc ggc acc agt agt gct cac acc acg tgc tac caa ccg ctt gat 403
 Gln Ile Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp
 90 95 100

gaa ttt ggc aat aat ttt ggc gac tgt acg cgt agc gtg cct aaa gag 451
 Glu Phe Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu
 105 110 115

cca gtg tgg tac gcc gat tat gta gct agt gtg ttc gca gaa cat ggc 499
Pro Val Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly
120 125 130

ttt gat gca cca gaa cct att gat aat tcg gtg ggt agc tgg ctg tta 547
Phe Asp Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu
135 140 145

ttt ggt cat gtg ggc att att cgg gtg acg ttt gtg att gcg gtt gca 595
Phe Gly His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala
150 155 160 165

gcg ggt gtg tat gcg atg tca cgc gca gca atg atg cgt cag cta gaa 643
Ala Gly Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu
170 175 180

aca caa aac gtc gct gtg gac acc acc gat att aac cag cac acc aat 691
Thr Gln Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn
185 190 195

gac gca cgt ttg gcg att ccg cag gag att gtg cgc gat ttg agt ctg 739
Asp Ala Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu
200 205 210

ttc ccc gat gtc ggt gca cac tca cca gtc cag ccc tca agc atg att 787
Phe Pro Asp Val Gly Ala His Ser Pro Val Gln Pro Ser Ser Met Ile
215 220 225

tcc cat gtg atg ctg tcg aat aag ggc ttg aaa aag gtg gat gta acg 835
Ser His Val Met Leu Ser Asn Lys Gly Leu Lys Lys Val Asp Val Thr
230 235 240 245

cag ttt gca cag gag aca att atc gac aat gac act ggt gaa att gtc 883
Gln Phe Ala Gln Glu Thr Ile Ile Asp Asn Asp Thr Gly Glu Ile Val
250 255 260

tct gaa aag ggt gaa gtg ctc tat gac ggt gca gga caa ccg atc aca 931
Ser Glu Lys Gly Glu Val Leu Tyr Asp Gly Ala Gly Gln Pro Ile Thr
265 270 275

aag agc ttg ccg atg att gac aac gaa ttt agc cat gcg att ttt gac 979
Lys Ser Leu Pro Met Ile Asp Asn Glu Phe Ser His Ala Ile Phe Asp
280 285 290

aaa tca gat gtc ccg aat ctt ccc gag ctg cga cgg ttc ttt aat cca 1027
Lys Ser Asp Val Pro Asn Leu Pro Glu Leu Arg Arg Phe Phe Asn Pro
295 300 305

gca aag att gag tgg aat cct ggt ggt agt 1057
Ala Lys Ile Glu Trp Asn Pro Gly Gly Ser
310 315

<210> 56

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Val Thr Asp Lys Ala Arg Asn Arg Asp Val His Asn Glu Gln Gln Leu

1	5	10	15
Ala Arg Gly Glu Ile Gly Glu Met Arg Ser Pro Met Trp Val Glu Val	20	25	30
Gly Ala Ala Ile Leu Gly Val Phe Val Leu Val Val Met Trp Leu Ala	35	40	45
Trp Gly Gly Ile Gly Leu Leu Ile Gln Thr Met Met Asn Thr Gly Ser	50	55	60
Pro Asn Asp Lys Glu Leu Phe Asp Glu Leu Gly Val Arg Pro Tyr Tyr	65	70	75
Val Ala Val Glu Gln Gln Ile Gly Thr Ser Ser Ala His Thr Thr Cys	85	90	95
Tyr Gln Pro Leu Asp Glu Phe Gly Asn Asn Phe Gly Asp Cys Thr Arg	100	105	110
Ser Val Pro Lys Glu Pro Val Trp Tyr Ala Asp Tyr Val Ala Ser Val	115	120	125
Phe Ala Glu His Gly Phe Asp Ala Pro Glu Pro Ile Asp Asn Ser Val	130	135	140
Gly Ser Trp Leu Leu Phe Gly His Val Gly Ile Ile Arg Val Thr Phe	145	150	155
Val Ile Ala Val Ala Ala Gly Val Tyr Ala Met Ser Arg Ala Ala Met	165	170	175
Met Arg Gln Leu Glu Thr Gln Asn Val Ala Val Asp Thr Thr Asp Ile	180	185	190
Asn Gln His Thr Asn Asp Ala Arg Leu Ala Ile Pro Gln Glu Ile Val	195	200	205
Arg Asp Leu Ser Leu Phe Pro Asp Val Gly Ala His Ser Pro Val Gln	210	215	220
Pro Ser Ser Met Ile Ser His Val Met Leu Ser Asn Lys Gly Leu Lys	225	230	235
Lys Val Asp Val Thr Gln Phe Ala Gln Glu Thr Ile Ile Asp Asn Asp	245	250	255
Thr Gly Glu Ile Val Ser Glu Lys Gly Glu Val Leu Tyr Asp Gly Ala	260	265	270
Gly Gln Pro Ile Thr Lys Ser Leu Pro Met Ile Asp Asn Glu Phe Ser	275	280	285
His Ala Ile Phe Asp Lys Ser Asp Val Pro Asn Leu Pro Glu Leu Arg	290	295	300
Arg Phe Phe Asn Pro Ala Lys Ile Glu Trp Asn Pro Gly Gly Ser	305	310	315

<211> 1824

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1801)

<223> RXN00022

<400> 57

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cacaccaccc accccttaac aaccacaaga aagatttata atg tcc gct cca acc 115
Met Ser Ala Pro Thr
1 5

atc tac ccc ggc acc aaa aca tct att gat ccg atc acc atg gat gac 163
Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro Ile Thr Met Asp Asp
10 15 20

gct cgc atc atc ttt ttc gat att gag tcg ctc cac aat att ttc acg 211
Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu His Asn Ile Phe Thr
25 30 35

gta gca acc tac gat tct ctg tcc cac cac gtc gat gtc ttt tac ctg 259
Val Ala Thr Tyr Asp Ser Leu Ser His His Val Asp Val Phe Tyr Leu
40 45 50

ctc gat cac aca acc agc cct cag atc acg gtg ctg ccg cac tca atg 307
Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val Leu Pro His Ser Met
55 60 65

gat tat ttc gat caa acg cgc agc gat gct gtt atg gct gcc atc att 355
Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val Met Ala Ala Ile Ile
70 75 80 85

gag caa aac cct gcg ttc gca gaa att aaa ggc tca ccc att aca acc 403
Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly Ser Pro Ile Thr Thr
90 95 100

gca gat gta gcc ctc cac aat ctc ggt gac acc aac gcc aac cga cgc 451
Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr Asn Ala Asn Arg Arg
105 110 115

tgg cag tct aac gtg ctg ctt gcc cgg cta ctc ggg ggt att agt gtg 499
Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu Gly Gly Ile Ser Val
120 125 130

cgc gga gag gta cct gag cac cag agc cac aac cat ctc gcc aag cag 547
Arg Gly Glu Val Pro Glu His Gln Ser His Asn His Leu Ala Lys Gln
135 140 145

ttt gcc gag gca acc ttg gtc acc agg gac ttc gat gtg aat tat gat 595
Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe Asp Val Asn Tyr Asp
150 155 160 165

cca aca agc gct cac cct ttt act gct ggc ttc aac tcg atc aac tat 643
Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe Asn Ser Ile Asn Tyr
170 175 180

gac acc acc ttg ctc agc ctg tac ttc gca atg ttg acc tca aat atc 691

Asp	Thr	Thr	Leu	Leu	Ser	Leu	Tyr	Phe	Ala	Met	Leu	Thr	Ser	Asn	Ile		
			185					190					195				
gga	agt	aca	ccg	acg	tat	ttc	ccg	gtg	atc	acc	gca	cag	gaa	ctt	cgt	739	
Gly	Ser	Thr	Pro	Thr	Tyr	Phe	Pro	Val	Ile	Thr	Ala	Gln	Glu	Leu	Arg		
		200					205					210					
gcg	cat	aac	gac	aag	ctc	ttt	agc	cct	gag	ttc	atc	aaa	aac	atg	cca	787	
Ala	His	Asn	Asp	Lys	Leu	Phe	Ser	Pro	Glu	Phe	Ile	Lys	Asn	Met	Pro		
	215					220					225						
aag	tat	ctc	tgg	gat	cgc	gac	agc	ggg	gct	gga	ctc	aga	gct	gca	tcg	835	
Lys	Tyr	Leu	Trp	Asp	Arg	Asp	Ser	Gly	Ala	Gly	Leu	Arg	Ala	Ala	Ser		
230					235					240					245		
ggg	ttc	cgc	aac	gcc	atg	ctc	aaa	tcg	ggg	cgc	cac	att	gat	att	caa	883	
Gly	Phe	Arg	Asn	Ala	Met	Leu	Lys	Ser	Gly	Arg	His	Ile	Asp	Ile	Gln		
				250					255					260			
cgc	ctc	aat	gaa	aaa	cag	ctc	ttt	gtt	gga	ctc	aag	cgc	ctg	ctt	ggg	931	
Arg	Leu	Asn	Glu	Lys	Gln	Leu	Phe	Val	Gly	Leu	Lys	Arg	Leu	Leu	Gly		
			265					270					275				
ctc	ctc	ggg	cac	cag	att	ctc	gaa	tct	gat	cgt	ctc	tct	ggg	gat	gat	979	
Leu	Leu	Gly	His	Gln	Ile	Leu	Glu	Ser	Asp	Arg	Leu	Ser	Gly	Asp	Asp		
		280					285					290					
gcc	cat	gtt	gat	act	aac	gag	gat	gta	ctt	gat	ctc	att	gcc	tac	aac	1027	
Ala	His	Val	Asp	Thr	Asn	Glu	Asp	Val	Leu	Asp	Leu	Ile	Ala	Tyr	Asn		
	295					300					305						
gtc	tca	gac	gtg	gtg	ggc	acc	aga	ctg	ctc	gct	gag	gac	ccg	gtg	tac	1075	
Val	Ser	Asp	Val	Val	Gly	Thr	Arg	Leu	Leu	Ala	Glu	Asp	Pro	Val	Tyr		
310					315				320						325		
tcc	ggc	tct	ttc	gat	ctg	cgg	gca	ggg	cta	ctg	agc	acc	tac	cca	gag	1123	
Ser	Gly	Ser	Phe	Asp	Leu	Arg	Ala	Gly	Leu	Leu	Ser	Thr	Tyr	Pro	Glu		
				330				335						340			
act	gtt	ttt	gat	cat	gat	ggg	act	ttc	cgt	cag	cca	tcc	acg	cag	atg	1171	
Thr	Val	Phe	Asp	His	Asp	Gly	Thr	Phe	Arg	Gln	Pro	Ser	Thr	Gln	Met		
			345				350						355				
cgt	aaa	gat	cgc	cta	acg	att	aat	acc	tca	tca	gct	cag	ttc	gca	gcg	1219	
Arg	Lys	Asp	Arg	Leu	Thr	Ile	Asn	Thr	Ser	Ser	Ala	Gln	Phe	Ala	Ala		
		360					365					370					
cgt	att	ttg	gcg	cca	tat	cgc	cca	ctc	cgc	gat	gtc	cct	gat	gcg	att	1267	
Arg	Ile	Leu	Ala	Pro	Tyr	Arg	Pro	Leu	Arg	Asp	Val	Pro	Asp	Ala	Ile		
	375					380					385						
ggc	gac	atg	ccg	gtg	gtg	tct	tac	ttg	tac	ccg	gat	gca	gca	gtc	gcc	1315	
Gly	Asp	Met	Pro	Val	Val	Ser	Tyr	Leu	Tyr	Pro	Asp	Ala	Ala	Val	Ala		
390					395					400					405		
gaa	gca	aca	ggg	caa	aaa	caa	gtc	aac	gtg	ctt	gat	gag	tca	aag	aag	1363	
Glu	Ala	Thr	Gly	Gln	Lys	Gln	Val	Asn	Val	Leu	Asp	Glu	Ser	Lys	Lys		
				410				415						420			
ttc	ttc	tat	gac	aac	atc	acc	gac	ccg	gaa	gca	cgt	gct	gcc	ttt	gat	1411	
Phe	Phe	Tyr	Asp	Asn	Ile	Thr	Asp	Pro	Glu	Ala	Arg	Ala	Ala	Phe	Asp		

425	430	435	
gag gtc ttt gct ttt tac gct gat att gag ggt cgc aac ttc aac agt			1459
Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly Arg Asn Phe Asn Ser			
440	445	450	
cac aat gag gct att gat acc cag att aac caa tta cgt gct tat ctc			1507
His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln Leu Arg Ala Tyr Leu			
455	460	465	
aac cag gtt gtc gca ttc gat gca gct ggg tat gcg ctc tat gat gta			1555
Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr Ala Leu Tyr Asp Val			
470	475	480	485
cgt aca cgt ttt gag cag atc ttc ccc aag gat cgc agc tac atc aac			1603
Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp Arg Ser Tyr Ile Asn			
490	495	500	
gat gct acg gat atg acc cct cgc gca gta tcg agc ttt gac gat ctg			1651
Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser Ser Phe Asp Asp Leu			
505	510	515	
gtt gca ctc tgt gat gat att cgc ggt gta ctt gat cga ggt tta gag			1699
Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu Asp Arg Gly Leu Glu			
520	525	530	
atc tca tct ccg aat cat cat gag atg gtg gat gct atg cgc aag cag			1747
Ile Ser Ser Pro Asn His His Glu Met Val Asp Ala Met Arg Lys Gln			
535	540	545	
ctg cac tat att cag gca ttt tac cgt gcc tgg gac cca tca acg ccg			1795
Leu His Tyr Ile Gln Ala Phe Tyr Arg Ala Trp Asp Pro Ser Thr Pro			
550	555	560	565
ctt caa tgacgctgac ccagcgggtga ccc			1824
Leu Gln			

<210> 58

<211> 567

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

Met Ser Ala Pro Thr Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro	
1	15

Ile Thr Met Asp Asp Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu	
20	30

His Asn Ile Phe Thr Val Ala Thr Tyr Asp Ser Leu Ser His His Val	
35	45

Asp Val Phe Tyr Leu Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val	
50	60

Leu Pro His Ser Met Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val	
65	75

Met Ala Ala Ile Ile Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly

85										90					95				
Ser	Pro	Ile	Thr	Thr	Ala	Asp	Val	Ala	Leu	His	Asn	Leu	Gly	Asp	Thr				
			100					105					110						
Asn	Ala	Asn	Arg	Arg	Trp	Gln	Ser	Asn	Val	Leu	Leu	Ala	Arg	Leu	Leu				
		115					120					125							
Gly	Gly	Ile	Ser	Val	Arg	Gly	Glu	Val	Pro	Glu	His	Gln	Ser	His	Asn				
	130					135					140								
His	Leu	Ala	Lys	Gln	Phe	Ala	Glu	Ala	Thr	Leu	Val	Thr	Arg	Asp	Phe				
145					150					155					160				
Asp	Val	Asn	Tyr	Asp	Pro	Thr	Ser	Ala	His	Pro	Phe	Thr	Ala	Gly	Phe				
				165					170					175					
Asn	Ser	Ile	Asn	Tyr	Asp	Thr	Thr	Leu	Leu	Ser	Leu	Tyr	Phe	Ala	Met				
			180					185					190						
Leu	Thr	Ser	Asn	Ile	Gly	Ser	Thr	Pro	Thr	Tyr	Phe	Pro	Val	Ile	Thr				
		195					200					205							
Ala	Gln	Glu	Leu	Arg	Ala	His	Asn	Asp	Lys	Leu	Phe	Ser	Pro	Glu	Phe				
	210					215					220								
Ile	Lys	Asn	Met	Pro	Lys	Tyr	Leu	Trp	Asp	Arg	Asp	Ser	Gly	Ala	Gly				
225					230				235						240				
Leu	Arg	Ala	Ala	Ser	Gly	Phe	Arg	Asn	Ala	Met	Leu	Lys	Ser	Gly	Arg				
				245					250					255					
His	Ile	Asp	Ile	Gln	Arg	Leu	Asn	Glu	Lys	Gln	Leu	Phe	Val	Gly	Leu				
			260					265					270						
Lys	Arg	Leu	Leu	Gly	Leu	Leu	Gly	His	Gln	Ile	Leu	Glu	Ser	Asp	Arg				
		275					280					285							
Leu	Ser	Gly	Asp	Asp	Ala	His	Val	Asp	Thr	Asn	Glu	Asp	Val	Leu	Asp				
	290					295					300								
Leu	Ile	Ala	Tyr	Asn	Val	Ser	Asp	Val	Val	Gly	Thr	Arg	Leu	Leu	Ala				
305					310					315					320				
Glu	Asp	Pro	Val	Tyr	Ser	Gly	Ser	Phe	Asp	Leu	Arg	Ala	Gly	Leu	Leu				
				325					330					335					
Ser	Thr	Tyr	Pro	Glu	Thr	Val	Phe	Asp	His	Asp	Gly	Thr	Phe	Arg	Gln				
			340					345					350						
Pro	Ser	Thr	Gln	Met	Arg	Lys	Asp	Arg	Leu	Thr	Ile	Asn	Thr	Ser	Ser				
		355					360					365							
Ala	Gln	Phe	Ala	Ala	Arg	Ile	Leu	Ala	Pro	Tyr	Arg	Pro	Leu	Arg	Asp				
	370					375					380								
Val	Pro	Asp	Ala	Ile	Gly	Asp	Met	Pro	Val	Val	Ser	Tyr	Leu	Tyr	Pro				
385					390					395					400				
Asp	Ala	Ala	Val	Ala	Glu	Ala	Thr	Gly	Gln	Lys	Gln	Val	Asn	Val	Leu				
				405					410					415					

Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala
 420 425 430
 Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly
 435 440 445
 Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln
 450 455 460
 Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
 465 470 475 480
 Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
 485 490 495
 Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
 500 505 510
 Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
 515 520 525
 Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
 530 535 540
 Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Tyr Arg Ala Trp
 545 550 555 560
 Asp Pro Ser Thr Pro Leu Gln
 565

<210> 59
 <211> 835
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(835)
 <223> FRXA00022

<400> 59
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 cacaccaccc accccttaac aaccacaaga aagattttatc atg tcc gct cca acc 115
 Met Ser Ala Pro Thr 5
 atc tac ccc ggc acc aaa aca tct att gat ccg atc acc atg gat gac 163
 Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro Ile Thr Met Asp Asp 20
 10 15
 gct cgc atc atc ttt ttc gat att gag tcg ctc cac aat att ttc acg 211
 Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu His Asn Ile Phe Thr 35
 25 30
 gta gca acc tac gat tct ctg tcc cac cac gtc gat gtc ttt tac ctg 259
 Val Ala Thr Tyr Asp Ser Leu Ser His His Val Asp Val Phe Tyr Leu 50
 40 45

ctc gat cac aca acc agc cct cag atc acg gtg ctg ccg cac tca atg 307
 Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val Leu Pro His Ser Met
 55 60 65
 gat tat ttc gat caa acg cgc agc gat gct gtt atg gct gcc atc att 355
 Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val Met Ala Ala Ile Ile
 70 75 80 85
 gag caa aac cct gcg ttc gca gaa att aaa ggc tca ccc att aca acc 403
 Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly Ser Pro Ile Thr Thr
 90 95 100
 gca gat gta gcc ctc cac aat ctc ggt gac acc aac gcc aac cga cgc 451
 Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr Asn Ala Asn Arg Arg
 105 110 115
 tgg cag tct aac gtg ctg ctt gcc cgg cta ctc ggg ggt att agt gtg 499
 Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu Gly Gly Ile Ser Val
 120 125 130
 cgc gga gag gta cct gag cac cag agc cac aac cat ctc gcc aag cag 547
 Arg Gly Glu Val Pro Glu His Gln Ser His Asn His Leu Ala Lys Gln
 135 140 145
 ttt gcc gag gca acc ttg gtc acc agg gac ttc gat gtg aat tat gat 595
 Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe Asp Val Asn Tyr Asp
 150 155 160 165
 cca aca agc gct cac cct ttt act gct ggc ttc aac tcg atc aac tat 643
 Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe Asn Ser Ile Asn Tyr
 170 175 180
 gac acc acc ttg ctc agc ctg tac ttc gca atg ttg acc tca aat atc 691
 Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met Leu Thr Ser Asn Ile
 185 190 195
 gga agt aca ccg acg tat ttc ccg gtg atc acc gca caa gaa ctt cgt 739
 Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr Ala Gln Glu Leu Arg
 200 205 210
 gcg cat aac gac aag ctc ttt agc cct gag ttc atc aaa aac atg cca 787
 Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe Ile Lys Asn Met Pro
 215 220 225
 aag tat ttc tgg gat cgc gac agc ggt gct gga ctc aga gct gca tcg 835
 Lys Tyr Phe Trp Asp Arg Asp Ser Gly Ala Gly Leu Arg Ala Ala Ser
 230 235 240 245

<210> 60

<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Met Ser Ala Pro Thr Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro
 1 5 10 15

Ile Thr Met Asp Asp Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu
 20 25 30

<400> 61																
cac	att	gat	att	caa	cgc	ctc	aat	gaa	aaa	cag	ctc	ttt	gtt	gga	ctc	48
His	Ile	Asp	Ile	Gln	Arg	Leu	Asn	Glu	Lys	Gln	Leu	Phe	Val	Gly	Leu	
1				5					10					15		
aag	cgc	ctg	ctt	ggt	ctc	ctc	ggt	cac	cag	att	ctc	gaa	tct	gat	cgt	96
Lys	Arg	Leu	Leu	Gly	Leu	Leu	Gly	His	Gln	Ile	Leu	Glu	Ser	Asp	Arg	
			20					25					30			

ctc tct ggt gat gat gcc cat gtt gat act aac gag gat gta ctt gat	144
Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp	
35 40 45	
ctc att gcc tac aac gtc tca gac gtg gtg ggc acc aga ctg ctc gct	192
Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala	
50 55 60	
gag gac ccg gtg tac tcc ggc tct ttc gat ctg cgg gca ggt cta ctg	240
Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu	
65 70 75 80	
agc acc tac cca gag act gtt ttt gat cat gat ggt act ttc cgt cag	288
Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln	
85 90 95	
cca tcc acg cag atg cgt aaa gat cgc cta acg att aat acc tca tca	336
Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser	
100 105 110	
gct cag ttc gca gcg cgt att ttg gcg cca tat cgc cca ctc cgc gat	384
Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp	
115 120 125	
gtc cct gat gcg att ggc gac atg ccg gtg gtg tct tac ttg tac ccg	432
Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro	
130 135 140	
gat gca gca gtc gcc gaa gca aca ggt caa aaa caa gtc aac gtg ctt	480
Asp Ala Ala Val Ala Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu	
145 150 155 160	
gat gag tca aag aag ttc ttc tat gac aac atc acc gac ccg gaa gca	528
Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala	
165 170 175	
cgt gct gcc ttt gat gag gtc ttt gct ttt tac gct gat att gag ggt	576
Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly	
180 185 190	
cgc aac ttc aac agt cac aat gag gct att gat acc cag att aac caa	624
Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln	
195 200 205	
tta cgt gct tat ctc aac cag gtt gtc gca ttc gat gca gct ggg tat	672
Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr	
210 215 220	
gcg ctc tat gat gta cgt aca cgt ttt gag cag atc ttc ccc aag gat	720
Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp	
225 230 235 240	
cgc agc tac atc aac gat gct acg gat atg acc cct cgc gca gta tcg	768
Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser	
245 250 255	
agc ttt gac gat ctg gtt gca ctc tgt gat gat att cgc ggt gta ctt	816
Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu	
260 265 270	

gat cga ggt tta gag atc tca tct ccg aat cat cat gag atg gtg gat 864
 Asp Arg Gly Leu Glu Ile Ser Pro Asn His His Glu Met Val Asp
 275 280 285

gct atg cgc aag cag ctg cac tat att cag gca ttt acc gtg cct ggg 912
 Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Thr Val Pro Gly
 290 295 300

acc cat caa cgc cgc ttc aat gac gct 939
 Thr His Gln Arg Arg Phe Asn Asp Ala
 305 310

<210> 62

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

His Ile Asp Ile Gln Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu
 1 5 10 15

Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
 20 25 30

Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
 35 40 45

Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
 50 55 60

Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu
 65 70 75 80

Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln
 85 90 95

Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser
 100 105 110

Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp
 115 120 125

Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro
 130 135 140

Asp Ala Ala Val Ala Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu
 145 150 155 160

Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala
 165 170 175

Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly
 180 185 190

Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln
 195 200 205

Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
 210 215 220

Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
 225 230 235 240
 Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
 245 250 255
 Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
 260 265 270
 Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
 275 280 285
 Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Thr Val Pro Gly
 290 295 300
 Thr His Gln Arg Arg Phe Asn Asp Ala
 305 310

<210> 63
 <211> 489
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(466)
 <223> RXN00027

<400> 63
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 gggaactggt ttagatttta ttcagggtag ggagattggt gtg gat gaa cga agc 115
 Val Asp Glu Arg Ser
 1 5
 cgg ttt gcg cgc agc gtt ttc ccg gac ggt gaa gaa cca gat cca cgt 163
 Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu Glu Pro Asp Pro Arg
 10 15 20
 ttc act ttg gcc aat gag cgc acg ttt cta gca tgg acg cgt acg tct 211
 Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala Trp Thr Arg Thr Ser
 25 30 35
 ttg gcg ttt ctt gcc ggt ggt att gct ttt gag gcg ttc cag atc agt 259
 Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu Ala Phe Gln Ile Ser
 40 45 50
 gga cta tcg gat act gtc cgt aca aca atc gcg gtt ttt atc att gcg 307
 Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala Val Phe Ile Ile Ala
 55 60 65
 gtt ggc atg atc att gcc gct ggt gct gcg gtg agg tgg atg aat gtg 355
 Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val Arg Trp Met Asn Val
 70 75 80 85
 gag cgt gca atg cgt aaa cag aag cca ctt ccc gta cct gcg att att 403
 Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro Val Pro Ala Ile Ile
 90 95 100
 ccg ttt ctg tct att gcg gct ttg gtg gcc tct gcg gct gtc ttg gtt 451

Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser Ala Ala Val Leu Val
 105 110 115

ctg att att gtt cag tagctatgcg cattcatgag gat
 Leu Ile Ile Val Gln
 120

489

<210> 64

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Val Asp Glu Arg Ser Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu
 1 5 10 15

Glu Pro Asp Pro Arg Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala
 20 25 30

Trp Thr Arg Thr Ser Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu
 35 40 45

Ala Phe Gln Ile Ser Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala
 50 55 60

Val Phe Ile Ile Ala Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val
 65 70 75 80

Arg Trp Met Asn Val Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro
 85 90 95

Val Pro Ala Ile Ile Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser
 100 105 110

Ala Ala Val Leu Val Leu Ile Ile Val Gln
 115 120

<210> 65

<211> 489

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(466)

<223> FRXA00027

<400> 65

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gggaactggt ttagatttta ttcagggttag ggagattggt gtg gat gaa cga agc 115
 Val Asp Glu Arg Ser
 1 5

cgg ttt gcg cgc agc gtt ttc ccg gac ggt gaa gaa cca gat cca cgt 163
 Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu Glu Pro Asp Pro Arg
 10 15 20

ttc act ttg gcc aat gag cgc acg ttt cta gca tgg acg cgt acg tct 211

Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala Trp Thr Arg Thr Ser
 25 30 35
 ttg gcg ttt ctt gcc ggt ggt att gct ttt gag gcg ttc cag atc agt 259
 Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu Ala Phe Gln Ile Ser
 40 45 50
 gga cta tcg gat act gtc cgt aca aca atc gcg gtt ttt atc att gcg 307
 Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala Val Phe Ile Ile Ala
 55 60 65
 gtt ggc atg atc att gcc gct ggt gct gcg gtg agg tgg atg aat gtg 355
 Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val Arg Trp Met Asn Val
 70 75 80 85
 gag cgt gca atg cgt aaa cag aag cca ctt ccc gta cct gcg att att 403
 Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro Val Pro Ala Ile Ile
 90 95 100
 ccg ttt ctg tct att gcg gct ttg gtg gcc tct gcg gct gtc ttg gtt 451
 Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser Ala Ala Val Leu Val
 105 110 115
 ctg att att gtt cag tagctatgcg cattcatgag gat 489
 Leu Ile Ile Val Gln
 120

<210> 66

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Val Asp Glu Arg Ser Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu
 1 5 10 15
 Glu Pro Asp Pro Arg Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala
 20 25 30
 Trp Thr Arg Thr Ser Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu
 35 40 45
 Ala Phe Gln Ile Ser Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala
 50 55 60
 Val Phe Ile Ile Ala Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val
 65 70 75 80
 Arg Trp Met Asn Val Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro
 85 90 95
 Val Pro Ala Ile Ile Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser
 100 105 110
 Ala Ala Val Leu Val Leu Ile Ile Val Gln
 115 120

<210> 67

<211> 2070

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2047)

<223> RXN00028

<400> 67

aaaagtctctg gccagaaaac tctctatact gtgcagcatg gcaccaacga tcaccgacat 60

ccatgttctg	cttcgtcgcg	gtgagcgaca	atcagtgatc	atg	acc	ctc	act	gcc	115
				Met	Thr	Leu	Thr	Ala	
				1				5	

tct	tcc	ttg	gag	gcc	ggg	aaa	atg	tct	ttt	agt	ggc	ggg	tat	atc	gtg	163
Ser	Ser	Leu	Glu	Ala	Gly	Lys	Met	Ser	Phe	Ser	Gly	Gly	Tyr	Ile	Val	
			10						15					20		

ggc	gag	acg	atg	atc	ttc	ctc	gtc	gat	ccc	gat	gaa	gtc	gag	ata	cga	211
Gly	Glu	Thr	Met	Ile	Phe	Leu	Val	Asp	Pro	Asp	Glu	Val	Glu	Ile	Arg	
			25					30					35			

cgc	agc	cct	aac	agc	ctc	cac	gtc	ctg	cgt	aac	ggt	agc	gat	att	ctg	259
Arg	Ser	Pro	Asn	Ser	Leu	His	Val	Leu	Arg	Asn	Gly	Ser	Asp	Ile	Leu	
		40					45					50				

cgc	cgc	aac	gag	cat	cat	tgc	tgg	gta	ttt	gag	aat	ttc	aat	aaa	ccc	307
Arg	Arg	Asn	Glu	His	His	Cys	Trp	Val	Phe	Glu	Asn	Phe	Asn	Lys	Pro	
		55				60					65					

att	gac	cca	cct	gtt	cga	ttg	ggt	cct	cgg	gat	atc	atc	tgc	ccg	agc	355
Ile	Asp	Pro	Pro	Val	Arg	Leu	Gly	Pro	Arg	Asp	Ile	Ile	Cys	Pro	Ser	
	70				75				80					85		

gcc	ttg	gcc	tgg	gtt	ctt	caa	cag	cat	tcc	atc	tcc	cgg	tcc	tta	tcc	403
Ala	Leu	Ala	Trp	Val	Leu	Gln	Gln	His	Ser	Ile	Ser	Arg	Ser	Leu	Ser	
			90						95					100		

cac	cac	ctt	cac	gcg	gat	aag	atc	act	gcg	gga	gag	att	gct	gga	cgc	451
His	His	Leu	His	Ala	Asp	Lys	Ile	Thr	Ala	Gly	Glu	Ile	Ala	Gly	Arg	
		105						110					115			

ccc	acc	tgg	atc	ctc	cgt	gag	gaa	cct	act	tca	gga	ggg	cag	gac	cca	499
Pro	Thr	Trp	Ile	Leu	Arg	Glu	Glu	Pro	Thr	Ser	Gly	Gly	Gln	Asp	Pro	
		120				125						130				

agt	cga	ttg	gtc	agt	ctt	gaa	atc	gac	cag	gaa	cac	ggt	gtc	atc	ctt	547
Ser	Arg	Leu	Val	Ser	Leu	Glu	Ile	Asp	Gln	Glu	His	Gly	Val	Ile	Leu	
	135					140					145					

gca	gtg	gag	act	gga	caa	gaa	cga	ctc	gaa	gcc	acg	gag	att	tct	ttt	595
Ala	Val	Glu	Thr	Gly	Gln	Glu	Arg	Leu	Glu	Ala	Thr	Glu	Ile	Ser	Phe	
	150				155				160					165		

cct	gac	act	ctt	cct	aat	cct	tcc	tgg	gac	gga	gcc	tgg	gaa	cca	ttc	643
Pro	Asp	Thr	Leu	Pro	Asn	Pro	Ser	Trp	Asp	Gly	Ala	Trp	Glu	Pro	Phe	
			170					175					180			

cat	tat	cca	gat	tcg	aca	cca	cac	act	gcc	cct	gat	gtt	gct	gaa	ata	691
His	Tyr	Pro	Asp	Ser	Thr	Pro	His	Thr	Ala	Pro	Asp	Val	Ala	Glu	Ile	

185	190	195	
ccc ggt tac att cag tca ctg ccg ccg cag tct gaa gat cct cgc aga Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser Glu Asp Pro Arg Arg 200 205 210			739
cta cga gtc ttc gtc aat gag ata gca ctc gaa ggt gat ttc cct gac Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu Gly Asp Phe Pro Asp 215 220 225			787
tac cgt caa gga caa tct gtg cga ctt act ttg gga att agc tcc tcc Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu Gly Ile Ser Ser Ser 230 235 240 245			835
cct gtg cca ctc gaa gga atg aca acc aga cgc cgg ggc cgg gta cgc Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg Arg Gly Arg Val Arg 250 255 260			883
aac ctt ggg gaa gaa gct agt cca ggc gat gac ggt atg ccc cag tgg Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp Gly Met Pro Gln Trp 265 270 275			931
cca atc ctg ctc act ggt gat ggg tgg acg gcg ctg gcc tac act ccc Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala Leu Ala Tyr Thr Pro 280 285 290			979
atc cca aaa cgt gga gat gca gag atc cag ggg tgg ttt tat tat tcc Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly Trp Phe Tyr Tyr Ser 295 300 305			1027
gcc tac gga att gtt gat gtt ccc aca gat cta cgg gta gag cgt att Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu Arg Val Glu Arg Ile 310 315 320 325			1075
ttc gct ggt atc ggc aca agt ggc acc aac gag cgt ttg tgg cag gag Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu Arg Leu Trp Gln Glu 330 335 340			1123
ata gac aat act tct tcg gct tat cac tcg gaa gat tgg tgg atc cgc Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu Asp Trp Trp Ile Arg 345 350 355			1171
gat gtc gtt tta gac gtc acg ttg gat gga gct gtt ccg cct ccg ctt Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala Val Pro Pro Pro Leu 360 365 370			1219
aga cgt gac gtc ttc act gct gtc gat cct att gtg gcg ggt gac aaa Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile Val Ala Gly Asp Lys 375 380 385			1267
ttg tgg ctg tgt gac gtg cac ttt ccg gta gcc cgc tgc tgg gag acc Leu Trp Leu Cys Asp Val His Phe Pro Val Ala Arg Cys Trp Glu Thr 390 395 400 405			1315
acg acc ggc cga tac ttg ggg cag act tta gtc cca gca cca ctg cga Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Val Pro Ala Pro Leu Arg 410 415 420			1363
gat cga tcg tac gtc ctt gag ctg cac agc gac caa caa tta gga gcc Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp Gln Gln Leu Gly Ala 425 430 435			1411

gta gcg gca agt ggg aag agt ggt tgg att ctc aca cct ggt caa gca 1459
 Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu Thr Pro Gly Gln Ala
 440 445 450

gta gcc act aaa gct cct gat tgg act cct ccc acc cgg gca acc gat 1507
 Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro Thr Arg Ala Thr Asp
 455 460 465

ctg cct cag gtc ccc tcc ccc tgg gag atc gtc gct gtc cgt ggc caa 1555
 Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val Ala Val Arg Gly Gln
 470 475 480 485

ggt ctg ttt gag ctg cag gtg gaa act agt aga cgc acc gcc ctc ggt 1603
 Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg Arg Thr Ala Leu Gly
 490 495 500

cga gtt aat gcg acc ggt ggc gtc gac atc ggt gaa ctc ccg ccc aac 1651
 Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly Glu Leu Pro Pro Asn
 505 510 515

ggc tat acc atc agt tct gtg gtt cag atc ggt gat gaa tac atc gtg 1699
 Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly Asp Glu Tyr Ile Val
 520 525 530

ggc agg tgg gta gag gaa tac cgg ctc aac tcc aaa ctg gag gtc att 1747
 Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser Lys Leu Glu Val Ile
 535 540 545

tct acc aaa gag cta gat atc tcc gca tcc gga tgg aag agc aag ggg 1795
 Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly Trp Lys Ser Lys Gly
 550 555 560 565

acg gtt gct tat ctg tcg gaa gac act cac ata tgt ttc ttc gac cag 1843
 Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile Cys Phe Phe Asp Gln
 570 575 580

gtc agc ggg gcc gag ctt ccc agc ctg ggt atc gcc gag gga cac cag 1891
 Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile Ala Glu Gly His Gln
 585 590 595

ggc gag gtt atg tca gca act tct tca gag agc atc gtg ctt atc tac 1939
 Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser Ile Val Leu Ile Tyr
 600 605 610

cgg cgc aac ccg aac aat tca atg tcg att gtc ccg act tcc gtt gcc 1987
 Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val Pro Thr Ser Val Ala
 615 620 625

acc tat gac aat ggc acc tgg acg act atg ccg cta cag gaa gct cca 2035
 Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro Leu Gln Glu Ala Pro
 630 635 640 645

gcg gaa ctg tcc taaactgctc atagactgct gag 2070
 Ala Glu Leu Ser

<210> 68

<211> 649

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Met Thr Leu Thr Ala Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser
 1 5 10 15
 Gly Gly Tyr Ile Val Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp
 20 25 30
 Glu Val Glu Ile Arg Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn
 35 40 45
 Gly Ser Asp Ile Leu Arg Arg Asn Glu His His Cys Trp Val Phe Glu
 50 55 60
 Asn Phe Asn Lys Pro Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp
 65 70 75 80
 Ile Ile Cys Pro Ser Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile
 85 90 95
 Ser Arg Ser Leu Ser His His Leu His Ala Asp Lys Ile Thr Ala Gly
 100 105 110
 Glu Ile Ala Gly Arg Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser
 115 120 125
 Gly Gly Gln Asp Pro Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu
 130 135 140
 His Gly Val Ile Leu Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala
 145 150 155 160
 Thr Glu Ile Ser Phe Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly
 165 170 175
 Ala Trp Glu Pro Phe His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro
 180 185 190
 Asp Val Ala Glu Ile Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser
 195 200 205
 Glu Asp Pro Arg Arg Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu
 210 215 220
 Gly Asp Phe Pro Asp Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu
 225 230 235 240
 Gly Ile Ser Ser Ser Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg
 245 250 255
 Arg Gly Arg Val Arg Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp
 260 265 270
 Gly Met Pro Gln Trp Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala
 275 280 285
 Leu Ala Tyr Thr Pro Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly
 290 295 300
 Trp Phe Tyr Tyr Ser Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu

305		310		315		320
Arg Val Glu Arg Ile Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu						
		325		330		335
Arg Leu Trp Gln Glu Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu						
		340		345		350
Asp Trp Trp Ile Arg Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala						
		355		360		365
Val Pro Pro Pro Leu Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile						
		370		375		380
Val Ala Gly Asp Lys Leu Trp Leu Cys Asp Val His Phe Pro Val Ala						
		385		390		395
Arg Cys Trp Glu Thr Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Val						
		405		410		415
Pro Ala Pro Leu Arg Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp						
		420		425		430
Gln Gln Leu Gly Ala Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu						
		435		440		445
Thr Pro Gly Gln Ala Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro						
		450		455		460
Thr Arg Ala Thr Asp Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val						
		465		470		475
Ala Val Arg Gly Gln Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg						
		485		490		495
Arg Thr Ala Leu Gly Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly						
		500		505		510
Glu Leu Pro Pro Asn Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly						
		515		520		525
Asp Glu Tyr Ile Val Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser						
		530		535		540
Lys Leu Glu Val Ile Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly						
		545		550		555
Trp Lys Ser Lys Gly Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile						
		565		570		575
Cys Phe Phe Asp Gln Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile						
		580		585		590
Ala Glu Gly His Gln Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser						
		595		600		605
Ile Val Leu Ile Tyr Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val						
		610		615		620
Pro Thr Ser Val Ala Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro						
		625		630		635
						640

Leu Gln Glu Ala Pro Ala Glu Leu Ser
645

<210> 69
<211> 2070
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2047)
<223> FRXA00028

<220>
<221> VARIANT
<222> 416
<223> Xaa = Val or Phe

<400> 69
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ccatgttctg cttcgtcgcg gtgagcgaca atcagtgatc atg acc ctc act gcc 115
Met Thr Leu Thr Ala
1 5
tct tcc ttg gag gcc ggg aaa atg tct ttt agt ggc ggg tat atc gtg 163
Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser Gly Gly Tyr Ile Val
10 15 20
ggc gag acg atg atc ttc ctc gtc gat ccc gat gaa gtc gag ata cga 211
Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp Glu Val Glu Ile Arg
25 30 35
cgc agc cct aac agc ctc cac gtc ctg cgt aac ggt agc gat att ctg 259
Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn Gly Ser Asp Ile Leu
40 45 50
cgc cgc aac gag cat cat tgc tgg gta ttt gag aat ttc aat aaa ccc 307
Arg Arg Asn Glu His His Cys Trp Val Phe Glu Asn Phe Asn Lys Pro
55 60 65
att gac cca cct gtt cga ttg ggt cct cgg gat atc atc tgc ccg agc 355
Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp Ile Ile Cys Pro Ser
70 75 80 85
gcc ttg gcc tgg gtt ctt caa cag cat tcc atc tcc cgg tcc tta tcc 403
Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile Ser Arg Ser Leu Ser
90 95 100
cac cac ctt cac gcg gat aag atc act gcg gga gag att gct gga cgc 451
His His Leu His Ala Asp Lys Ile Thr Ala Gly Glu Ile Ala Gly Arg
105 110 115
ccc acc tgg atc ctc cgt gag gaa cct act tca gga ggg cag gac cca 499
Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser Gly Gly Gln Asp Pro
120 125 130
agt cga ttg gtc agt ctt gaa atc gac cag gaa cac ggt gtc atc ctt 547
Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu His Gly Val Ile Leu

135	140	145	
gca gtg gag act gga caa gaa cga ctc gaa gcc acg gag att tct ttt			595
Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala Thr Glu Ile Ser Phe			
150	155	160	165
cct gac act ctt cct aat cct tcc tgg gac gga gcc tgg gaa cca ttc			643
Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly Ala Trp Glu Pro Phe			
	170	175	180
cat tat cca gat tcg aca cca cac act gcc cct gat gtt gct gaa ata			691
His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro Asp Val Ala Glu Ile			
	185	190	195
ccc ggt tac att cag tca ctg ccg ccg cag tct gaa gat cct cgc aga			739
Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser Glu Asp Pro Arg Arg			
	200	205	210
cta cga gtc ttc gtc aat gag ata gca ctc gaa ggt gat ttc cct gac			787
Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu Gly Asp Phe Pro Asp			
	215	220	225
tac cgt caa gga caa tct gtg cga ctt act ttg gga att agc tcc tcc			835
Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu Gly Ile Ser Ser Ser			
	230	235	240
cct gtg cca ctc gaa gga atg aca acc aga cgc cgg ggc cgg gta cgc			883
Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg Arg Gly Arg Val Arg			
	250	255	260
aac ctt ggg gaa gaa gct agt cca ggc gat gac ggt atg ccc cag tgg			931
Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp Gly Met Pro Gln Trp			
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cca atc ctg ctc act ggt gat ggg tgg acg gcg ctg gcc tac act ccc			979
Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala Leu Ala Tyr Thr Pro			
	280	285	290
atc cca aaa cgt gga gat gca gag atc cag ggg tgg ttt tat tat tcc			1027
Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly Trp Phe Tyr Tyr Ser			
	295	300	305
gcc tac gga att gtt gat gtt ccc aca gat cta cgg gta gag cgt att			1075
Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu Arg Val Glu Arg Ile			
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ttc gct ggt atc ggc aca agt ggc acc aac gag cgt ttg tgg cag gag			1123
Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu Arg Leu Trp Gln Glu			
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ata gac aat act tct tcg gct tat cac tcg gaa gat tgg tgg atc cgc			1171
Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu Asp Trp Trp Ile Arg			
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gat gtc gtt tta gac gtc acg ttg gat gga gct gtt ccg cct ccg ctt			1219
Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala Val Pro Pro Pro Leu			
	360	365	370
aga cgt gac gtc ttc act gct gtc gat cct att gtg gcg ggt gac aaa			1267
Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile Val Ala Gly Asp Lys			
	375	380	385

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Leu Trp Leu Cys Asp Val His Phe Pro Val Ala Arg Cys Trp Glu Thr	
390 395 400 405	
acg acc ggc cga tac ttg ggg cag act tta ktc cca gca cca ctg cga	1363
Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Xaa Pro Ala Pro Leu Arg	
410 415 420	
gat cga tcg tac gtc ctt gag ctg cac agc gac caa caa tta gga gcc	1411
Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp Gln Gln Leu Gly Ala	
425 430 435	
gta gcg gca agt ggg aag agt ggt tgg att ctc aca cct ggt caa gca	1459
Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu Thr Pro Gly Gln Ala	
440 445 450	
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Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro Thr Arg Ala Thr Asp	
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Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val Ala Val Arg Gly Gln	
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Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg Arg Thr Ala Leu Gly	
490 495 500	
cga gtt aat gcg acc ggt ggc gtc gac atc ggt gaa ctc ccg ccc aac	1651
Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly Glu Leu Pro Pro Asn	
505 510 515	
ggc tat acc atc agt tct gtg gtt cag atc ggt gat gaa tac atc gtg	1699
Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly Asp Glu Tyr Ile Val	
520 525 530	
ggc agg tgg gta gag gaa tac ccg ctc aac tcc aaa ctg gag gtc att	1747
Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser Lys Leu Glu Val Ile	
535 540 545	
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Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly Trp Lys Ser Lys Gly	
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acg gtt gct tat ctg tcg gaa gac act cac ata tgt ttc ttc gac cag	1843
Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile Cys Phe Phe Asp Gln	
570 575 580	
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Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile Ala Glu Gly His Gln	
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Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser Ile Val Leu Ile Tyr	
600 605 610	
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Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val Pro Thr Ser Val Ala	
615 620 625	

acc tat gac aat ggc acc tgg acg act atg ccg cta cag gaa gct cca 2035
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 Ala Glu Leu Ser

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 35 40 45
 Gly Ser Asp Ile Leu Arg Arg Asn Glu His His Cys Trp Val Phe Glu
 50 55 60
 Asn Phe Asn Lys Pro Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp
 65 70 75 80
 Ile Ile Cys Pro Ser Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile
 85 90 95
 Ser Arg Ser Leu Ser His His Leu His Ala Asp Lys Ile Thr Ala Gly
 100 105 110
 Glu Ile Ala Gly Arg Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser
 115 120 125
 Gly Gly Gln Asp Pro Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu
 130 135 140
 His Gly Val Ile Leu Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala
 145 150 155 160
 Thr Glu Ile Ser Phe Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly
 165 170 175
 Ala Trp Glu Pro Phe His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro
 180 185 190
 Asp Val Ala Glu Ile Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser
 195 200 205
 Glu Asp Pro Arg Arg Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu
 210 215 220

Gly Asp Phe Pro Asp Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu
 225 230 235 240
 Gly Ile Ser Ser Ser Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg
 245 250 255
 Arg Gly Arg Val Arg Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp
 260 265 270
 Gly Met Pro Gln Trp Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala
 275 280 285
 Leu Ala Tyr Thr Pro Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly
 290 295 300
 Trp Phe Tyr Tyr Ser Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu
 305 310 315 320
 Arg Val Glu Arg Ile Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu
 325 330 335
 Arg Leu Trp Gln Glu Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu
 340 345 350
 Asp Trp Trp Ile Arg Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala
 355 360 365
 Val Pro Pro Pro Leu Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile
 370 375 380
 Val Ala Gly Asp Lys Leu Trp Leu Cys Asp Val His Phe Pro Val Ala
 385 390 395 400
 Arg Cys Trp Glu Thr Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Xaa
 405 410 415
 Pro Ala Pro Leu Arg Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp
 420 425 430
 Gln Gln Leu Gly Ala Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu
 435 440 445
 Thr Pro Gly Gln Ala Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro
 450 455 460
 Thr Arg Ala Thr Asp Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val
 465 470 475 480
 Ala Val Arg Gly Gln Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg
 485 490 495
 Arg Thr Ala Leu Gly Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly
 500 505 510
 Glu Leu Pro Pro Asn Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly
 515 520 525
 Asp Glu Tyr Ile Val Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser
 530 535 540

Lys Leu Glu Val Ile Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly
 545 550 555 560
 Trp Lys Ser Lys Gly Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile
 565 570 575
 Cys Phe Phe Asp Gln Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile
 580 585 590
 Ala Glu Gly His Gln Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser
 595 600 605
 Ile Val Leu Ile Tyr Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val
 610 615 620
 Pro Thr Ser Val Ala Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro
 625 630 635 640
 Leu Gln Glu Ala Pro Ala Glu Leu Ser
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 <223> RXN00033

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 Met Ser Val Gln Gln 5
 agc ggg ttg ctc gaa cgt ctc ggc att ccc cga ccc ttg att ttc gga 163
 Ser Gly Leu Leu Glu Arg Leu Gly Ile Pro Arg Pro Leu Ile Phe Gly 20
 10 15
 ttt atc ggc ctc acc atc ttc atg atc ggt gac ggt gtc gaa acc aac 211
 Phe Ile Gly Leu Thr Ile Phe Met Ile Gly Asp Gly Val Glu Thr Asn 35
 25 30
 att ttg gaa cct ttc ctc agt tcc gaa cat ggt ttc agc gtt tcc ctc 259
 Ile Leu Glu Pro Phe Leu Ser Ser Glu His Gly Phe Ser Val Ser Leu 50
 40 45
 gcg gga acc ctg gtg act gtt tac ggt gtt gcc gtg gcg atc gca gca 307
 Ala Gly Thr Leu Val Thr Val Tyr Gly Val Ala Val Ala Ile Ala Ala 65
 55 60
 ttc ttc gcg gcg gca ctt tcg gac ctg tgg ggt cca cga aaa gtg atg 355
 Phe Phe Ala Ala Ala Leu Ser Asp Leu Trp Gly Pro Arg Lys Val Met 85
 70 75 80
 atc ctc ggt gct tca atc tgg atc gtc ttt gag ctg atc ttc ctc acc 403
 Ile Leu Gly Ala Ser Ile Trp Ile Val Phe Glu Leu Ile Phe Leu Thr

	90	95	100	
gtg gca ctg acc acc gac cat act tgg ttg atc ttc ctt gct tat ggt				451
Val Ala Leu Thr Thr Asp His Thr Trp Leu Ile Phe Leu Ala Tyr Gly				
	105	110	115	
ctc cgc ggc ttt ggt tat cca ttc ttc gcc tac gga ttc ttg gtg tgg				499
Leu Arg Gly Phe Gly Tyr Pro Phe Phe Ala Tyr Gly Phe Leu Val Trp				
	120	125	130	
atc acc gca act gcc tca cct aag caa ttg ggt acc ggt gtg ggt tgg				547
Ile Thr Ala Thr Ala Ser Pro Lys Gln Leu Gly Thr Gly Val Gly Trp				
	135	140	145	
ttc tac gtt gcc ttc tct gca ggt ctt cct acc ttg ggt gcg ctg gtt				595
Phe Tyr Val Ala Phe Ser Ala Gly Leu Pro Thr Leu Gly Ala Leu Val				
	150	155	160	165
gcc acc att tcc atg cag tac gtg aac ttg acc ttc tat gaa acg ttg				643
Ala Thr Ile Ser Met Gln Tyr Val Asn Leu Thr Phe Tyr Glu Thr Leu				
	170	175	180	
tgg gtt tcc ctc gtg ctg gtg gtc atc gga tcg ctc atc gca ctg ctg				691
Trp Val Ser Leu Val Leu Val Val Ile Gly Ser Leu Ile Ala Leu Leu				
	185	190	195	
gga gtg aag gaa cgt cgc gga cgc cac cca ctg gtt gcc aac ccc gac				739
Gly Val Lys Glu Arg Arg Gly Arg His Pro Leu Val Ala Asn Pro Asp				
	200	205	210	
gat gtg aag caa aca ctt ggc cag ggc ttc aaa ctt ctg cgc aat gat				787
Asp Val Lys Gln Thr Leu Gly Gln Gly Phe Lys Leu Leu Arg Asn Asp				
	215	220	225	
cga cgt gca cgt ttt gtc acc tac atc cgc acc atc aac tcc att ccg				835
Arg Arg Ala Arg Phe Val Thr Tyr Ile Arg Thr Ile Asn Ser Ile Pro				
	230	235	240	245
acc tac gcg atg gct gtg ttc ttc cca tca ttt ttc act gac gat ctg				883
Thr Tyr Ala Met Ala Val Phe Phe Pro Ser Phe Phe Thr Asp Asp Leu				
	250	255	260	
aag tgg cag cta agc tgg ttc ctc atc ctc acc act gta att tac gca				931
Lys Trp Gln Leu Ser Trp Phe Leu Ile Leu Thr Thr Val Ile Tyr Ala				
	265	270	275	
gtc aac ctg ccg ttc aat cct ttc ttc ggt agc ttc ggc gac cgc cac				979
Val Asn Leu Pro Phe Asn Pro Phe Phe Gly Ser Phe Gly Asp Arg His				
	280	285	290	
ggt tgg gca cga act gtg ttc tgg ggc gga tca atc ggt ggc gca gtc				1027
Gly Trp Ala Arg Thr Val Phe Trp Gly Gly Ser Ile Gly Gly Ala Val				
	295	300	305	
acc ctc gcg ttg gtt tac ttc att ccg atg ttc ggc gtt cag gct ggc				1075
Thr Leu Ala Leu Val Tyr Phe Ile Pro Met Phe Gly Val Gln Ala Gly				
	310	315	320	325
atg tcc aac ggt gtc gtt ttc gga atc acc atc gca gcc ggc gca ctc				1123
Met Ser Asn Gly Val Val Phe Gly Ile Thr Ile Ala Ala Gly Ala Leu				
	330	335	340	

ttt ggt gtg tcc ctc gcg ggc ttc gtg cca ctt tcc gca atc gct gtc 1171
 Phe Gly Val Ser Leu Ala Gly Phe Val Pro Leu Ser Ala Ile Ala Val
 345 350 355

tcc ctt gat ccc aag cac ccc ggc gca gcg atg gcc aca tac aac ctc 1219
 Ser Leu Asp Pro Lys His Pro Gly Ala Ala Met Ala Thr Tyr Asn Leu
 360 365 370

ggc gtt ggt ggc gct gta gct gtg gga ccg ctc ctg gtt gca gtc ttc 1267
 Gly Val Gly Gly Ala Val Ala Val Gly Pro Leu Leu Val Ala Val Phe
 375 380 385

cac cca ctg att ggt cca acc gga ttg atc ctg gtc atg atc gcc ctc 1315
 His Pro Leu Ile Gly Pro Thr Gly Leu Ile Leu Val Met Ile Ala Leu
 390 395 400 405

tac ctg ctc tcc ggt tgg atg act ctt caa ctt cgc ggc acc caa cca 1363
 Tyr Leu Leu Ser Gly Trp Met Thr Leu Gln Leu Arg Gly Thr Gln Pro
 410 415 420

gga ttc gac gga gtg cca gca ctt gct gaa gac gcc cac atc gaa gac 1411
 Gly Phe Asp Gly Val Pro Ala Leu Ala Glu Asp Ala His Ile Glu Asp
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 Leu Ala Asp Val Asn Ala Asn Ala
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<210> 72

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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Gly Val Glu Thr Asn Ile Leu Glu Pro Phe Leu Ser Ser Glu His Gly
 35 40 45

Phe Ser Val Ser Leu Ala Gly Thr Leu Val Thr Val Tyr Gly Val Ala
 50 55 60

Val Ala Ile Ala Ala Phe Phe Ala Ala Ala Leu Ser Asp Leu Trp Gly
 65 70 75 80

Pro Arg Lys Val Met Ile Leu Gly Ala Ser Ile Trp Ile Val Phe Glu
 85 90 95

Leu Ile Phe Leu Thr Val Ala Leu Thr Thr Asp His Thr Trp Leu Ile
 100 105 110

Phe Leu Ala Tyr Gly Leu Arg Gly Phe Gly Tyr Pro Phe Phe Ala Tyr
 115 120 125

Gly Phe Leu Val Trp Ile Thr Ala Thr Ala Ser Pro Lys Gln Leu Gly

130	135	140
Thr Gly Val Gly Trp Phe Tyr Val Ala Phe Ser Ala Gly Leu Pro Thr 145 150 155 160		
Leu Gly Ala Leu Val Ala Thr Ile Ser Met Gln Tyr Val Asn Leu Thr 165 170 175		
Phe Tyr Glu Thr Leu Trp Val Ser Leu Val Leu Val Val Ile Gly Ser 180 185 190		
Leu Ile Ala Leu Leu Gly Val Lys Glu Arg Arg Gly Arg His Pro Leu 195 200 205		
Val Ala Asn Pro Asp Asp Val Lys Gln Thr Leu Gly Gln Gly Phe Lys 210 215 220		
Leu Leu Arg Asn Asp Arg Arg Ala Arg Phe Val Thr Tyr Ile Arg Thr 225 230 235 240		
Ile Asn Ser Ile Pro Thr Tyr Ala Met Ala Val Phe Phe Pro Ser Phe 245 250 255		
Phe Thr Asp Asp Leu Lys Trp Gln Leu Ser Trp Phe Leu Ile Leu Thr 260 265 270		
Thr Val Ile Tyr Ala Val Asn Leu Pro Phe Asn Pro Phe Phe Gly Ser 275 280 285		
Phe Gly Asp Arg His Gly Trp Ala Arg Thr Val Phe Trp Gly Gly Ser 290 295 300		
Ile Gly Gly Ala Val Thr Leu Ala Leu Val Tyr Phe Ile Pro Met Phe 305 310 315 320		
Gly Val Gln Ala Gly Met Ser Asn Gly Val Val Phe Gly Ile Thr Ile 325 330 335		
Ala Ala Gly Ala Leu Phe Gly Val Ser Leu Ala Gly Phe Val Pro Leu 340 345 350		
Ser Ala Ile Ala Val Ser Leu Asp Pro Lys His Pro Gly Ala Ala Met 355 360 365		
Ala Thr Tyr Asn Leu Gly Val Gly Gly Ala Val Ala Val Gly Pro Leu 370 375 380		
Leu Val Ala Val Phe His Pro Leu Ile Gly Pro Thr Gly Leu Ile Leu 385 390 395 400		
Val Met Ile Ala Leu Tyr Leu Leu Ser Gly Trp Met Thr Leu Gln Leu 405 410 415		
Arg Gly Thr Gln Pro Gly Phe Asp Gly Val Pro Ala Leu Ala Glu Asp 420 425 430		
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<223> RXN00056
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Leu Leu Asn Arg Val 5															
1															
agt cgt att gca ggc gct tct gca atc aca cta tgc atc ggc tta acc 163															
Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu Cys Ile Gly Leu Thr 20															
10 15															
aca ata cta agc cct act tcc act gca caa agc ctc gaa cag atc acc 211															
Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser Leu Glu Gln Ile Thr 35															
25 30															
cct tta cct gaa tct gca atc gac ctc aac gcc gag att cac gta aac 259															
Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala Glu Ile His Val Asn 50															
40 45															
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Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly Ala Gln Asp Glu Ile 65															
55 60															
aca act atg tac gat tct cat gac ccc tac gag tac ttc gat acc ctc 355															
Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu Tyr Phe Asp Thr Leu 85															
70 75 80															
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Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala Leu Lys Arg Asp Pro 100															
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Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu Ala Ala Gln Ser Asp 115															
105 110															
ccc tac aaa att tac ata tca ggc ctc gaa atg ctt tca tgc atc aat 499															
Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met Leu Ser Cys Ile Asn 130															
120 125															
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Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn Gln Ala Ala Thr Lys 145															
135 140															
gca aat aat gag gct gtc gca cga tac cca ggc gat tcc ctt cgc aac 595															
Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly Asp Ser Leu Arg Asn 165															
150 155 160															
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Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp Asn Ala Leu Met Thr 180															
170 175															
ata cga atc ggg agc aat gga gct gaa aga att gca aca aac cac gag 691															

Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile Ala Thr Asn His Glu
 185 190 195

aca atc ggg gac ggt ccg gcc gat gaa aat gca atg gac cta ttc aat 739
 Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala Met Asp Leu Phe Asn
 200 205 210

aat gca caa ggc cga cag atc gga gcc gga ttc att aat agt aag gat 787
 Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe Ile Asn Ser Lys Asp
 215 220 225

gaa act agc gcg ctc gcg ata tgc gcg ctg tgg aca aat ctc ggt aga 835
 Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp Thr Asn Leu Gly Arg
 230 235 240 245

cta aaa act cta aaa taagcaagggt gccctctgat gct 873
 Leu Lys Thr Leu Lys
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<210> 74

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

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Cys Ile Gly Leu Thr Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser
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Leu Glu Gln Ile Thr Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala
 35 40 45

Glu Ile His Val Asn Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly
 50 55 60

Ala Gln Asp Glu Ile Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu
 65 70 75 80

Tyr Phe Asp Thr Leu Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala
 85 90 95

Leu Lys Arg Asp Pro Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu
 100 105 110

Ala Ala Gln Ser Asp Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met
 115 120 125

Leu Ser Cys Ile Asn Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn
 130 135 140

Gln Ala Ala Thr Lys Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly
 145 150 155 160

Asp Ser Leu Arg Asn Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp
 165 170 175

Asn Ala Leu Met Thr Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile
 180 185 190

Ala Thr Asn His Glu Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala
 195 200 205

Met Asp Leu Phe Asn Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe
 210 215 220

Ile Asn Ser Lys Asp Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp
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Thr Asn Leu Gly Arg Leu Lys Thr Leu Lys
 245 250

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 <223> FRXA00056

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 Leu Leu Asn Arg Val
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agt cgt att gca ggc gct tct gca atc aca cta tgc atc ggc tta acc 163
 Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu Cys Ile Gly Leu Thr
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aca ata cta agc cct act tcc act gca caa agc ctc gaa cag atc acc 211
 Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser Leu Glu Gln Ile Thr
 25 30 35

cct tta cct gaa tct gca atc gac ctc aac gcc gag att cac gta aac 259
 Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala Glu Ile His Val Asn
 40 45 50

aca agc gac att tca gct gaa cag atc ctt ggt gct caa gat gaa atc 307
 Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly Ala Gln Asp Glu Ile
 55 60 65

aca act atg tac gat tct cat gac ccc tac gag tac ttc gat acc ctc 355
 Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu Tyr Phe Asp Thr Leu
 70 75 80 85

acc gac atc gaa cag cgt tca ata ata gca gcg ctt aaa cgg gat ccg 403
 Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala Leu Lys Arg Asp Pro
 90 95 100

agt tca ctc caa caa cgc caa gaa acc cgt ctc gcg gca cag tcc gac 451
 Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu Ala Ala Gln Ser Asp
 105 110 115

ccc tac aaa att tac ata tca ggc ctc gaa atg ctt tca tgc atc aat 499
 Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met Leu Ser Cys Ile Asn

120	125	130	
cta gtt gat gtt gta tca tgc ggg att gca aac caa gca gca acc aaa			547
Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn Gln Ala Ala Thr Lys			
135	140	145	
gca aat aat gag gct gtc gca cga tac cca ggc gat tcc ctt cgc aac			595
Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly Asp Ser Leu Arg Asn			
150	155	160	165
ggc aaa ggc gat gca ttt cgg cat tgc tca tgg aac gct ctg atg acg			643
Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp Asn Ala Leu Met Thr			
170	175		180
ata cga atc ggg agc aat gga gct gaa aga att gca aca aac cac gag			691
Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile Ala Thr Asn His Glu			
185	190		195
aca atc ggg gac ggt ccg gcc gat gaa aat gca atg gac cta ttc aat			739
Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala Met Asp Leu Phe Asn			
200	205		210
aat gca caa ggc cga cag atc gga gcc gga ttc att aat agt aag gat			787
Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe Ile Asn Ser Lys Asp			
215	220		225
gaa act agc gcg ctc gcg ata tgc gcg ctg tgg aca aat ctc ggt aga			835
Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp Thr Asn Leu Gly Arg			
230	235	240	245
cta aaa act cta aaa taagcaaggt gccctctgat gct			873
Leu Lys Thr Leu Lys			
250			

<210> 76

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

Leu	Leu	Asn	Arg	Val	Ser	Arg	Ile	Ala	Gly	Ala	Ser	Ala	Ile	Thr	Leu
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Cys	Ile	Gly	Leu	Thr	Thr	Ile	Leu	Ser	Pro	Thr	Ser	Thr	Ala	Gln	Ser
			20					25					30		

Leu	Glu	Gln	Ile	Thr	Pro	Leu	Pro	Glu	Ser	Ala	Ile	Asp	Leu	Asn	Ala
		35					40					45			

Glu	Ile	His	Val	Asn	Thr	Ser	Asp	Ile	Ser	Ala	Glu	Gln	Ile	Leu	Gly
	50					55					60				

Ala	Gln	Asp	Glu	Ile	Thr	Thr	Met	Tyr	Asp	Ser	His	Asp	Pro	Tyr	Glu
65					70				75						80

Tyr	Phe	Asp	Thr	Leu	Thr	Asp	Ile	Glu	Gln	Arg	Ser	Ile	Ile	Ala	Ala
				85				90						95	

Leu	Lys	Arg	Asp	Pro	Ser	Ser	Leu	Gln	Arg	Gln	Glu	Thr	Arg	Leu	
			100					105				110			

Ala Ala Gln Ser Asp Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met
 115 120 125

Leu Ser Cys Ile Asn Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn
 130 135 140

Gln Ala Ala Thr Lys Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly
 145 150 155 160

Asp Ser Leu Arg Asn Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp
 165 170 175

Asn Ala Leu Met Thr Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile
 180 185 190

Ala Thr Asn His Glu Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala
 195 200 205

Met Asp Leu Phe Asn Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe
 210 215 220

Ile Asn Ser Lys Asp Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp
 225 230 235 240

Thr Asn Leu Gly Arg Leu Lys Thr Leu Lys
 245 250

<210> 77
 <211> 609
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(586)
 <223> RXN00067

<400> 77
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aatcattatt ttcctcactt tcagctaaaa ggaccatgca atg gta gac gct cag 115
 Met Val Asp Ala Gln
 1 5

cgc ccc aaa gca ggc atc ttc ggt agc cac aca gaa gaa aca tgg gtg 163
 Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr Glu Glu Thr Trp Val
 10 15 20

tgg ctc ggt aat gaa ctt ttc gac gag tcc ggc gag gtc atc gcc gac 211
 Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly Glu Val Ile Ala Asp
 25 30 35

gtt cgc tcc gac gtc ctc tac gtg gat cgc gaa cga cta ctc atc gaa 259
 Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu Arg Leu Leu Ile Glu
 40 45 50

tcc acc ccc ggc acc atg cgt ttt cgt tgc cgc gca aca ctg tcc ggg 307
 Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg Ala Thr Leu Ser Gly
 55 60 65

ggt gag gtc tat acg atg act cag aat tct ttc act gtg ggg gat ctc 355
 Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe Thr Val Gly Asp Leu 85
 70 75 80

act gcg gtg tgc ggg cgc cgg acg tat tca cta aaa agg gtg tcg ccg 403
 Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu Lys Arg Val Ser Pro 100
 90 95

tgg cgt aaa gaa cgc ctg atc acc aac aat ggg gtg gaa gtg gcg cgg 451
 Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly Val Glu Val Ala Arg 115
 105 110

ctt cgc ccg atg acc agc ggt aaa gtc gaa ttc att gtg ggc acc gcg 499
 Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe Ile Val Gly Thr Ala 130
 120 125

ggc agc gag gcg ttg ccg ttc gtc gac gca gta ttt ttg agc tgg gcg 547
 Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val Phe Leu Ser Trp Ala 145
 135 140

tgc gtc ctg gtg gat tcg gcc gtg cgc cgg ccg aaa att taaaagcttt 596
 Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro Lys Ile 160
 150 155

ttgcttatcg acg 609

<210> 78

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 78

Met Val Asp Ala Gln Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr
 1 5 10 15

Glu Glu Thr Trp Val Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly
 20 25 30

Glu Val Ile Ala Asp Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu
 35 40 45

Arg Leu Leu Ile Glu Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg
 50 55 60

Ala Thr Leu Ser Gly Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe
 65 70 75 80

Thr Val Gly Asp Leu Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu
 85 90 95

Lys Arg Val Ser Pro Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly
 100 105 110

Val Glu Val Ala Arg Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe
 115 120 125

Ile Val Gly Thr Ala Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val
 130 135 140

Phe Leu Ser Trp Ala Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro
 145 150 155 160

Lys Ile

<210> 79

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> FRXA00067

<400> 79

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aatcattatt ttcctcactt tcagctaaaa ggaccatgca atg gta gac gct cag 115
 Met Val Asp Ala Gln
 1 5

cgc ccc aaa gca ggc atc ttc ggt agc cac aca gaa gaa aca tgg gtg 163
 Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr Glu Glu Thr Trp Val
 10 15 20

tgg ctc ggt aat gaa ctt ttc gac gag tcc ggc gag gtc atc gcc gac 211
 Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly Glu Val Ile Ala Asp
 25 30 35

gtt cgc tcc gac gtc ctc tac gtg gat cgc gaa cga cta ctc atc gaa 259
 Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu Arg Leu Leu Ile Glu
 40 45 50

tcc acc ccc ggc acc atg cgt ttt cgt tgc cgc gca aca ctg tcc ggg 307
 Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg Ala Thr Leu Ser Gly
 55 60 65

ggg gag gtc tat acg atg act cag aat tct ttc act gtg ggg gat ctc 355
 Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe Thr Val Gly Asp Leu
 70 75 80 85

act gcg gtg tgc ggg cgc cgg acg tat tca cta aaa agg gtg tcg ccg 403
 Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu Lys Arg Val Ser Pro
 90 95 100

tgg cgt aaa gaa cgc ctg atc acc aac aat ggg gtg gaa gtg gcg cgg 451
 Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly Val Glu Val Ala Arg
 105 110 115

ctt cgc ccg atg acc agc ggt aaa gtc gaa ttc att gtg ggc acc gcg 499
 Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe Ile Val Gly Thr Ala
 120 125 130

ggc agc gag gcg ttg ccg ttc gtc gac gca gta ttt ttg agc tgg gcg 547
 Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val Phe Leu Ser Trp Ala
 135 140 145

tgc gtc ctg gtg gat tcg gcc gtg cgc cgg ccg aaa att taaaagcttt 596

Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro Lys Ile
 150 155 160

ttgcttatcg acg

609

<210> 80
 <211> 162
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 80
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Glu Glu Thr Trp Val Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly
 20 25 30

Glu Val Ile Ala Asp Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu
 35 40 45

Arg Leu Leu Ile Glu Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg
 50 55 60

Ala Thr Leu Ser Gly Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe
 65 70 75 80

Thr Val Gly Asp Leu Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu
 85 90 95

Lys Arg Val Ser Pro Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly
 100 105 110

Val Glu Val Ala Arg Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe
 115 120 125

Ile Val Gly Thr Ala Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val
 130 135 140

Phe Leu Ser Trp Ala Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro
 145 150 155 160

Lys Ile

<210> 81
 <211> 1485
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1462)
 <223> RXN00077

<400> 81
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ctttccggga taaaattgc aacgcactac actgagcagt atg aat gat gag aat 115
 Met Asn Asp Glu Asn

	1	5	
att caa agc tcc aac tat cag cca ttc ccg agt ttt gac gat tgg aaa			163
Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser Phe Asp Asp Trp Lys			
	10	15	20
cag atc gag gtg tcg ctc tta gat gtc atc gaa tcc tca cgc cat ttt			211
Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu Ser Ser Arg His Phe			
	25	30	35
tct gat ttg aaa gat agc act gat cgt tct gcg tta gat gct gcg cta			259
Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala Leu Asp Ala Ala Leu			
	40	45	50
gag aga gca aaa aga gct gcc gca gtt gat acc aat gcc ata gaa gga			307
Glu Arg Ala Lys Arg Ala Ala Val Asp Thr Asn Ala Ile Glu Gly			
	55	60	65
atc ttc caa act gat cgc ggt ttt acc cat aca gtt gca acg cag gta			355
Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr Val Ala Thr Gln Val			
	70	75	80
ggg gct tgg gag caa caa atg gcg atg aaa ggc aaa cat gtt aag cct			403
Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly Lys His Val Lys Pro			
	90	95	100
gcg ttt gac gat act cta gaa ggc ttt gag tat gtt ctc gat gca gta			451
Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr Val Leu Asp Ala Val			
	105	110	115
act ggt aga act cca atc tct cag caa tgg att aga aat ttg cac gcc			499
Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile Arg Asn Leu His Ala			
	120	125	130
gtc att ctg cgg agc caa gaa agc cac gag gtt ttt aca gcc gtt gga			547
Val Ile Leu Arg Ser Gln Glu Ser His Glu Val Phe Thr Ala Val Gly			
	135	140	145
gtc caa aat cag gcg ctt cag aaa ggc gag tat aaa act cag cca aat			595
Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr Lys Thr Gln Pro Asn			
	150	155	160
agt cca cag cgc tca gat gga tct gta cat gca tac gcc cca gtt gaa			643
Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala Tyr Ala Pro Val Glu			
	170	175	180
gat act cct gct gaa atg gct aga ttt att tca gaa ctt gaa tct aag			691
Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser Glu Leu Glu Ser Lys			
	185	190	195
gaa ttc tta gca gcc gag aag gtt att caa gct gcc tat gcc cac tat			739
Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala Ala Tyr Ala His Tyr			
	200	205	210
gct ttc gta tgt att cat cct ttt gca gat ggg aat gga cga gtt gca			787
Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly Asn Gly Arg Val Ala			
	215	220	225
cga gcc ttg gct agt gtt ttt cta tac aaa gat cct ggt gtc cct ctc			835
Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp Pro Gly Val Pro Leu			
	230	235	240
			245

gta atc tac caa gat caa cgc aga gat tac atc cat gct cta gaa gca 883
 Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile His Ala Leu Glu Ala
 250 255 260

gcg gac aag aat aac ccg ctc ctg ctg att aga ttc ttt gct gaa cga 931
 Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg Phe Phe Ala Glu Arg
 265 270 275

gtg acc gat act att aac tct att atc gtt gat ctc act acc ccg atc 979
 Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp Leu Thr Thr Pro Ile
 280 285 290

gcg ggt aaa tct ggt tcg gct aag ctt tcg gat gcg cta cgc ccc act 1027
 Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp Ala Leu Arg Pro Thr
 295 300 305

cgc gta tta cca gaa tta cat gat gct gca cat agg ctc caa gaa agt 1075
 Arg Val Leu Pro Glu Leu His Asp Ala Ala His Arg Leu Gln Glu Ser
 310 315 320 325

tta ttt aca gaa atc cga tct cga ttg gat gaa gaa gga aaa agg aat 1123
 Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu Glu Gly Lys Arg Asn
 330 335 340

ggg ttg gag ttt cta ctt caa cgg att ttt atc ggt tcc cca ttc aat 1171
 Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile Gly Ser Pro Phe Asn
 345 350 355

ctg cca gag ggc tat aac gct ttc cct gat agc tat tgt ctg acc tta 1219
 Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser Tyr Cys Leu Thr Leu
 360 365 370

gct ttc aat agc aac tct cca aaa caa atc ttc cac ccg cta tcc ata 1267
 Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe His Pro Leu Ser Ile
 375 380 385

gta ata gca gct cga gat ggg aaa aga gcg agc agc gac ctc gtg gca 1315
 Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser Ser Asp Leu Val Ala
 390 395 400 405

gct act tct att gga tac aac ttt cac gct tac gga cgt gaa gtc gag 1363
 Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr Gly Arg Glu Val Glu
 410 415 420

cct gtt gtt act gaa agc ttt cga gaa cgt gtg aaa att tac gcc gac 1411
 Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val Lys Ile Tyr Ala Asp
 425 430 435

ggg att gta gat cac ttc tta acc gaa ctg gct aaa aag ttt caa cag 1459
 Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala Lys Lys Phe Gln Gln
 440 445 450

aat taattagcct atctcggcctt tcg 1485
 Asn

<210> 82
 <211> 454
 <212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Asn Asp Glu Asn Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser
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 Phe Asp Asp Trp Lys Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu
 20 25 30
 Ser Ser Arg His Phe Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala
 35 40 45
 Leu Asp Ala Ala Leu Glu Arg Ala Lys Arg Ala Ala Val Asp Thr
 50 55 60
 Asn Ala Ile Glu Gly Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr
 65 70 75 80
 Val Ala Thr Gln Val Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly
 85 90 95
 Lys His Val Lys Pro Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr
 100 105 110
 Val Leu Asp Ala Val Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile
 115 120 125
 Arg Asn Leu His Ala Val Ile Leu Arg Ser Gln Glu Ser His Glu Val
 130 135 140
 Phe Thr Ala Val Gly Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr
 145 150 155 160
 Lys Thr Gln Pro Asn Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala
 165 170 175
 Tyr Ala Pro Val Glu Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser
 180 185 190
 Glu Leu Glu Ser Lys Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala
 195 200 205
 Ala Tyr Ala His Tyr Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly
 210 215 220
 Asn Gly Arg Val Ala Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp
 225 230 235 240
 Pro Gly Val Pro Leu Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile
 245 250 255
 His Ala Leu Glu Ala Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg
 260 265 270
 Phe Phe Ala Glu Arg Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp
 275 280 285
 Leu Thr Thr Pro Ile Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp
 290 295 300
 Ala Leu Arg Pro Thr Arg Val Leu Pro Glu Leu His Asp Ala Ala His

55	60	65	
atc ttc caa act gat cgc ggt ttt acc cat aca gtt gca acg cag gta Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr Val Ala Thr Gln Val 70 75 80 85			355
ggg gct tgg gag caa caa atg gcg atg aaa ggc aaa cat gtt aag cct Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly Lys His Val Lys Pro 90 95 100			403
gcg ttt gac gat act cta gaa ggc ttt gag tat gtt ctc gat gca gta Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr Val Leu Asp Ala Val 105 110 115			451
act ggt aga act cca atc tct cag caa tgg att aga aat ttg cac gcc Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile Arg Asn Leu His Ala 120 125 130			499
gtc att ctg cgg agc caa gaa agc cac gag gtt ttt aca gcc gtt gga Val Ile Leu Arg Ser Gln Glu Ser His Glu Val Phe Thr Ala Val Gly 135 140 145			547
gtc caa aat cag gcg ctt cag aaa ggc gag tat aaa act cag cca aat Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr Lys Thr Gln Pro Asn 150 155 160 165			595
agt cca cag cgc tca gat gga tct gta cat gca tac gcc cca gtt gaa Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala Tyr Ala Pro Val Glu 170 175 180			643
gat act cct gct gaa atg gct aga ttt att tca gaa ctt gaa tct aag Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser Glu Leu Glu Ser Lys 185 190 195			691
gaa ttc tta gca gcc gag aag gtt att caa gct gcc tat gcc cac tat Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala Ala Tyr Ala His Tyr 200 205 210			739
gct ttc gta tgt att cat cct ttt gca gat ggg aat gga cga gtt gca Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly Asn Gly Arg Val Ala 215 220 225			787
cga gcc ttg gct agt gtt ttt cta tac aaa gat cct ggt gtc cct ctc Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp Pro Gly Val Pro Leu 230 235 240 245			835
gta atc tac caa gat caa cgc aga gat tac atc cat gct cta gaa gca Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile His Ala Leu Glu Ala 250 255 260			883
gcg gac aag aat aac ccg ctc ctg ctg att aga ttc ttt gct gaa cga Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg Phe Phe Ala Glu Arg 265 270 275			931
gtg acc gat act att aac tct att atc gtt gat ctc act acc ccg atc Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp Leu Thr Thr Pro Ile 280 285 290			979
gcg ggt aaa tct ggt tcg gct aag ctt tcg gat gcg cta cgc ccc act Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp Ala Leu Arg Pro Thr 295 300 305			1027

cgc gta tta cca gaa tta cat gat gct gca cat agg ctc caa gaa agt 1075
 Arg Val Leu Pro Glu Leu His Asp Ala Ala His Arg Leu Gln Glu Ser
 310 315 320 325
 tta ttt aca gaa atc cga tct cga ttg gat gaa gaa gga aaa agg aat 1123
 Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu Glu Gly Lys Arg Asn
 330 335 340
 ggg ttg gag ttt cta ctt caa cgg att ttt atc ggt tcc cca ttc aat 1171
 Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile Gly Ser Pro Phe Asn
 345 350 355
 ctg cca gag ggc tat aac gct ttc cct gat agc tat tgt ctg acc tta 1219
 Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser Tyr Cys Leu Thr Leu
 360 365 370
 gct ttc aat agc aac tct cca aaa caa atc ttc cac ccg cta tcc ata 1267
 Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe His Pro Leu Ser Ile
 375 380 385
 gta ata gca gct cga gat ggg aaa aga gcg agc agc gac ctc gtg gca 1315
 Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser Ser Asp Leu Val Ala
 390 395 400 405
 gct act tct att gga tac aac ttt cac gct tac gga cgt gaa gtc gag 1363
 Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr Gly Arg Glu Val Glu
 410 415 420
 cct gtt gtt act gaa agc ttt cga gaa cgt gtg aaa att tac gcc gac 1411
 Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val Lys Ile Tyr Ala Asp
 425 430 435
 ggg att gta gat cac ttc tta acc gaa ctg gct aaa aag ttt caa cag 1459
 Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala Lys Lys Phe Gln Gln
 440 445 450
 aat taattagcct atctcggctt tcg 1485
 Asn

<210> 84

<211> 454

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Asn Asp Glu Asn Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser
 1 5 10 15

Phe Asp Asp Trp Lys Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu
 20 25 30

Ser Ser Arg His Phe Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala
 35 40 45

Leu Asp Ala Ala Leu Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr
 50 55 60

Asn Ala Ile Glu Gly Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr

65		70		75		80
Val Ala Thr Gln	Val Gly Ala Trp Glu	Gln Gln Met Ala Met Lys Gly				
	85		90			95
Lys His Val Lys	Pro Ala Phe Asp Asp	Thr Leu Glu Gly Phe Glu Tyr				
	100		105			110
Val Leu Asp Ala	Val Thr Gly Arg Thr	Pro Ile Ser Gln Gln Trp Ile				
	115		120			125
Arg Asn Leu His	Ala Val Ile Leu Arg Ser	Gln Glu Ser His Glu Val				
	130		135			140
Phe Thr Ala Val	Gly Val Gln Asn Gln Ala	Leu Gln Lys Gly Glu Tyr				
	145		150			155
Lys Thr Gln Pro	Asn Ser Pro Gln Arg Ser	Asp Gly Ser Val His Ala				
	165		170			175
Tyr Ala Pro Val	Glu Asp Thr Pro Ala	Glu Met Ala Arg Phe Ile Ser				
	180		185			190
Glu Leu Glu Ser	Lys Glu Phe Leu Ala	Ala Glu Lys Val Ile Gln Ala				
	195		200			205
Ala Tyr Ala His	Tyr Ala Phe Val Cys Ile	His Pro Phe Ala Asp Gly				
	210		215			220
Asn Gly Arg Val	Ala Arg Ala Leu Ala	Ser Val Phe Leu Tyr Lys Asp				
	225		230			235
Pro Gly Val Pro	Leu Val Ile Tyr Gln	Asp Gln Arg Arg Asp Tyr Ile				
	245		250			255
His Ala Leu Glu	Ala Ala Asp Lys Asn	Asn Pro Leu Leu Leu Ile Arg				
	260		265			270
Phe Phe Ala Glu	Arg Val Thr Asp Thr	Ile Asn Ser Ile Ile Val Asp				
	275		280			285
Leu Thr Thr Pro	Ile Ala Gly Lys Ser	Gly Ser Ala Lys Leu Ser Asp				
	290		295			300
Ala Leu Arg Pro	Thr Arg Val Leu Pro	Glu Leu His Asp Ala Ala His				
	305		310			315
Arg Leu Gln Glu	Ser Leu Phe Thr Glu	Ile Arg Ser Arg Leu Asp Glu				
	325		330			335
Glu Gly Lys Arg	Asn Gly Leu Glu Phe	Leu Leu Gln Arg Ile Phe Ile				
	340		345			350
Gly Ser Pro Phe	Asn Leu Pro Glu Gly	Tyr Asn Ala Phe Pro Asp Ser				
	355		360			365
Tyr Cys Leu Thr	Leu Ala Phe Asn Ser	Asn Ser Pro Lys Gln Ile Phe				
	370		375			380
His Pro Leu Ser	Ile Val Ile Ala Ala	Arg Asp Gly Lys Arg Ala Ser				
	385		390			395
						400

Ser Asp Leu Val Ala Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr
 405 410 415

Gly Arg Glu Val Glu Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val
 420 425 430

Lys Ile Tyr Ala Asp Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala
 435 440 445

Lys Lys Phe Gln Gln Asn
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<210> 85
 <211> 1653
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1630)
 <223> RXN00080

<400> 85
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gacttaatct tccttcogga cttttgggtg gtggctttta atg gat att ttg tcc 115
 Met Asp Ile Leu Ser
 1 5

ctc ttg atg gaa ggt ttc gcc ggc gcg cta acg ccg atg aac ctc ctc 163
 Leu Leu Met Glu Gly Phe Ala Gly Ala Leu Thr Pro Met Asn Leu Leu
 10 15 20

tgg gtg att gtc ggc tgt ttg ctc ggc acc gcg gtt ggc gtc atg cct 211
 Trp Val Ile Val Gly Cys Leu Leu Gly Thr Ala Val Gly Val Met Pro
 25 30 35

ggt ctt gga tcc tcc atg gct gtg gcg ctg ctg ctg cca atg acc ttc 259
 Gly Leu Gly Ser Ser Met Ala Val Ala Leu Leu Leu Pro Met Thr Phe
 40 45 50

gcg ctt gat cca act gcc gcg ttc att atg ttc tct ggc gta tat ttc 307
 Ala Leu Asp Pro Thr Ala Ala Phe Ile Met Phe Ser Gly Val Tyr Phe
 55 60 65

ggt ggt ctc ttc ggt gac tcc acg atg gca att ttg atg aac acc cca 355
 Gly Gly Leu Phe Gly Asp Ser Thr Met Ala Ile Leu Met Asn Thr Pro
 70 75 80 85

ggt cag gca tcg gca atc gcc tca aca ttc gag ggc cac cgc atg gct 403
 Gly Gln Ala Ser Ala Ile Ala Ser Thr Phe Glu Gly His Arg Met Ala
 90 95 100

ctt aac ggc cgt gcg cca cag gct ctg gct acc gca gcg atc ggt gcc 451
 Leu Asn Gly Arg Ala Pro Gln Ala Leu Ala Thr Ala Ala Ile Gly Ala
 105 110 115

ttc atc ggc ggt atc gtc tcc tcc ttc atc gtg gtc ttc ctc gca cca 499
 Phe Ile Gly Gly Ile Val Ser Ser Phe Ile Val Val Phe Leu Ala Pro

120	125	130	
acc ctg gcg gaa ctg tcc acc gca ttc ggc ccc gcc gag tac ttc gca			547
Thr Leu Ala Glu Leu Ser Thr Ala Phe Gly Pro Ala Glu Tyr Phe Ala			
135	140	145	
ctg gca ctc ttc gcg ttc gtc gcc acc tcc tcc gtg gtg tcc gac tcc			595
Leu Ala Leu Phe Ala Phe Val Ala Thr Ser Ser Val Val Ser Asp Ser			
150	155	160	165
gtg ttt aag gga ctt gcg tcc ctc att ttc ggc ctc ggc att gcg acc			643
Val Phe Lys Gly Leu Ala Ser Leu Ile Phe Gly Leu Gly Ile Ala Thr			
	170	175	180
atc ggc atc gat tcc gtc acc ggc atc gag cgc ttc acg ctc ggg gca			691
Ile Gly Ile Asp Ser Val Thr Gly Ile Glu Arg Phe Thr Leu Gly Ala			
	185	190	195
ccg cag ctt ttc gac gga att tcc ctc gtt act gtt acc gtc gcg att			739
Pro Gln Leu Phe Asp Gly Ile Ser Leu Val Thr Val Thr Val Ala Ile			
	200	205	210
ttg gca ctg gga gaa gtg ttt tac att gca gcc cgc gca cgc cgt gac			787
Leu Ala Leu Gly Glu Val Phe Tyr Ile Ala Ala Arg Ala Arg Arg Asp			
	215	220	225
aaa gca aat ctg gag acg cgc tct gca ggc cgt ccg tgg ctt acc gga			835
Lys Ala Asn Leu Glu Thr Arg Ser Ala Gly Arg Pro Trp Leu Thr Gly			
	230	235	240
acg gaa ttc aaa gaa gcc gct cca gcc tgg gca cgc gga acc atc att			883
Thr Glu Phe Lys Glu Ala Ala Pro Ala Trp Ala Arg Gly Thr Ile Ile			
	250	255	260
ggt ctg cct ttc ggt gtg atc cct gtt ggt gga tct gaa gtt cca acc			931
Gly Leu Pro Phe Gly Val Ile Pro Val Gly Gly Ser Glu Val Pro Thr			
	265	270	275
ttc ttg gct tac tcc acc gag cgc gca ttg gat aaa cga cgc aaa gat			979
Phe Leu Ala Tyr Ser Thr Glu Arg Ala Leu Asp Lys Arg Arg Lys Asp			
	280	285	290
ccg cag ttc ggc gat aaa ggt gca atc cga gga ctc gct gct cct gaa			1027
Pro Gln Phe Gly Asp Lys Gly Ala Ile Arg Gly Leu Ala Ala Pro Glu			
	295	300	305
gct gca ggt aac gcc acc aca ggc atg gcg atg ggc gct ctt ctt gcc			1075
Ala Ala Gly Asn Ala Thr Thr Gly Met Ala Met Gly Ala Leu Leu Ala			
	310	315	320
ctg ggt ctc cca gtc tct gca act gcg gcc atc atg ttg gca gcg ttc			1123
Leu Gly Leu Pro Val Ser Ala Thr Ala Ala Ile Met Leu Ala Ala Phe			
	330	335	340
cgc cag tac gga atc cag ccc gga cca cta ctc ttc gat cgc aac cct			1171
Arg Gln Tyr Gly Ile Gln Pro Gly Pro Leu Leu Phe Asp Arg Asn Pro			
	345	350	355
gaa ctt gtc tgg gca ctt ctt gcc agc ttc ttc atc gcg atg atc gtc			1219
Glu Leu Val Trp Ala Leu Leu Ala Ser Phe Phe Ile Ala Met Ile Val			
	360	365	370

ctg ctg ttc atc aac ctg ccg ttc gca cag ctg tgg gca aag ctc ctg 1267
 Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala Lys Leu Leu
 375 380 385

 ctc att cca aac cac tac ctc tac tcc ggc atc gca ttg ttc tgt ggc 1315
 Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu Phe Cys Gly
 390 395 400 405

 ctg ggc att tac gcc acc tcc ggc gca gtg ttc gac ctg ctc atg ctg 1363
 Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu Leu Met Leu
 410 415 420

 ctc ggc atc ggt gtc gtg gct ttg atc atg cgt cgc tac ggt tac ccg 1411
 Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr Gly Tyr Pro
 425 430 435

 ctg gca ccg ctg atg atc ggt atg gtt ctt gga cct ttg gct gaa acc 1459
 Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu Ala Glu Thr
 440 445 450

 tcc ctc cgc gac gca cta ctg tcc tcg gtt ggc gat ttc tcc atc ctc 1507
 Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe Ser Ile Leu
 455 460 465

 gtc tcc agc ccc atc acc tgg tct ctc tac gca gtg ctc gcc atc ttc 1555
 Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu Ala Ile Phe
 470 475 480 485

 atc gcg gtc agt gtc atc act gca atc cgc ggt cgt cgc aag cac ctg 1603
 Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg Lys His Leu
 490 495 500

 act tct cag ctc gaa acc atc gac gct taaagtcccc gtatagaaac 1650
 Thr Ser Gln Leu Glu Thr Ile Asp Ala
 505 510

 agg 1653

<210> 86

<211> 510

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

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Pro Met Asn Leu Leu Trp Val Ile Val Gly Cys Leu Leu Gly Thr Ala
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Val Gly Val Met Pro Gly Leu Gly Ser Ser Met Ala Val Ala Leu Leu
 35 40 45

Leu Pro Met Thr Phe Ala Leu Asp Pro Thr Ala Ala Phe Ile Met Phe
 50 55 60

Ser Gly Val Tyr Phe Gly Gly Leu Phe Gly Asp Ser Thr Met Ala Ile
 65 70 75 80

Leu Met Asn Thr Pro Gly Gln Ala Ser Ala Ile Ala Ser Thr Phe Glu
 85 90 95
 Gly His Arg Met Ala Leu Asn Gly Arg Ala Pro Gln Ala Leu Ala Thr
 100 105 110
 Ala Ala Ile Gly Ala Phe Ile Gly Gly Ile Val Ser Ser Phe Ile Val
 115 120 125
 Val Phe Leu Ala Pro Thr Leu Ala Glu Leu Ser Thr Ala Phe Gly Pro
 130 135 140
 Ala Glu Tyr Phe Ala Leu Ala Leu Phe Ala Phe Val Ala Thr Ser Ser
 145 150 155 160
 Val Val Ser Asp Ser Val Phe Lys Gly Leu Ala Ser Leu Ile Phe Gly
 165 170 175
 Leu Gly Ile Ala Thr Ile Gly Ile Asp Ser Val Thr Gly Ile Glu Arg
 180 185 190
 Phe Thr Leu Gly Ala Pro Gln Leu Phe Asp Gly Ile Ser Leu Val Thr
 195 200 205
 Val Thr Val Ala Ile Leu Ala Leu Gly Glu Val Phe Tyr Ile Ala Ala
 210 215 220
 Arg Ala Arg Arg Asp Lys Ala Asn Leu Glu Thr Arg Ser Ala Gly Arg
 225 230 235 240
 Pro Trp Leu Thr Gly Thr Glu Phe Lys Glu Ala Ala Pro Ala Trp Ala
 245 250 255
 Arg Gly Thr Ile Ile Gly Leu Pro Phe Gly Val Ile Pro Val Gly Gly
 260 265 270
 Ser Glu Val Pro Thr Phe Leu Ala Tyr Ser Thr Glu Arg Ala Leu Asp
 275 280 285
 Lys Arg Arg Lys Asp Pro Gln Phe Gly Asp Lys Gly Ala Ile Arg Gly
 290 295 300
 Leu Ala Ala Pro Glu Ala Ala Gly Asn Ala Thr Thr Gly Met Ala Met
 305 310 315 320
 Gly Ala Leu Leu Ala Leu Gly Leu Pro Val Ser Ala Thr Ala Ala Ile
 325 330 335
 Met Leu Ala Ala Phe Arg Gln Tyr Gly Ile Gln Pro Gly Pro Leu Leu
 340 345 350
 Phe Asp Arg Asn Pro Glu Leu Val Trp Ala Leu Leu Ala Ser Phe Phe
 355 360 365
 Ile Ala Met Ile Val Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu
 370 375 380
 Trp Ala Lys Leu Leu Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile
 385 390 395 400
 Ala Leu Phe Cys Gly Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe

405	410	415
Asp Leu Leu Met Leu Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg 420 425 430		
Arg Tyr Gly Tyr Pro Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly 435 440 445		
Pro Leu Ala Glu Thr Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly 450 455 460		
Asp Phe Ser Ile Leu Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala 465 470 475 480		
Val Leu Ala Ile Phe Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly 485 490 495		
Arg Arg Lys His Leu Thr Ser Gln Leu Glu Thr Ile Asp Ala 500 505 510		

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 <211> 543
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(520)
 <223> FRXA00080

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 Met Ile Val Leu Leu 5
 1 5
 ttc atc aac ctg ccg ttc gca cag ctg tgg gca aag ctc ctg ctc att 163
 Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala Lys Leu Leu Leu Ile 20
 10 15 20
 cca aac cac tac ctc tac tcc ggc atc gca ttg ttc tgt ggc ctg ggc 211
 Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu Phe Cys Gly Leu Gly 35
 25 30 35
 att tac gcc acc tcc ggc gca gtg ttc gac ctg ctc atg ctg ctc ggc 259
 Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu Leu Met Leu Leu Gly 50
 40 45 50
 atc ggt gtc gtg gct ttg atc atg cgt cgc tac ggt tac ccg ctg gca 307
 Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr Gly Tyr Pro Leu Ala 65
 55 60 65
 ccg ctg atg atc ggt atg gtt ctt gga cct ttg gct gaa acc tcc ctc 355
 Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu Ala Glu Thr Ser Leu 85
 70 75 80 85
 cgc gac gca cta ctg tcc tcg gtt ggc gat ttc tcc atc ctc gtc tcc 403
 Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe Ser Ile Leu Val Ser 100
 90 95 100

agc ccc atc acc tgg tct ctc tac gca gtg ctc gcc atc ttc atc gcg 451
Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu Ala Ile Phe Ile Ala
105 110 115

gtc agt gtc atc act gca atc cgc ggt cgt cgc aag cac ctg act tct 499
Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg Lys His Leu Thr Ser
120 125 130

cag ctc gaa acc atc gac gct taaagtcccc gtatagaaac agg 543
Gln Leu Glu Thr Ile Asp Ala
135 140

<210> 88

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

Met Ile Val Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala
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Lys Leu Leu Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu
20 25 30

Phe Cys Gly Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu
35 40 45

Leu Met Leu Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr
50 55 60

Gly Tyr Pro Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu
65 70 75 80

Ala Glu Thr Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe
85 90 95

Ser Ile Leu Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu
100 105 110

Ala Ile Phe Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg
115 120 125

Lys His Leu Thr Ser Gln Leu Glu Thr Ile Asp Ala
130 135 140

<210> 89

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXN00087

<400> 89

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                                   Met Ile Gly Gly Ile
                                   1 5

atc ggc ctc att ttg tgc gtg atc atc atg gcc gaa aaa ctt gcc atc 163
Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala Glu Lys Leu Ala Ile
      10 15 20

ctc gag gat ccc ggt cac atc acc agc tgc gat ttc aat gca gtc cta 211
Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp Phe Asn Ala Val Leu
      25 30 35

gct tgt ggc gat gtc atg cgt tcc ggc caa gct aac gcg ttc ggc atc 259
Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala Asn Ala Phe Gly Ile
      40 45 50

ccg aat ccg ctc atc ggc atc gcc ggt ttc gcc gct gtc gcc atc atc 307
Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala Ala Val Ala Ile Ile
      55 60 65

ggc gcc ggc atc ctc gcg ggc ggc ggg ttc cgc ggt tgg ttc tgg ttc 355
Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg Gly Trp Phe Trp Phe
      70 75 80 85

ggc gcc cag gcc gga ctc act ttt gcc atg atg ttc tgc cac tgg ctc 403
Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met Phe Cys His Trp Leu
      90 95 100

gcc tac caa tcc atg tcc gtc atc cgc gcg ctc tgc cct tac tgc atg 451
Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu Cys Pro Tyr Cys Met
      105 110 115

ggc gtg tgg acc gta tgc atc atc atg ttc gtg ctg gtc act gca tgg 499
Gly Val Trp Thr Val Ser Ile Ile Met Phe Val Leu Val Thr Ala Trp
      120 125 130

aat gtg aaa act ttc agc ggc tcc gac agc acg ttc gtc aac gca ctg 547
Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr Phe Val Asn Ala Leu
      135 140 145

tac aaa tac aag tgg gtc atc gcg atc gtc tgg ctg ctg ctc atc gca 595
Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp Leu Leu Leu Ile Ala
      150 155 160 165

gcc gca gct gtg tgg tca ttc cgc tac atg ttc taggcattta aggctttcag 648
Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
      170 175

gcc 651

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<210> 90

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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Glu Lys Leu Ala Ile Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp

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20										25					30				
Phe	Asn	Ala	Val	Leu	Ala	Cys	Gly	Asp	Val	Met	Arg	Ser	Gly	Gln	Ala				
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Asn	Ala	Phe	Gly	Ile	Pro	Asn	Pro	Leu	Ile	Gly	Ile	Ala	Gly	Phe	Ala				
	50					55					60								
Ala	Val	Ala	Ile	Ile	Gly	Ala	Gly	Ile	Leu	Ala	Gly	Gly	Gly	Phe	Arg				
	65				70				75						80				
Gly	Trp	Phe	Trp	Phe	Gly	Ala	Gln	Ala	Gly	Leu	Thr	Phe	Ala	Met	Met				
				85					90					95					
Phe	Cys	His	Trp	Leu	Ala	Tyr	Gln	Ser	Met	Ser	Val	Ile	Arg	Ala	Leu				
			100					105					110						
Cys	Pro	Tyr	Cys	Met	Gly	Val	Trp	Thr	Val	Ser	Ile	Ile	Met	Phe	Val				
		115					120					125							
Leu	Val	Thr	Ala	Trp	Asn	Val	Lys	Thr	Phe	Ser	Gly	Ser	Asp	Ser	Thr				
	130					135					140								
Phe	Val	Asn	Ala	Leu	Tyr	Lys	Tyr	Lys	Trp	Val	Ile	Ala	Ile	Val	Trp				
	145				150				155						160				
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<210> 91

<211> 651

<212> DNA

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<220>

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<222> (101)..(628)

<223> FRXA00087

<400> 91

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				Met	Ile	Gly	Gly	Ile	
				1				5	

atc	ggc	ctc	att	ttg	tcg	gtg	atc	atc	atg	gcc	gaa	aaa	ctt	gcc	atc	163
Ile	Gly	Leu	Ile	Leu	Ser	Val	Ile	Ile	Met	Ala	Glu	Lys	Leu	Ala	Ile	
			10					15						20		

ctc	gag	gat	ccc	ggt	cac	atc	acc	agc	tgc	gat	ttc	aat	gca	gtc	cta	211
Leu	Glu	Asp	Pro	Gly	His	Ile	Thr	Ser	Cys	Asp	Phe	Asn	Ala	Val	Leu	
			25					30					35			

gct	tgt	ggc	gat	gtc	atg	cgt	tcc	ggc	caa	gct	aac	gcg	ttc	ggc	atc	259
Ala	Cys	Gly	Asp	Val	Met	Arg	Ser	Gly	Gln	Ala	Asn	Ala	Phe	Gly	Ile	
		40					45					50				

ccg	aat	ccg	ctc	atc	ggc	atc	gcc	ggt	ttc	gcc	gct	gtc	gcc	atc	atc	307
Pro	Asn	Pro	Leu	Ile	Gly	Ile	Ala	Gly	Phe	Ala	Ala	Val	Ala	Ile	Ile	

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ggc gcc ggc atc ctc gcg ggc ggc ggg ttc cgc ggt tgg ttc tgg ttc			355
Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg Gly Trp Phe Trp Phe			
70	75	80	85
ggc gcc cag gcc gga ctc act ttt gcc atg atg ttc tgc cac tgg ctc			403
Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met Phe Cys His Trp Leu			
	90	95	100
gcc tac caa tcc atg tcc gtc atc cgc gcg ctc tgc cct tac tgc atg			451
Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu Cys Pro Tyr Cys Met			
	105	110	115
ggc gtg tgg acc gta tgc atc atc atg ttc gtg ctg gtc act gca tgg			499
Gly Val Trp Thr Val Ser Ile Ile Met Phe Val Leu Val Thr Ala Trp			
	120	125	130
aat gtg aaa act ttc agc ggc tcc gac agc acg ttc gtc aac gca ctg			547
Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr Phe Val Asn Ala Leu			
	135	140	145
tac aaa tac aag tgg gtc atc gcg atc gtc tgg ctg ctg ctc atc gca			595
Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp Leu Leu Leu Ile Ala			
	150	155	160
gcc gca gct gtg tgg tca ttc cgc tac atg ttc taggcattta aggcatttcag			648
Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe			
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gcc			651
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<213> Corynebacterium glutamicum			
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Glu Lys Leu Ala Ile Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp			
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Phe Asn Ala Val Leu Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala			
	35	40	45
Asn Ala Phe Gly Ile Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala			
	50	55	60
Ala Val Ala Ile Ile Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg			
	65	70	75
Gly Trp Phe Trp Phe Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met			
	85	90	95
Phe Cys His Trp Leu Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu			
	100	105	110
Cys Pro Tyr Cys Met Gly Val Trp Thr Val Ser Ile Ile Met Phe Val			

115	120	125
Leu Val Thr Ala Trp Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr		
130	135	140
Phe Val Asn Ala Leu Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp		
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Leu Leu Leu Ile Ala Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe		
165	170	175

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 <211> 426
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(403)
 <223> RXN00096

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 Met Thr Asn Ala Gly
 1 5
 gac aac ttc gag atc agg atg cct tct ggc acg gat gac cca ttg tcc 163
 Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr Asp Asp Pro Leu Ser
 10 15 20
 gat gcg gag atc caa aag tat cgc gag gag atc aac cgc ttg gac cgc 211
 Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile Asn Arg Leu Asp Arg
 25 30 35
 gaa atc ctc gat gcg gtg aaa cgc cgc acg aag att tcc caa acc atc 259
 Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys Ile Ser Gln Thr Ile
 40 45 50
 gga aaa aca cgc atg agc tcg ggc gga aca cgt ctc gtg cac acc cga 307
 Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg Leu Val His Thr Arg
 55 60 65
 gaa gta gca atc atc aac caa ttc cgt gaa gag atc ggc gag gaa ggc 355
 Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu Ile Gly Glu Glu Gly
 70 75 80 85
 cct gcc ctc gct gga att ttg ctg cgc atg gga cgc gga aaa ctc gga 403
 Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly Arg Gly Lys Leu Gly
 90 95 100
 taagttatcc acaggtagaa aaa 426

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 94

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 20 25 30
 Asn Arg Leu Asp Arg Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys
 35 40 45
 Ile Ser Gln Thr Ile Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg
 50 55 60
 Leu Val His Thr Arg Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu
 65 70 75 80
 Ile Gly Glu Glu Gly Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly
 85 90 95
 Arg Gly Lys Leu Gly
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<210> 95

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(403)

<223> FRXA00096

<400> 95

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 Met Thr Asn Ala Gly
 1 5
 gac aac ttc gag atc agg atg cct tct ggc acg gat gac cca ttg tcc 163
 Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr Asp Asp Pro Leu Ser
 10 15 20
 gat gcg gag atc caa aag tat cgc gag gag atc aac cgc ttg gac cgc 211
 Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile Asn Arg Leu Asp Arg
 25 30 35
 gaa atc ctc gat gcg gtg aaa cgc cgc acg aag att tcc caa acc atc 259
 Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys Ile Ser Gln Thr Ile
 40 45 50
 gga aaa aca cgc atg agc tcg ggc gga aca cgt ctc gtg cac acc cga 307
 Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg Leu Val His Thr Arg
 55 60 65
 gaa gta gca atc atc aac cag ttc cgt gaa gag atc ggc gag gaa ggc 355
 Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu Ile Gly Glu Glu Gly
 70 75 80 85
 cct gcc ctc gct gga att ttg ctg cgc atg gga cgc gga aaa ctc gga 403

Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly Arg Gly Lys Leu Gly
 90 95 100

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426

<210> 96
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 96
 Met Thr Asn Ala Gly Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr
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 20 25 30
 Asn Arg Leu Asp Arg Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys
 35 40 45
 Ile Ser Gln Thr Ile Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg
 50 55 60
 Leu Val His Thr Arg Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu
 65 70 75 80
 Ile Gly Glu Glu Gly Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly
 85 90 95
 Arg Gly Lys Leu Gly
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<210> 97
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1276)
 <223> RXN00097

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 Met Glu Val Pro Ser
 1 5
 ttg ttt acc aac ttc ttc gca gtc aac aac cca gac agt ccg ccc gca 163
 Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala
 10 15 20
 cga caa aaa acc aaa ctc aga gaa ctg gaa cac cgc ttc tgg caa gaa 211
 Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu
 25 30 35
 cac ctg cca ggc gac gac gat gac cat tcc acc gca atc tcc agc ctc 259
 His Leu Pro Gly Asp Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu

40	45	50	
gcc atc gtc aca ggt cta aca aaa gcg cag gtc tcc cgc ata tcc atc Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile 55 60 65			307
gcg ttt gcc acg ctc gcc gac ttg ccc gaa ctc aaa gcc ctg caa caa Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln 70 75 80 85			355
aag ctg tac cac ctc gac ctc tcc cga ctg atc acc att agc aac gaa Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu 90 95 100			403
ctc gcc ggc atc aac ccc gac aac ctc gcc ggc gcc gac gca atc ctc Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu 105 110 115			451
acc gaa tac ctc acc gcc acc agc ccc aac cag att ctg cca agc ccg Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro 120 125 130			499
gcg tcc ata gga cgc aag ata aaa gaa ata aga gat ttg ctt gac gac Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp 135 140 145			547
gca aga gcc acc ggt tcg cgc ggt acc caa gac gac agc tct ttc gga Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly 150 155 160 165			595
gtg acc ttc tcc cca gac gga acc gcc gaa atc gga gcc tcc gtc gat Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp 170 175 180			643
gct gtg gac ggg cac atc atc aac gac gcc gtc acc caa cac gcg aag Ala Val Asp Gly His Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys 185 190 195			691
aaa aac gac ctc acc tac ggc gaa gct ttc agc gac atc ctt cgg aac Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn 200 205 210			739
aat atc caa gtc aag gta gtc ctc aac ttg tac acc gcc aaa gac ctc Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu 215 220 225			787
gcc aac gcc cca gtg tgg gcc agc gga atc ggc tgg ttg gat gcc aag Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys 230 235 240 245			835
act gga aca ttc tgg tca gag aaa gcc aac aaa gaa caa gac atg gat Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp 250 255 260			883
gcg gct gcc aaa atc agc acc gac aaa cac gat cct cca cca gcg ttg Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu 265 270 275			931
cgt gac gca ctc att ggt cgt gat ggc acc tgc cga ttc cct ggc tgt Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys 280 285 290			979

tca gtc cca gcg ctc aaa acc caa gcc gac cac cgc atc ccc tac gaa 1027
 Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu
 295 300 305

gaa ggc gga gaa act tgc cta ggc gga atc ggc tgc ctc tgt caa cac 1075
 Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His
 310 315 320 325

cac cac aac atg aaa acc gac ggc cga gtc acc tac ctt ctc gat ccc 1123
 His His Asn Met Lys Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro
 330 335 340

ttc tcc ggc atc atc gtc tgg ctc atg gga gac gga aca tgg gca gtg 1171
 Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val
 345 350 355

tca gaa ccc aac ggg ccg ctc aat ccc aaa aat gcg aga tgg gcg caa 1219
 Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln
 360 365 370

aca gtc gcc caa cac cgg gca cgc cac cac aag cgt tgg gtt aag gag 1267
 Thr Val Ala Gln His Arg Ala Arg His His Lys Arg Trp Val Lys Glu
 375 380 385

gac gcc aag tagccggatg gccacgtcga aaa 1299
 Asp Ala Lys
 390

<210> 98

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

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 20 25 30

Arg Phe Trp Gln Glu His Leu Pro Gly Asp Asp Asp Asp His Ser Thr
 35 40 45

Ala Ile Ser Ser Leu Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val
 50 55 60

Ser Arg Ile Ser Ile Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu
 65 70 75 80

Lys Ala Leu Gln Gln Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile
 85 90 95

Thr Ile Ser Asn Glu Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly
 100 105 110

Ala Asp Ala Ile Leu Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln
 115 120 125

Ile Leu Pro Ser Pro Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg

130	135	140
Asp Leu Leu Asp Asp	Ala Arg Ala Thr Gly Ser	Arg Gly Thr Gln Asp
145	150	155 160
Asp Ser Ser Phe Gly Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile		
	165	170 175
Gly Ala Ser Val Asp Ala Val Asp Gly His Ile Ile Asn Asp Ala Val		
	180	185 190
Thr Gln His Ala Lys Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser		
	195	200 205
Asp Ile Leu Arg Asn Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr		
	210	215 220
Thr Ala Lys Asp Leu Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly		
	225	230 235 240
Trp Leu Asp Ala Lys Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys		
	245	250 255
Glu Gln Asp Met Asp Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp		
	260	265 270
Pro Pro Pro Ala Leu Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys		
	275	280 285
Arg Phe Pro Gly Cys Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His		
	290	295 300
Arg Ile Pro Tyr Glu Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly		
	305	310 315 320
Cys Leu Cys Gln His His His Asn Met Lys Thr Asp Gly Arg Val Thr		
	325	330 335
Tyr Leu Leu Asp Pro Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp		
	340	345 350
Gly Thr Trp Ala Val Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn		
	355	360 365
Ala Arg Trp Ala Gln Thr Val Ala Gln His Arg Ala Arg His His Lys		
	370	375 380
Arg Trp Val Lys Glu Asp Ala Lys		
385	390	

<210> 99
 <211> 1284
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1261)
 <223> FRXA00097

<400> 99

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gatagggttac agggcagaat cccgaatgga ggtgccttcc ttg ttt acc aac ttc 115
                                   Leu Phe Thr Asn Phe
                                   1 5

ttc gca gtc aac aac cca gac agt ccg ccc gca cga caa aaa acc aaa 163
Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala Arg Gln Lys Thr Lys
                                   10 15 20

ctc aga gaa ctg gaa cac cgc ttc tgg caa gaa cac ctg cca ggc gac 211
Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu His Leu Pro Gly Asp
                                   25 30 35

gac gat gac cat tcc acc gca atc tcc agc ctc gcc atc gtc aca ggt 259
Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu Ala Ile Val Thr Gly
                                   40 45 50

cta aca aaa gcg cag gtc tcc cgc ata tcc atc gcg ttt gcc acg ctc 307
Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile Ala Phe Ala Thr Leu
                                   55 60 65

gcc gac ttg ccc gaa ctc aaa gcc ctg caa caa aag ctg tac cac ctc 355
Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln Lys Leu Tyr His Leu
                                   70 75 80 85

gac ctc tcc cga ctg atc acc att agc aac gaa ctc gcc ggc atc aac 403
Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu Leu Ala Gly Ile Asn
                                   90 95 100

ccc gac aac ctc gcc ggc gcc gac gca atc ctc acc gaa tac ctc acc 451
Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu Thr Glu Tyr Leu Thr
                                   105 110 115

gcc acc agc ccc aac cag att ctg cca agc ccg gcg tcc ata gga cgc 499
Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro Ala Ser Ile Gly Arg
                                   120 125 130

aag ata aaa gaa ata aga gat ttg ctt gac gac gca aga gcc acc ggt 547
Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp Ala Arg Ala Thr Gly
                                   135 140 145

tcg cgc ggt acc caa gac gac agc tct ttc gga gtg acc ttc tcc cca 595
Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly Val Thr Phe Ser Pro
                                   150 155 160 165

gac gga acc gcc gaa atc gga gcc tcc gtc gat gct gtg gac ggg cac 643
Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp Ala Val Asp Gly His
                                   170 175 180

atc atc aac gac gcc gtc acc caa cac gcg aag aaa aac gac ctc acc 691
Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys Lys Asn Asp Leu Thr
                                   185 190 195

tac ggc gaa gct ttc agc gac atc ctt cgg aac aat atc caa gtc aag 739
Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn Asn Ile Gln Val Lys
                                   200 205 210

gta gtc ctc aac ttg tac acc gcc aaa gac ctc gcc aac gcc cca gtg 787
Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu Ala Asn Ala Pro Val

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215	220	225	
tgg gcc agc gga atc ggc tgg ttg gat gcc aag act gga aca ttc tgg			835
Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys Thr Gly Thr Phe Trp			
230	235	240	245
tca gag aaa gcc aac aaa gaa caa gac atg gat gcg gct gcc aaa atc			883
Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp Ala Ala Ala Lys Ile			
	250	255	260
agc acc gac aaa cac gat cct cca cca gcg ttg cgt gac gca ctc att			931
Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu Arg Asp Ala Leu Ile			
	265	270	275
ggc cgt gat ggc acc tgc cga ttc cct ggc tgt tca gtc cca gcg ctc			979
Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys Ser Val Pro Ala Leu			
	280	285	290
aaa acc caa gcc gac cac cgc atc ccc tac gaa gaa ggc gga gaa act			1027
Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu Glu Gly Gly Glu Thr			
	295	300	305
tgc cta ggc gga atc ggc tgc ctc tgt caa cac cac cac aac atg aaa			1075
Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His His His Asn Met Lys			
	310	315	325
acc gac ggc cga gtc acc tac ctt ctc gat ccc ttc tcc ggc atc atc			1123
Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro Phe Ser Gly Ile Ile			
	330	335	340
gtc tgg ctc atg gga gac gga aca tgg gca gtg tca gaa ccc aac ggg			1171
Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val Ser Glu Pro Asn Gly			
	345	350	355
ccg ctc aat ccc aaa aat gcg aga tgg gcg caa aca gtc gcc caa cac			1219
Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln Thr Val Ala Gln His			
	360	365	370
cgg gca cgc cac cac aag cgt tgg gtt aag gag gac gcc aag			1261
Arg Ala Arg His His Lys Arg Trp Val Lys Glu Asp Ala Lys			
	375	380	385
tagccggatg gccacgtcga aaa			1284

<210> 100

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

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Arg	Gln	Lys	Thr	Lys	Leu	Arg	Glu	Leu	Glu	His	Arg	Phe	Trp	Gln	Glu
			20					25					30		

His	Leu	Pro	Gly	Asp	Asp	Asp	Asp	His	Ser	Thr	Ala	Ile	Ser	Ser	Leu
		35					40					45			

Ala	Ile	Val	Thr	Gly	Leu	Thr	Lys	Ala	Gln	Val	Ser	Arg	Ile	Ser	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln 65 70 75 80		
Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu 85 90 95		
Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu 100 105 110		
Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro 115 120 125		
Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp 130 135 140		
Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly 145 150 155 160		
Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp 165 170 175		
Ala Val Asp Gly His Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys 180 185 190		
Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn 195 200 205		
Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu 210 215 220		
Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys 225 230 235 240		
Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp 245 250 255		
Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu 260 265 270		
Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys 275 280 285		
Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu 290 295 300		
Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His 305 310 315 320		
His His Asn Met Lys Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro 325 330 335		
Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val 340 345 350		
Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln 355 360 365		
Thr Val Ala Gln His Arg Ala Arg His His Lys Arg Trp Val Lys Glu 370 375 380		

Asp Ala Lys
385

<210> 101
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXN00114

<400> 101
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atttacttaa aacctaatta aatctactat cggagatctc atg aaa ctt ctc aag 115
Met Lys Leu Leu Lys
1 5
ttt gct gca gca gga acc ttc gca cta gcc ctg gct ggc tgc aca cag 163
Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu Ala Gly Cys Thr Gln
10 15 20
act gag tct ctc gta gca aca atc gaa tct gca acc tct gca gca cag 211
Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala Thr Ser Ala Ala Gln
25 30 35
gca tcc gga aac gac gta gaa gga gac caa acc tcc gcg ttc gaa ctc 259
Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr Ser Ala Phe Glu Leu
40 45 50
tcc gtt ggc gaa tgc ttc aac gac acc tac gaa gaa gaa atc tcc gaa 307
Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu Glu Glu Ile Ser Glu
55 60 65
gta ccc atc gtc gac tgc gca gaa cct cac gac aac gag atc tac tac 355
Val Pro Ile Val Asp Cys Ala Glu Pro His Asp Asn Glu Ile Tyr Tyr
70 75 80 85
ctc tac gac atc gaa ggc gac gac ttc cca acc gac atc acc acc aca 403
Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr Asp Ile Thr Thr Thr
90 95 100
ggc tac gaa ggc tgc ctc cca aca ttt gaa ggc ttc gta gga gct cct 451
Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly Phe Val Gly Ala Pro
105 110 115
tac gaa acc tcc atc tac gag gtc tac cca atg acc cca acc ttt ggc 499
Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met Thr Pro Thr Phe Gly
120 125 130
tcc tgg aca aac ggc gac cgc gag gta gtg tgc tcc gtg tac ttg gcc 547
Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys Ser Val Tyr Leu Ala
135 140 145
acc ggt gag cag atg acc gga acc gca gca gga acc gcg cag 589
Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly Thr Ala Gln
150 155 160

tagatttttg ataggaatt ttg

612

<210> 102

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Met Lys Leu Leu Lys Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu
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Ala Gly Cys Thr Gln Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala
 20 25 30

Thr Ser Ala Ala Gln Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr
 35 40 45

Ser Ala Phe Glu Leu Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu
 50 55 60

Glu Glu Ile Ser Glu Val Pro Ile Val Asp Cys Ala Glu Pro His Asp
 65 70 75 80

Asn Glu Ile Tyr Tyr Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr
 85 90 95

Asp Ile Thr Thr Thr Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly
 100 105 110

Phe Val Gly Ala Pro Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met
 115 120 125

Thr Pro Thr Phe Gly Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys
 130 135 140

Ser Val Tyr Leu Ala Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly
 145 150 155 160

Thr Ala Gln

<210> 103

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> FRXA00114

<400> 103

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atttacttaa aacctaat aatctactat cggagatctc atg aaa ctt ctc aag 115
 Met Lys Leu Leu Lys
 1 5

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ttt gct gca gca gga acc ttc gca cta gcc ctg gct ggc tgc aca cag 163
Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu Ala Gly Cys Thr Gln
      10                      15                      20

act gag tct ctc gta gca aca atc gaa tct gca acc tct gca gca cag 211
Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala Thr Ser Ala Ala Gln
      25                      30                      35

gca tcc gga aac gac gta gaa gga gac caa acc tcc gcg ttc gaa ctc 259
Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr Ser Ala Phe Glu Leu
      40                      45                      50

tcc gtt ggc gaa tgc ttc aac gac acc tac gaa gaa gaa atc tcc gaa 307
Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu Glu Glu Ile Ser Glu
      55                      60                      65

gta ccc atc gtc gac tgc gca gaa cct cac gac aac gag atc tac tac 355
Val Pro Ile Val Asp Cys Ala Glu Pro His Asp Asn Glu Ile Tyr Tyr
      70                      75                      80                      85

ctc tac gac atc gaa ggc gac gac ttc cca acc gac atc acc acc aca 403
Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr Asp Ile Thr Thr Thr
      90                      95                      100

ggc tac gaa ggc tgc ctc cca aca ttt gaa ggc ttc gta gga gct cct 451
Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly Phe Val Gly Ala Pro
      105                      110                      115

tac gaa acc tcc atc tac gag gtc tac cca atg acc cca acc ttt ggc 499
Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met Thr Pro Thr Phe Gly
      120                      125                      130

tcc tgg aca aac ggc gac cgc gag gta gtg tgc tcc gtg tac ttg gcc 547
Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys Ser Val Tyr Leu Ala
      135                      140                      145

acc ggt gag cag atg acc gga acc gca gca gga acc gcg cag 589
Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly Thr Ala Gln
      150                      155                      160

tagattttgg atagggaatt ttg 612

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<210> 104

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

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Ala Gly Cys Thr Gln Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala
      20                      25                      30

Thr Ser Ala Ala Gln Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr
      35                      40                      45

Ser Ala Phe Glu Leu Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu
      50                      55                      60

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Glu Glu Ile Ser Glu Val Pro Ile Val Asp Cys Ala Glu Pro His Asp
 65 70 75 80
 Asn Glu Ile Tyr Tyr Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr
 85 90 95
 Asp Ile Thr Thr Thr Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly
 100 105 110
 Phe Val Gly Ala Pro Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met
 115 120 125
 Thr Pro Thr Phe Gly Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys
 130 135 140
 Ser Val Tyr Leu Ala Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly
 145 150 155 160
 Thr Ala Gln

<210> 105
 <211> 963
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(940)
 <223> RXN00120

<400> 105
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 Met Leu Ile Gly Met
 1 5
 agc aat caa aca gtc aat caa gca gtg tcg tca ggg gtg aaa gca tcc 163
 Ser Asn Gln Thr Val Asn Gln Ala Val Ser Ser Gly Val Lys Ala Ser
 10 15 20
 ccg cac agg ttc aat cgt ttt gaa atc aaa tac ttg att aca gag caa 211
 Pro His Arg Phe Asn Arg Phe Glu Ile Lys Tyr Leu Ile Thr Glu Gln
 25 30 35
 gat gta cct gca ctc cgc gag cag ttg gca acg agg atg agc acg gat 259
 Asp Val Pro Ala Leu Arg Glu Gln Leu Ala Thr Arg Met Ser Thr Asp
 40 45 50
 ccg ctt tcc cca ccc gga ggc tac cga gtg gaa tcc ctt tac ttc gat 307
 Pro Leu Ser Pro Pro Gly Gly Tyr Arg Val Glu Ser Leu Tyr Phe Asp
 55 60 65
 tca gcc gat tta cgg tgc tac acc gaa aag atc gag ggt ctg aaa ttc 355
 Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile Glu Gly Leu Lys Phe
 70 75 80 85
 cga agg aaa cta cgg atc cgt acc tac ggt gat gga gtg ctc act cca 403
 Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp Gly Val Leu Thr Pro

90	95	100	
gaa tcc acc gtg tgc gta gag atc aag cag cgg gtt aac aaa gta act			451
Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg Val Asn Lys Val Thr			
105	110	115	
caa aag cgt cgg ctg gat ttg ccc ttt ata tat gcg ctc gcc ctg ggc			499
Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr Ala Leu Ala Leu Gly			
120	125	130	
gat agc acg ggc gcc gcg gta ggc gag cag gtg gac gtc gag aag ctt			547
Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val Asp Val Glu Lys Leu			
135	140	145	
ctt gaa atc tct ccg gaa aac cag cac gct ttg att cac gaa atg gcg			595
Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu Ile His Glu Met Ala			
150	155	160	165
tcg ttt gct aaa aat tat cgg ctg cga ccc atc gcc acc acg aag tat			643
Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile Ala Thr Thr Lys Tyr			
170	175	180	
cac cgc gag gca ttc gtc ggc gct gat gcg gag gaa agt tcg cga gtc			691
His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu Glu Ser Ser Arg Val			
185	190	195	
acc att gac cac ggt gtt tca ggc cgt gat cgt gat ttt ctg ctt ggc			739
Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg Asp Phe Leu Leu Gly			
200	205	210	
caa gac ctt gaa gac cgc cca acg gtg gcg caa gga ttg gca gtc gtg			787
Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln Gly Leu Ala Val Val			
215	220	225	
gaa atc aaa tgc gat gaa cgc gtg ccg ttt tgg ctc act gat atg act			835
Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp Leu Thr Asp Met Thr			
230	235	240	245
gct caa ctg gaa atg tcc gtg att cgg atg tcc aaa tac tgc gaa acc			883
Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser Lys Tyr Cys Glu Thr			
250	255	260	
atc gaa gcg ttt cac aac cgt ccg gca tca gct ttc ggc gct gtc gac			931
Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala Phe Gly Ala Val Asp			
265	270	275	
ccc atc ttc taaacaagaa aggcccctcc aat			963
Pro Ile Phe			
280			

<210> 106

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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1				5				10						15	

Gly Val Lys Ala Ser Pro His Arg Phe Asn Arg Phe Glu Ile Lys Tyr

20	25	30
Leu Ile Thr Glu Gln Asp Val Pro Ala Leu Arg Glu Gln Leu Ala Thr 35 40 45		
Arg Met Ser Thr Asp Pro Leu Ser Pro Pro Gly Gly Tyr Arg Val Glu 50 55 60		
Ser Leu Tyr Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile 65 70 75 80		
Glu Gly Leu Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp 85 90 95		
Gly Val Leu Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg 100 105 110		
Val Asn Lys Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr 115 120 125		
Ala Leu Ala Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val 130 135 140		
Asp Val Glu Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu 145 150 155 160		
Ile His Glu Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile 165 170 175		
Ala Thr Thr Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu 180 185 190		
Glu Ser Ser Arg Val Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg 195 200 205		
Asp Phe Leu Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln 210 215 220		
Gly Leu Ala Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp 225 230 235 240		
Leu Thr Asp Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser 245 250 255		
Lys Tyr Cys Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala 260 265 270		
Phe Gly Ala Val Asp Pro Ile Phe 275 280		

<210> 107

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> FRXA00120

<400> 107

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gatgagcacg gatccgcttt cccccccgg aggctaccga gtg gaa tcc ctt tac 115
Val Glu Ser Leu Tyr
1 5
ttc gat tca gcc gat tta cgg tgc tac acc gaa aag atc gag ggt ctg 163
Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile Glu Gly Leu
10 15 20
aaa ttc cga agg aaa cta cgg atc cgt acc tac ggt gat gga gtg ctc 211
Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp Gly Val Leu
25 30 35
act cca gaa tcc acc gtg tcg gta gag atc aag cag cgg gtt aac aaa 259
Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg Val Asn Lys
40 45 50
gta act caa aag cgt cgg ctg gat ttg ccc ttt ata tat gcg ctc gcc 307
Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr Ala Leu Ala
55 60 65
ctg ggc gat agc acg ggc gcc gcg gta ggc gag cag gtg gac gtc gag 355
Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val Asp Val Glu
70 75 80 85
aag ctt ctt gaa atc tct ccg gaa aac cag cac gct ttg att cac gaa 403
Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu Ile His Glu
90 95 100
atg gcg tcg ttt gct aaa aat tat cgg ctg cga ccc atc gcc acc acg 451
Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile Ala Thr Thr
105 110 115
aag tat cac cgc gag gca ttc gtc ggc gct gat gcg gag gaa agt tcg 499
Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu Glu Ser Ser
120 125 130
cga gtc acc att gac cac ggt gtt tca ggc cgt gat cgt gat ttt ctg 547
Arg Val Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg Asp Phe Leu
135 140 145
ctt ggc caa gac ctt gaa gac cgc cca acg gtg gcg caa gga ttg gca 595
Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln Gly Leu Ala
150 155 160 165
gtc gtg gaa atc aaa tgc gat gaa cgc gtg ccg ttt tgg ctc act gat 643
Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp Leu Thr Asp
170 175 180
atg act gct caa ctg gaa atg tcc gtg att cgg atg tcc aaa tac tgc 691
Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser Lys Tyr Cys
185 190 195
gaa acc atc gaa gcg ttt cac aac cgt ccg gca tca gct ttc ggc gct 739
Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala Phe Gly Ala
200 205 210
gtc gac ccc atc ttc taaacaagaa aggccctcc aat 777
Val Asp Pro Ile Phe

215

<210> 108

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Val Glu Ser Leu Tyr Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu
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Lys Ile Glu Gly Leu Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr
20 25 30

Gly Asp Gly Val Leu Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys
35 40 45

Gln Arg Val Asn Lys Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe
50 55 60

Ile Tyr Ala Leu Ala Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu
65 70 75 80

Gln Val Asp Val Glu Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His
85 90 95

Ala Leu Ile His Glu Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg
100 105 110

Pro Ile Ala Thr Thr Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp
115 120 125

Ala Glu Glu Ser Ser Arg Val Thr Ile Asp His Gly Val Ser Gly Arg
130 135 140

Asp Arg Asp Phe Leu Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val
145 150 155 160

Ala Gln Gly Leu Ala Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro
165 170 175

Phe Trp Leu Thr Asp Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg
180 185 190

Met Ser Lys Tyr Cys Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala
195 200 205

Ser Ala Phe Gly Ala Val Asp Pro Ile Phe
210 215

<210> 109

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXN00128

<400> 109

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca  gtg agt aaa att tcg 115
                                         Val Ser Lys Ile Ser
                                         1                               5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
                        10                        15                        20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
                        25                        30                        35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
                        40                        45                        50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
                        55                        60                        65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
                        70                        75                        80                        85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
                        90                        95                        100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
                        105                        110                        115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
                        120                        125                        130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
                        135                        140                        145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
150                        155                        160                        165

aga aac gat ctg ccg aac cat tac act ccg cac gat gtg tat ttc ttt 643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
                        170                        175                        180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat 691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
                        185                        190                        195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly
200                        205                        210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat 787

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Pro 215	Ser	Pro	Ala	Ile	Ser	Pro 220	Gly	Val	Val	Asn	Gln 225	Leu	Ser	Thr	Asp	
gcg	tcg	ttc	gtg	ggg	ttc	aat	gat	ggg	gag	tat	cag	ttc	act	ggt	ttg	835
Ala	Ser	Phe	Val	Gly	Phe	Asn	Asp	Gly	Glu	Tyr	Gln	Phe	Thr	Gly	Leu	
230					235					240					245	
gga	aat	ttg	gat	gat	gat	gcg	cgt	ttg	cgt	ttc	gcc	gcc	cag	gcc	gtg	883
Gly	Asn	Leu	Asp	Asp	Asp	Ala	Arg	Leu	Arg	Phe	Ala	Ala	Gln	Ala	Val	
				250					255						260	
tgg	acg	ttg	gcg	cat	gct	gat	gtc	gca	ggc	ccc	tac	act	ttg	gtc	gct	931
Trp	Thr	Leu	Ala	His	Ala	Asp	Val	Ala	Gly	Pro	Tyr	Thr	Leu	Val	Ala	
			265					270						275		
gac	ggc	gcg	ccg	ttg	ctg	tcg	gag	ttc	cca	acg	ctc	acc	acc	gat	gac	979
Asp	Gly	Ala	Pro	Leu	Leu	Ser	Glu	Phe	Pro	Thr	Leu	Thr	Thr	Asp	Asp	
		280					285					290				
ctc	gcc	gaa	tac	aac	cca	gag	gct	tac	acc	aac	acg	gtg	tcc	acg	ttg	1027
Leu	Ala	Glu	Tyr	Asn	Pro	Glu	Ala	Tyr	Thr	Asn	Thr	Val	Ser	Thr	Leu	
	295					300					305					
ttt	gcg	ttg	cag	gat	gga	tcg	ttg	tcg	agg	gtc	agt	tcc	ggc	aat	gtg	1075
Phe	Ala	Leu	Gln	Asp	Gly	Ser	Leu	Ser	Arg	Val	Ser	Ser	Gly	Asn	Val	
310					315					320					325	
agt	cca	cta	cag	ggc	att	tgg	agc	ggt	gga	gat	atc	gat	tct	gca	gcg	1123
Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp	Ile	Asp	Ser	Ala	Ala	
				330					335						340	
att	tcc	tcc	tcc	gcc	aat	gtg	gtg	gca	gcg	gta	cgc	cac	gaa	aac	aac	1171
Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val	Arg	His	Glu	Asn	Asn	
			345					350						355		
gag	gca	gtg	ctt	act	gtt	ggc	tcc	atg	gaa	ggc	gtg	act	tca	gat	gcg	1219
Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly	Val	Thr	Ser	Asp	Ala	
		360					365					370				
ttg	agg	agt	gaa	acg	atc	act	cgt	ccc	acc	ttt	gaa	tac	gcg	tcg	agt	1267
Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe	Glu	Tyr	Ala	Ser	Ser	
	375					380					385					
ggg	ttg	tgg	gct	gtg	gtg	gat	ggg	gag	acg	cct	gtc	cga	gtc	gca	cga	1315
Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro	Val	Arg	Val	Ala	Arg	
390					395					400					405	
tcg	gca	aca	acc	ggt	gag	ctc	gtc	cag	acg	gag	gcg	gag	att	gtg	ctg	1363
Ser	Ala	Thr	Thr	Gly	Glu	Leu	Val	Gln	Thr	Glu	Ala	Glu	Ile	Val	Leu	
				410				415						420		
cca	agg	gat	gtg	acg	ggt	ccg	atc	tct	gaa	ttc	caa	ctg	tca	cga	act	1411
Pro	Arg	Asp	Val	Thr	Gly	Pro	Ile	Ser	Glu	Phe	Gln	Leu	Ser	Arg	Thr	
			425					430						435		
ggg	gtc	cgg	gcc	gcc	atg	atc	att	gaa	ggc	aag	gtg	tac	gtg	ggc	gtc	1459
Gly	Val	Arg	Ala	Ala	Met	Ile	Ile	Glu	Gly	Lys	Val	Tyr	Val	Gly	Val	
		440				445						450				
gta	acg	cgt	cct	ggt	ccg	ggc	gag	cgg	cgc	gtg	aca	aat	atc	acg	gag	1507
Val	Thr	Arg	Pro	Gly	Pro	Gly	Glu	Arg	Arg	Val	Thr	Asn	Ile	Thr	Glu	

455	460	465	
gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca			1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro			
470	475	480	485
gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg			1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp			
	490	495	500
cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat			1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn			
	505	510	515
ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac			1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr			
	520	525	530
gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat			1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp			
	535	540	545
att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg			1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val			
550	555	560	565
ggt gcg tac tgatggagct gttcttcccg cgc			1827
Val Ala Tyr			

<210> 110

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

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20	30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile	
35	45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe	
50	60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala	
65	75

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr	
85	95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn	
100	110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu	
115	125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val

450	455	460
Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser		
465	470	475 480
Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro		
	485	490 495
Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser		
	500	505 510
Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser		
	515	520 525
Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro		
	530	535 540
Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr		
545	550	555 560
Arg Ala Ala Pro Val Val Ala Tyr		
	565	

<210> 111
 <211> 1827
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1804)
 <223> FRXA00128

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 Val Ser Lys Ile Ser
 1 5
 acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
 10 15 20
 gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
 25 30 35
 tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
 40 45 50
 aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
 55 60 65
 tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
 70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg 90 95 100	403
att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile 105 110 115	451
gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr 120 125 130	499
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu 135 140 145	547
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu 150 155 160 165	595
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe 170 175 180	643
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn 185 190 195	691
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly 200 205 210	739
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp 215 220 225	787
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu 230 235 240 245	835
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val 250 255 260	883
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala 265 270 275	931
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp 280 285 290	979
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu 295 300 305	1027
ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val 310 315 320 325	1075
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg	1123

Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp	Ile	Asp	Ser	Ala	Ala		
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att	tcc	tcc	tcc	gcc	aat	gtg	gtg	gca	gcg	gta	cgc	cac	gaa	aac	aac	1171	
Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val	Arg	His	Glu	Asn	Asn		
				345					350					355			
gag	gca	gtg	ctt	act	gtt	ggc	tcc	atg	gaa	ggc	gtg	act	tca	gat	gcg	1219	
Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly	Val	Thr	Ser	Asp	Ala		
				360					365					370			
ttg	agg	agt	gaa	acg	atc	act	cgt	ccc	acc	ttt	gaa	tac	gcg	tcg	agt	1267	
Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe	Glu	Tyr	Ala	Ser	Ser		
				375					380					385			
ggg	ttg	tgg	gct	gtg	gtg	gat	ggg	gag	acg	cct	gtc	cga	gtc	gca	cga	1315	
Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro	Val	Arg	Val	Ala	Arg		
				395					400					405			
tcg	gca	aca	acc	ggc	gag	ctc	gtc	cag	acg	gag	gcg	gag	att	gtg	ctg	1363	
Ser	Ala	Thr	Thr	Gly	Glu	Leu	Val	Gln	Thr	Glu	Ala	Glu	Ile	Val	Leu		
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cca	agg	gat	gtg	acg	ggc	ccg	atc	tct	gaa	ttc	caa	ctg	tca	cga	act	1411	
Pro	Arg	Asp	Val	Thr	Gly	Pro	Ile	Ser	Glu	Phe	Gln	Leu	Ser	Arg	Thr		
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ggg	gtc	cgg	gcc	gcc	atg	atc	att	gaa	ggc	aag	gtg	tac	gtg	ggc	gtc	1459	
Gly	Val	Arg	Ala	Ala	Met	Ile	Ile	Glu	Gly	Lys	Val	Tyr	Val	Gly	Val		
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gta	acg	cgt	cct	ggc	ccg	ggc	gag	cgg	cgc	gtg	aca	aat	atc	acg	gag	1507	
Val	Thr	Arg	Pro	Gly	Pro	Gly	Glu	Arg	Arg	Val	Thr	Asn	Ile	Thr	Glu		
				455					460					465			
gtg	gcg	ccg	agc	ttg	ggc	gag	gcg	gcg	ctg	tcg	atc	aac	tgg	cgc	cca	1555	
Val	Ala	Pro	Ser	Leu	Gly	Glu	Ala	Ala	Leu	Ser	Ile	Asn	Trp	Arg	Pro		
				470					475					480			485
gac	ggc	att	ttg	ctt	gtg	ggc	acg	tca	att	cca	gag	acg	ccg	ctg	tgg	1603	
Asp	Gly	Ile	Leu	Leu	Val	Gly	Thr	Ser	Ile	Pro	Glu	Thr	Pro	Leu	Trp		
				490					495					500			
cgc	gtc	gag	cag	gac	gga	tcg	gcg	att	tcg	tcg	atg	ccg	agc	ggg	aat	1651	
Arg	Val	Glu	Gln	Asp	Gly	Ser	Ala	Ile	Ser	Ser	Met	Pro	Ser	Gly	Asn		
				505					510					515			
ctc	agc	gcg	ccg	gtg	gtg	gcg	gtg	gca	agt	tcc	gcg	acg	acg	gtc	tac	1699	
Leu	Ser	Ala	Pro	Val	Val	Ala	Val	Ala	Ser	Ser	Ala	Thr	Thr	Val	Tyr		
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gtc	act	gat	tcg	cat	gcg	atg	ctt	cag	ctg	ccg	act	gcc	gat	aat	gat	1747	
Val	Thr	Asp	Ser	His	Ala	Met	Leu	Gln	Leu	Pro	Thr	Ala	Asp	Asn	Asp		
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<212> PRT
<213> Corynebacterium glutamicum

<400> 112
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Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60
Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
65 70 75 80
Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
85 90 95
Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
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Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
115 120 125
Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
130 135 140
Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145 150 155 160
Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
165 170 175
Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
180 185 190
Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
195 200 205
Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
210 215 220
Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
225 230 235 240
Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
245 250 255
Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
260 265 270
Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr

275					280					285					
Leu	Thr	Thr	Asp	Asp	Leu	Ala	Glu	Tyr	Asn	Pro	Glu	Ala	Tyr	Thr	Asn
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Thr	Val	Ser	Thr	Leu	Phe	Ala	Leu	Gln	Asp	Gly	Ser	Leu	Ser	Arg	Val
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Ser	Ser	Gly	Asn	Val	Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp
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Ile	Asp	Ser	Ala	Ala	Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val
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Arg	His	Glu	Asn	Asn	Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly
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Val	Thr	Ser	Asp	Ala	Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe
	370					375					380				
Glu	Tyr	Ala	Ser	Ser	Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro
385					390					395					400
Val	Arg	Val	Ala	Arg	Ser	Ala	Thr	Thr	Gly	Glu	Leu	Val	Gln	Thr	Glu
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Ala	Glu	Ile	Val	Leu	Pro	Arg	Asp	Val	Thr	Gly	Pro	Ile	Ser	Glu	Phe
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Gln	Leu	Ser	Arg	Thr	Gly	Val	Arg	Ala	Ala	Met	Ile	Ile	Glu	Gly	Lys
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Val	Tyr	Val	Gly	Val	Val	Thr	Arg	Pro	Gly	Pro	Gly	Glu	Arg	Arg	Val
	450					455					460				
Thr	Asn	Ile	Thr	Glu	Val	Ala	Pro	Ser	Leu	Gly	Glu	Ala	Ala	Leu	Ser
465					470					475					480
Ile	Asn	Trp	Arg	Pro	Asp	Gly	Ile	Leu	Leu	Val	Gly	Thr	Ser	Ile	Pro
				485					490					495	
Glu	Thr	Pro	Leu	Trp	Arg	Val	Glu	Gln	Asp	Gly	Ser	Ala	Ile	Ser	Ser
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Met	Pro	Ser	Gly	Asn	Leu	Ser	Ala	Pro	Val	Val	Ala	Val	Ala	Ser	Ser
		515					520					525			
Ala	Thr	Thr	Val	Tyr	Val	Thr	Asp	Ser	His	Ala	Met	Leu	Gln	Leu	Pro
	530					535					540				
Thr	Ala	Asp	Asn	Asp	Ile	Trp	Arg	Glu	Val	Pro	Gly	Leu	Leu	Gly	Thr
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Arg	Ala	Ala	Pro	Val	Val	Ala	Tyr								
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<211> 966

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(943)

<223> RXN00154

<400> 113

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                               Met Ser Phe Ser Asp
                               1           5

ccc tat gca ggc aat att ttt ggt gga cac tcc cgc aac aag cag ccg 163
Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser Arg Asn Lys Gln Pro
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gag tat ccc gat gtg ccc gca aaa cca ggc ctt gtg gtg gaa gtt cgt 211
Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu Val Val Glu Val Arg
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gga gat ggc ttc gtc ggc gct gtg acc ggt ttt gaa cgc acc tac gat 259
Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe Glu Arg Thr Tyr Asp
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ggt gat ttt gtg cgt ctc gag gac cgc cgc gga cgc gat gcg ctg tac 307
Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly Arg Asp Ala Leu Tyr
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aag ctg cgc aag ggt gcg ttc atg att gat ggg cag atc gtt aac ctc 355
Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly Gln Ile Val Asn Leu
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acc cgt ttc gtg gaa aaa caa gca cca cgt aaa tct aat tct ggt tcc 403
Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys Ser Asn Ser Gly Ser
                90                95                100

agg cgt gta gaa aac gcg caa gca aag gtc gcg gcg ccg tca cgc atc 451
Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala Ala Pro Ser Arg Ile
                105                110                115

tgg gta gaa ggc atc cat gac gcc gcc atc gtg gag aaa gtg tgg gga 499
Trp Val Glu Gly Ile His Asp Ala Ala Ile Val Glu Lys Val Trp Gly
                120                125                130

cac gac ctt cgc gtt gag ggc gtc gtg gtg gag tac ctg gaa ggt cta 547
His Asp Leu Arg Val Glu Gly Val Val Val Glu Tyr Leu Glu Gly Leu
                135                140                145

gac aac ctg gag gaa cgt ctc gcg gaa ttt cag cct ggg cct gga cga 595
Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln Pro Gly Pro Gly Arg
                150                155                160                165

cgc atc gga gtg ctc gct gat cac ctt gtt gag gga tct aaa gaa act 643
Arg Ile Gly Val Leu Ala Asp His Leu Val Glu Gly Ser Lys Glu Thr
                170                175                180

cgg atg act aaa tca cta ccc gcg gat gtc gct gtc acc ggc cac ccc 691
Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala Val Thr Gly His Pro
                185                190                195

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tac atc gat att tgg gct gct gtg aaa cca gag cgt ttg ggg ctt aag 739
 Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu Arg Leu Gly Leu Lys
 200 205 210

gcg tgg cct gag gtg cca tac ggg gag gat tgg aaa acc ggc atc tgc 787
 Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp Lys Thr Gly Ile Cys
 215 220 225

aaa cga gtt ggc tgg tca gac ccc aaa gaa ggc tgg cac cgt gtg tat 835
 Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly Trp His Arg Val Tyr
 230 235 240 245

aac gcc gtg aat tcc ttc cgc gat ttg gac tac acc cta att ggg gca 883
 Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr Thr Leu Ile Gly Ala
 250 255 260

gtg gaa cgt ttg gtg gat ttt gtg acc aac ctc gat ttg agt aaa gag 931
 Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu Asp Leu Ser Lys Glu
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 Asp Val Leu Ala
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<210> 114
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45

Glu Arg Thr Tyr Asp Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly
 50 55 60

Arg Asp Ala Leu Tyr Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly
 65 70 75 80

Gln Ile Val Asn Leu Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys
 85 90 95

Ser Asn Ser Gly Ser Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala
 100 105 110

Ala Pro Ser Arg Ile Trp Val Glu Gly Ile His Asp Ala Ala Ile Val
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Glu Lys Val Trp Gly His Asp Leu Arg Val Glu Gly Val Val Val Glu
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Tyr Leu Glu Gly Leu Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln
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				Met	Ser	Phe	Ser	Asp									
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ccc	tat	gca	ggc	aat	att	ttt	ggt	gga	cac	tcc	cgc	aac	aag	cag	ccg	163	
Pro	Tyr	Ala	Gly	Asn	Ile	Phe	Gly	Gly	His	Ser	Arg	Asn	Lys	Gln	Pro		
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Glu	Tyr	Pro	Asp	Val	Pro	Ala	Lys	Pro	Gly	Leu	Val	Val	Glu	Val	Arg		
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gga	gat	ggc	ttc	gtc	ggc	gct	gtg	acc	ggg	ttt	gaa	cgc	acc	tac	gat	259	
Gly	Asp	Gly	Phe	Val	Gly	Ala	Val	Thr	Gly	Phe	Glu	Arg	Thr	Tyr	Asp		
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Gly	Asp	Phe	Val	Arg	Leu	Glu	Asp	Arg	Arg	Gly	Arg	Asp	Ala	Leu	Tyr		
	55					60					65						
aag	ctg	cgc	aag	ggg	gcg	ttc	atg	att	gat	ggg	cag	atc	gtt	aac	ctc	355	
Lys	Leu	Arg	Lys	Gly	Ala	Phe	Met	Ile	Asp	Gly	Gln	Ile	Val	Asn	Leu		
70					75					80					85		

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 Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys Ser Asn Ser Gly Ser
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agg cgt gta gaa aac gcg caa gca aag gtc gcg gcg ccg tca cgc atc 451
 Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala Ala Pro Ser Arg Ile
 105 110 115

tgg gta gaa ggc atc cat gac gcc gcc atc gtg gag aaa gtg tgg gga 499
 Trp Val Glu Gly Ile His Asp Ala Ala Ile Val Glu Lys Val Trp Gly
 120 125 130

cac gac ctt cgc gtt gag ggc gtc gtg gtg gag tac ctg gaa ggt cta 547
 His Asp Leu Arg Val Glu Gly Val Val Val Glu Tyr Leu Glu Gly Leu
 135 140 145

gac aac ctg gag gaa cgt ctc gcg gaa ttt cag cct ggg cct gga cga 595
 Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln Pro Gly Pro Gly Arg
 150 155 160 165

cgc atc gga gtg ctc gct gat cac ctt gtt gag gga tct aaa gaa act 643
 Arg Ile Gly Val Leu Ala Asp His Leu Val Glu Gly Ser Lys Glu Thr
 170 175 180

cgg atg act aaa tca cta ccc gcg gat gtc gct gtc acc ggc cac ccc 691
 Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala Val Thr Gly His Pro
 185 190 195

tac atc gat att tgg gct gct gtg aaa cca gag cgt ttg ggg ctt aag 739
 Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu Arg Leu Gly Leu Lys
 200 205 210

gcg tgg cct gag gtg cca tac ggg gag gat tgg aaa acc ggc atc tgc 787
 Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp Lys Thr Gly Ile Cys
 215 220 225

aaa cga gtt ggc tgg tca gac ccc aaa gaa ggc tgg cac cgt gtg tat 835
 Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly Trp His Arg Val Tyr
 230 235 240 245

aac gcc gtg aat tcc ttc cgc gat ttg gac tac acc cta att ggg gca 883
 Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr Thr Leu Ile Gly Ala
 250 255 260

gtg gaa cgt ttg gtg gat ttt gtg acc aac ctc gat ttg agt aaa gag 931
 Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu Asp Leu Ser Lys Glu
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 Asp Val Leu Ala
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<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Met Ser Phe Ser Asp Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser

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Glu Arg Thr Tyr Asp Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly	50	55	60
Arg Asp Ala Leu Tyr Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly	65	70	75
Gln Ile Val Asn Leu Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys	85	90	95
Ser Asn Ser Gly Ser Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala	100	105	110
Ala Pro Ser Arg Ile Trp Val Glu Gly Ile His Asp Ala Ala Ile Val	115	120	125
Glu Lys Val Trp Gly His Asp Leu Arg Val Glu Gly Val Val Val Glu	130	135	140
Tyr Leu Glu Gly Leu Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln	145	150	155
Pro Gly Pro Gly Arg Arg Ile Gly Val Leu Ala Asp His Leu Val Glu	165	170	175
Gly Ser Lys Glu Thr Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala	180	185	190
Val Thr Gly His Pro Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu	195	200	205
Arg Leu Gly Leu Lys Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp	210	215	220
Lys Thr Gly Ile Cys Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly	225	230	235
Trp His Arg Val Tyr Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr	245	250	255
Thr Leu Ile Gly Ala Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu	260	265	270
Asp Leu Ser Lys Glu Asp Val Leu Ala	275	280	

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(454)

<223> RXN00162

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                                   Val Ser Thr Thr Thr
                                   1 5
cca atc cac cct gag cgc aag aaa cgc gtt cgt cag gcc ctc acc atg 163
Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg Gln Ala Leu Thr Met
                                   10 15 20
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Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe Leu Leu Ala Leu Val
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gcg gag atg atc atg aag tac ata att ggc atg gat ctt cct gag tgg 259
Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met Asp Leu Pro Glu Trp
                                   40 45 50
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Ala Arg Phe Val Pro Ile Ala His Gly Trp Val Tyr Ile Val Phe Leu
                                   55 60 65
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Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg Trp Asn Pro Thr Arg
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tgg gtg acc acc gct atc gca ggt gtg gtt ccg ctg ctg tcg ttt ttt 403
Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro Leu Leu Ser Phe Phe
                                   90 95 100
gtt gag cac aac cgc cgc aag gaa gtt act cag aca ttc cag ctg aac 451
Val Glu His Asn Arg Arg Lys Glu Val Thr Gln Thr Phe Gln Leu Asn
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Ser

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<210> 118

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<400> 118

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  35 40 45
Asp Leu Pro Glu Trp Ala Arg Phe Val Pro Ile Ala His Gly Trp Val
  50 55 60

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Tyr Ile Val Phe Leu Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg
 65 70 75 80
 Trp Asn Pro Thr Arg Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro
 85 90 95
 Leu Leu Ser Phe Phe Val Glu His Asn Arg Arg Lys Glu Val Thr Gln
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 Thr Phe Gln Leu Asn Ser
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 Val Ser Thr Thr Thr
 1 5
 cca atc cac cct gag cgc aag aaa cgc gtt cgt cag gcc ctc acc atg 163
 Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg Gln Ala Leu Thr Met
 10 15 20
 ttc tcc atc gct gcg tgg gtg act ggt gtg ttt ttg ctg gcg ctg gtg 211
 Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe Leu Leu Ala Leu Val
 25 30 35
 gcg gag atg atc atg aag tac ata att ggc atg gat ctt cct gag tgg 259
 Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met Asp Leu Pro Glu Trp
 40 45 50
 gca cga ttc gtt ccg att gca cat gga tgg gtt tac att gtt ttc ttg 307
 Ala Arg Phe Val Pro Ile Ala His Gly Trp Val Tyr Ile Val Phe Leu
 55 60 65
 atg acc acc ctg aac ctg ggt ctg aag gcg cgt tgg aat ccg act cgt 355
 Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg Trp Asn Pro Thr Arg
 70 75 80 85
 tgg gtg acc acc gct atc gca ggt gtg gtt ccg ctg ctg tcg ttt ttt 403
 Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro Leu Leu Ser Phe Phe
 90 95 100
 gtt gag cac aac cgc cgc aag gaa gtt act cag aca ttc cag ctg aac 451
 Val Glu His Asn Arg Arg Lys Glu Val Thr Gln Thr Phe Gln Leu Asn
 105 110 115
 tca tagttaaata cacaaaaacc tcc 477
 Ser

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 <211> 118
 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Leu Leu Ala Leu Val Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met
 35 40 45
 Asp Leu Pro Glu Trp Ala Arg Phe Val Pro Ile Ala His Gly Trp Val
 50 55 60
 Tyr Ile Val Phe Leu Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg
 65 70 75 80
 Trp Asn Pro Thr Arg Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro
 85 90 95
 Leu Leu Ser Phe Phe Val Glu His Asn Arg Arg Lys Glu Val Thr Gln
 100 105 110
 Thr Phe Gln Leu Asn Ser
 115

<210> 121
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> RXN00167

<400> 121
 ccgacaatcc agtggaaactt ccctatcgct gtgatgcatt tttactttca cggtccggta 60
 ccctggcagg cagatcttcc aatcttttagg agccctcgcc atg tac ctg ttg aat 115
 Met Tyr Leu Leu Asn
 1 5
 cca cca gtc act gaa ccc gag atc ctc act gtc aac gag att ccg acc 163
 Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val Asn Glu Ile Pro Thr
 10 15 20
 gtc gtc gct gtc ttt gac aac cac ccc atg aac gac atg ccc gca gca 211
 Val Val Ala Val Phe Asp Asn His Pro Met Asn Asp Met Pro Ala Ala
 25 30 35
 ttc gat caa acc tac caa gtg ctc ttc ccc acc ttg ggt gcc aag ggc 259
 Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr Leu Gly Ala Lys Gly
 40 45 50

atc gcg cca att ggc ccc gga ttt gct ctg tac acc tcc gaa cca act 307
 Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr Thr Ser Glu Pro Thr
 55 60 65
 gac acc gtc agc ttt gaa gtg ggc atc cca gtc agc caa cca ctt gag 355
 Asp Thr Val Ser Phe Glu Val Gly Ile Pro Val Ser Gln Pro Leu Glu
 70 75 80 85
 gga gat gtt tca gcc gcc agc ggc atc gtg ctg aaa aac tca gtg gtc 403
 Gly Asp Val Ser Ala Ala Ser Gly Ile Val Leu Lys Asn Ser Val Val
 90 95 100
 cct gcc gga aaa att gcg cga atc agc cac atc ggc tca ttc gac gga 451
 Pro Ala Gly Lys Ile Ala Arg Ile Ser His Ile Gly Ser Phe Asp Gly
 105 110 115
 ctg agc caa gca tgg ggt tca ttc gtg gaa gct ctt gaa tct gca ggc 499
 Leu Ser Gln Ala Trp Gly Ser Phe Val Glu Ala Leu Glu Ser Ala Gly
 120 125 130
 cat gag atc gat atg ccg tgt tgg gag gta tat gtc acc gag cct tcc 547
 His Glu Ile Asp Met Pro Cys Trp Glu Val Tyr Val Thr Glu Pro Ser
 135 140 145
 ccc gac atg gat ccc gca aca ctc caa act gat cta tac gtc ctg ttg 595
 Pro Asp Met Asp Pro Ala Thr Leu Gln Thr Asp Leu Tyr Val Leu Leu
 150 155 160 165
 aag tagagaagct ttctggtcaa gtt 621
 Lys

<210> 122
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 122
 Met Tyr Leu Leu Asn Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val
 1 5 10 15
 Asn Glu Ile Pro Thr Val Val Ala Val Phe Asp Asn His Pro Met Asn
 20 25 30
 Asp Met Pro Ala Ala Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr
 35 40 45
 Leu Gly Ala Lys Gly Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr
 50 55 60
 Thr Ser Glu Pro Thr Asp Thr Val Ser Phe Glu Val Gly Ile Pro Val
 65 70 75 80
 Ser Gln Pro Leu Glu Gly Asp Val Ser Ala Ala Ser Gly Ile Val Leu
 85 90 95
 Lys Asn Ser Val Val Pro Ala Gly Lys Ile Ala Arg Ile Ser His Ile
 100 105 110

Gly Ser Phe Asp Gly Leu Ser Gln Ala Trp Gly Ser Phe Val Glu Ala
 115 120 125
 Leu Glu Ser Ala Gly His Glu Ile Asp Met Pro Cys Trp Glu Val Tyr
 130 135 140
 Val Thr Glu Pro Ser Pro Asp Met Asp Pro Ala Thr Leu Gln Thr Asp
 145 150 155 160
 Leu Tyr Val Leu Leu Lys
 165

<210> 123
 <211> 361
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> FRXA00167

<400> 123
 ccgacaatcc agtgggaactt ccctatcgct gtgatgcatt tttactttca cgttccggta 60
 ccctggcagg cagatcttcc aatctttagg agccctcgcc atg tac ctg ttg aat 115
 Met Tyr Leu Leu Asn
 1 5
 cca cca gtc act gaa ccc gag atc ctc act gtc aac gag att ccg acc 163
 Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val Asn Glu Ile Pro Thr
 10 15 20
 gtc gtc gct gtc ttt gac aac cac ccc atg aac gac atg ccc gca gca 211
 Val Val Ala Val Phe Asp Asn His Pro Met Asn Asp Met Pro Ala Ala
 25 30 35
 ttc gat caa acc tac caa gtg ctc ttc ccc acc ttg ggt gcc aag ggc 259
 Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr Leu Gly Ala Lys Gly
 40 45 50
 atc gcg cca att ggc ccc gga ttt gct ctg tac acc tcc gaa cca act 307
 Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr Thr Ser Glu Pro Thr
 55 60 65
 gac acc gtc agc ttt gaa gtg ggc atg cca gtc agc caa cca ctt gag 355
 Asp Thr Val Ser Phe Glu Val Gly Met Pro Val Ser Gln Pro Leu Glu
 70 75 80 85
 gga gag 361
 Gly Glu

<210> 124
 <211> 87
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 124

Met Tyr Leu Leu Asn Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val
 1 5 10 15
 Asn Glu Ile Pro Thr Val Val Ala Val Phe Asp Asn His Pro Met Asn
 20 25 30
 Asp Met Pro Ala Ala Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr
 35 40 45
 Leu Gly Ala Lys Gly Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr
 50 55 60
 Thr Ser Glu Pro Thr Asp Thr Val Ser Phe Glu Val Gly Met Pro Val
 65 70 75 80
 Ser Gln Pro Leu Glu Gly Glu
 85

<210> 125
 <211> 281
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(258)
 <223> RXN00171

<400> 125
 aaa gat cag cag aag cag att cat aac ttg gca gct gag gta aag cgt 48
 Lys Asp Gln Gln Lys Gln Ile His Asn Leu Ala Ala Glu Val Lys Arg
 1 5 10 15
 ctt cgt gag cgt gac gat gca cga gat cag cag cta gga gtg ctt aat 96
 Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val Leu Asn
 20 25 30
 gaa gcc atg ttt tca cta cta gga gat gga ctt gac cgt ttt cgt gaa 144
 Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe Arg Glu
 35 40 45
 tct ggc gat gag gca tcc ttc aat gct gca ttg aac tat cag gca gtg 192
 Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln Ala Val
 50 55 60
 gtg gca cca gaa atg ttt aag acc gtg tat ggt gtc gat ccg tct acc 240
 Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro Ser Thr
 65 70 75 80
 gga gag cct att ccc act taaagtacaa cacagtcttt tca 281
 Gly Glu Pro Ile Pro Thr
 85

<210> 126
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 126

Lys Asp Gln Gln Lys Gln Ile His Asn Leu Ala Ala Glu Val Lys Arg
 1 5 10 15
 Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val Leu Asn
 20 25 30
 Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe Arg Glu
 35 40 45
 Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln Ala Val
 50 55 60
 Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro Ser Thr
 65 70 75 80
 Gly Glu Pro Ile Pro Thr
 85

<210> 127
 <211> 354
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(331)
 <223> FRXA00171

<400> 127
 cgattaaggt aggggcctta aaaaggggaa taaagaatat tgggccccaga cgaaaactgc 60
 tggcgagatc atcaaagatc agcagaagca gattcataac ttg gca gct gag gta 115
 Leu Ala Ala Glu Val
 1 5
 aag cgt ctt cgt gag cgt gac gat gca cga gat cag cag cta gga gtg 163
 Lys Arg Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val
 10 15 20
 ctt aat gaa gcc atg ttt tca cta cta gga gat gga ctt gac cgt ttt 211
 Leu Asn Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe
 25 30 35
 cgt gaa tct ggc gat gag gca tcc ttc aat gct gca ttg aac tat cag 259
 Arg Glu Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln
 40 45 50
 gca gtg gtg gca cca gaa atg ttt aag acc gtg tat ggt gtc gat ccg 307
 Ala Val Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro
 55 60 65
 tct acc gga gag cct att ccc act taaagtacaa cacagtcttt tca 354
 Ser Thr Gly Glu Pro Ile Pro Thr
 70 75

<210> 128
 <211> 77
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 128

Leu Ala Ala Glu Val Lys Arg Leu Arg Glu Arg Asp Asp Ala Arg Asp
 1 5 10 15

Gln Gln Leu Gly Val Leu Asn Glu Ala Met Phe Ser Leu Leu Gly Asp
 20 25 30

Gly Leu Asp Arg Phe Arg Glu Ser Gly Asp Glu Ala Ser Phe Asn Ala
 35 40 45

Ala Leu Asn Tyr Gln Ala Val Val Ala Pro Glu Met Phe Lys Thr Val
 50 55 60

Tyr Gly Val Asp Pro Ser Thr Gly Glu Pro Ile Pro Thr
 65 70 75

<210> 129

<211> 564

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(541)

<223> RXN00194

<400> 129

aaatatgaga acatagtgag agttaaacca agttctgtag gtgcttggtg cagcgggcg 60
 gaaggcgtag cactgcaact tgcgaataaa ggagtaaaac gtg gct ggt tcc tcc 115
 Val Ala Gly Ser Ser
 1 5

cac acg att gag cct gag atc tac cgc ggt gta tcc acc ctt gat gag 163
 His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val Ser Thr Leu Asp Glu
 10 15 20

cct tcg gct gca tgg gga tgg cac ggt ctc aag cgc aac acc atc caa 211
 Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys Arg Asn Thr Ile Gln
 25 30 35

ctc gct ggc tgg att tcc gtt ctg ttc atg ctt gga tac aac ttc ggt 259
 Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu Gly Tyr Asn Phe Gly
 40 45 50

aac cac aag ggc cac gtt gaa acc atc tgg ctt ctc gtc atc acc gcc 307
 Asn His Lys Gly His Val Glu Thr Ile Trp Leu Leu Val Ile Thr Ala
 55 60 65

ctt ctg gtc atc ggc ctg ctg atc cac ctg ttc gag cca aag ctc ttc 355
 Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe Glu Pro Lys Leu Phe
 70 75 80 85

cag gtt cgc acc atc act tcc cgc aac aag cct gtc ggc cac gtc gag 403
 Gln Val Arg Thr Ile Thr Ser Arg Asn Lys Pro Val Gly His Val Glu
 90 95 100

cca gac tgg acc tac gac cag gca acc ctc acc ggc acc tgg ggt aac 451
 Pro Asp Trp Thr Tyr Asp Gln Ala Thr Leu Thr Gly Thr Trp Gly Asn

105	110	115	
ctc act gac tcc cag ctt cgc tcc gtc aac atc gag cca agc cgt gtc			499
Leu Thr Asp Ser Gln Leu Arg Ser Val Asn Ile Glu Pro Ser Arg Val			
120	125	130	
gct cac ctg cgt gct gca gat tct gcg aaa gaa cta gac aac			541
Ala His Leu Arg Ala Ala Asp Ser Ala Lys Glu Leu Asp Asn			
135	140	145	
tagtttttta aaaagaaaat gcg			564

<210> 130
 <211> 147
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 130
 Val Ala Gly Ser Ser His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val
 1 5 10 15
 Ser Thr Leu Asp Glu Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys
 20 25 30
 Arg Asn Thr Ile Gln Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu
 35 40 45
 Gly Tyr Asn Phe Gly Asn His Lys Gly His Val Glu Thr Ile Trp Leu
 50 55 60
 Leu Val Ile Thr Ala Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe
 65 70 75 80
 Glu Pro Lys Leu Phe Gln Val Arg Thr Ile Thr Ser Arg Asn Lys Pro
 85 90 95
 Val Gly His Val Glu Pro Asp Trp Thr Tyr Asp Gln Ala Thr Leu Thr
 100 105 110
 Gly Thr Trp Gly Asn Leu Thr Asp Ser Gln Leu Arg Ser Val Asn Ile
 115 120 125
 Glu Pro Ser Arg Val Ala His Leu Arg Ala Ala Asp Ser Ala Lys Glu
 130 135 140
 Leu Asp Asn
 145

<210> 131
 <211> 385
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> FRXA00194

<400> 131

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<210> 132
<211> 95
<212> PRT
<213> Corynebacterium glutamicum
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<400> 132
Val Ala Gly Ser Ser His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val
  1          5          10          15
Ser Thr Leu Asp Glu Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys
          20          25          30
Arg Asn Thr Ile Gln Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu
          35          40          45
Gly Tyr Asn Phe Gly Asn His Lys Gly His Val Glu Thr Ile Trp Leu
          50          55          60
Leu Val Ile Thr Ala Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe
          65          70          75          80
Glu Pro Lys Ala Leu Pro Gly Ser His His His Phe Ser Gln Gln
          85          90          95

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<210> 133
<211> 1335
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (101)..(1312)

<223> RXN00197

<400> 133

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gtc gat gata ttttggcaac cgaatctgag gcacgcgcgc gtgcgaatgc tttgatcaac 60

cggttggcaa ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt 115
                               Val Ala Ala Tyr Leu
                               1 5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt 163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
                               10 15 20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg 211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
                               25 30 35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc 259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
                               40 45 50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt 307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
                               55 60 65

gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg 355
Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
                               70 75 80 85

ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt 403
Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
                               90 95 100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac 451
Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
                               105 110 115

ggc gtg gcg gtg agc tcc gga atc ccg aat ccg gat gtg gat acc acc 499
Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr
                               120 125 130

gcg aca gtc gac acc gtt cag tgc gtg ccg gaa acc caa att tcc gca 547
Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala
                               135 140 145

act gaa ctg tcc tcc tgc gta ggt tca ggc cca gcg ggc gac gcc ggc 595
Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly
                               150 155 160 165

att gag cac ggc gat aag att ttg gcc gtc aac ggc caa gag atg gca 643
Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala
                               170 175 180

agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca ggc gaa acg 691
Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr
                               185 190 195

gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc 739

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Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu	
200 205 210	
cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc	787
Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr	
215 220 225	
gtc ggc gcg gtg ggc atg tcg agc ctt cca ccg acc gat gtg tac aaa	835
Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro Thr Asp Val Tyr Lys	
230 235 240 245	
aaa tac ggc cca atc gag ggt gtg gga gca act gca cgt ttc acc ggc	883
Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly	
250 255 260	
gac atg atc agc gcc acg tgg gat ggc ctc aaa gcc ttc ccg gcg aaa	931
Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys	
265 270 275	
atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa	979
Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu	
280 285 290	
agc ccc atg agt gtg gtg ggc gcc gta cgc atc ggc ggc gaa ttt gtc	1027
Ser Pro Met Ser Val Val Gly Ala Val Arg Ile Gly Gly Glu Phe Val	
295 300 305	
gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac	1075
Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn	
310 315 320 325	
ttc ttc ctc gcg ctg ttt aac ctc gtg ccg ctg cca cca ctt gat ggc	1123
Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu Pro Pro Leu Asp Gly	
330 335 340	
gga cac att gcc gtg gtg atc tat gaa aaa atc cgc gac ttc ttc cgc	1171
Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile Arg Asp Phe Phe Arg	
345 350 355	
aaa ctg cgc gga aaa cca gcg ggc ggc cca gcg gat tac acc aaa cta	1219
Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala Asp Tyr Thr Lys Leu	
360 365 370	
atg ccc gtc acc gta gct gtc gca gcc ttg ctg atg aca gtg gga ggc	1267
Met Pro Val Thr Val Ala Val Ala Ala Leu Leu Met Thr Val Gly Gly	
375 380 385	
ctg gtc att gtc gcc gat gtg gtc aat ccc atc cga ctc ttt ggc	1312
Leu Val Ile Val Ala Asp Val Val Asn Pro Ile Arg Leu Phe Gly	
390 395 400	
taacgatacg gaattgaact gcc	1335

<210> 134

<211> 404

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala

1	5	10	15
Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile	20	25	30
Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val	35	40	45
Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro	50	55	60
Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu	65	70	75
Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln	85	90	95
Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly	100	105	110
Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro	115	120	125
Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu	130	135	140
Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro	145	150	155
Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn	165	170	175
Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu	180	185	190
Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu	195	200	205
Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp	210	215	220
Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro	225	230	235
Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr	245	250	255
Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys	260	265	270
Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala	275	280	285
Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Val Arg Ile	290	295	300
Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met	305	310	315
Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu	325	330	335

Pro Pro Leu Asp Gly Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile
 340 345 350

Arg Asp Phe Phe Arg Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala
 355 360 365

Asp Tyr Thr Lys Leu Met Pro Val Thr Val Ala Val Ala Ala Leu Leu
 370 375 380

Met Thr Val Gly Gly Leu Val Ile Val Ala Asp Val Val Asn Pro Ile
 385 390 395 400

Arg Leu Phe Gly

<210> 135
 <211> 1111
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1111)
 <223> FRXA00197

<400> 135
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cggttggcaa ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt 115
 Val Ala Ala Tyr Leu
 1 5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt 163
 Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
 10 15 20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg 211
 His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
 25 30 35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc 259
 Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
 40 45 50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt 307
 Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
 55 60 65

gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg 355
 Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
 70 75 80 85

ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt 403
 Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
 90 95 100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac 451
 Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
 105 110 115

ggc gtg gcg gtg agc tcc gga atc ccg aat ccg gat gtg gat acc acc 499
 Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr
 120 125 130

gcg aca gtc gac acc gtt cag tgc gtg ccg gaa acc caa att tcc gca 547
 Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala
 135 140 145

act gaa ctg tcc tcc tgc gta ggt tca ggc cca gcg ggc gac gcc ggc 595
 Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly
 150 155 160 165

att gag cac ggc gat aag att ttg gcc gtc aac ggc caa gag atg gca 643
 Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala
 170 175 180

agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca ggc gaa acg 691
 Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr
 185 190 195

gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc 739
 Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu
 200 205 210

cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc 787
 Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr
 215 220 225

gtc ggc gcg gtg ggc atg tcg agc ctt cca ccg acc gat gtg tac aaa 835
 Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro Thr Asp Val Tyr Lys
 230 235 240 245

aaa tac ggc cca atc gag ggt gtg gga gca act gca cgt ttc acc ggc 883
 Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly
 250 255 260

gac atg atc agc gcc acg tgg gat ggc ctc aaa gcc ttc ccg gcg aaa 931
 Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys
 265 270 275

atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa 979
 Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu
 280 285 290

agc ccc atg agt gtg gtg ggc gcg tca cgc atc ggc ggc gaa ttt gtc 1027
 Ser Pro Met Ser Val Val Gly Ala Ser Arg Ile Gly Gly Glu Phe Val
 295 300 305

gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac 1075
 Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn
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<210> 136

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
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 Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
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 Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
 35 40 45
 Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
 50 55 60
 Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
 65 70 75 80
 Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
 85 90 95
 Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
 100 105 110
 Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
 115 120 125
 Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
 130 135 140
 Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
 145 150 155 160
 Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
 165 170 175
 Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
 180 185 190
 Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
 195 200 205
 Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
 210 215 220
 Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
 225 230 235 240
 Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
 245 250 255
 Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys
 260 265 270
 Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
 275 280 285
 Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Ser Arg Ile
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 Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met

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Leu Gly Ala Tyr Gly																	115
1 5																	
tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att																	163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile																	
10 15 20																	
cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga																	211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg																	
25 30 35																	
ggt ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg																	259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met																	
40 45 50																	
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Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro																	
55 60 65																	
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Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp																	
70 75 80 85																	
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Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln																	
90 95 100																	
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Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly																	
105 110 115																	
cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg																	499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala																	
120 125 130																	
ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt																	547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe																	
135 140 145																	

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt 595
 Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu
 150 155 160 165

 atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg 643
 Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala
 170 175 180

 gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg 691
 Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser
 185 190 195

 att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg 739
 Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp
 200 205 210

 gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat 787
 Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp
 215 220 225

 caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc 835
 Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr
 230 235 240 245

 agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta 883
 Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val
 250 255 260

 gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc 931
 Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg
 265 270 275

 ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979
 Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
 280 285 290

 gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc 1027
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
 295 300 305

 gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag 1075
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
 310 315 320 325

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 Asp Ser Cys Asp Leu
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<210> 138

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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 20 25 30

Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
 35 40 45
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
 50 55 60
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65 70 75 80
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
 85 90 95
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
 100 105 110
 Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
 115 120 125
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
 130 135 140
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
 145 150 155 160
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
 165 170 175
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
 180 185 190
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
 195 200 205
 Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
 210 215 220
 Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
 225 230 235 240
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
 245 250 255
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
 260 265 270
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
 275 280 285
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
 290 295 300
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
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 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
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<210> 139

<211> 1269

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1246)

<223> RXN00222

<400> 139

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				Met	Thr	Pro	Thr	Ala	
				1				5	

gat	atc	tg	ttt	aaa	gat	act	ttg	gct	gct	cat	ttc	aca	cgc	gac	ggc	163
Asp	Ile	Trp	Phe	Lys	Asp	Thr	Leu	Ala	Ala	His	Phe	Thr	Arg	Asp	Gly	
			10					15						20		

gac	cag	acc	aca	ttc	tcc	tac	aca	gct	gat	tac	gca	gg	cca	ccg	att	211
Asp	Gln	Thr	Thr	Phe	Ser	Tyr	Thr	Ala	Asp	Tyr	Ala	Gly	Pro	Pro	Ile	
			25					30					35			

gcc	acg	tcc	ctg	ccc	atc	aat	tct	gaa	ccc	gtg	att	acg	cgc	tct	gga	259
Ala	Thr	Ser	Leu	Pro	Ile	Asn	Ser	Glu	Pro	Val	Ile	Thr	Arg	Ser	Gly	
		40				45					50					

gcg	atc	cca	cca	ttt	ttc	gcg	gga	tta	ctc	ccc	gaa	gg	cgt	cgc	tta	307
Ala	Ile	Pro	Pro	Phe	Phe	Ala	Gly	Leu	Leu	Pro	Glu	Gly	Arg	Arg	Leu	
	55					60					65					

agt	tca	ctc	cgg	aga	aac	att	aaa	gcc	tct	gcc	gat	gat	gaa	ctt	tca	355
Ser	Ser	Leu	Arg	Arg	Asn	Ile	Lys	Ala	Ser	Ala	Asp	Asp	Glu	Leu	Ser	
70					75				80					85		

ctc	ctt	cta	gca	gtg	gga	gct	gat	cct	ggt	gg	gca	gtc	gct	atc	ttc	403
Leu	Leu	Leu	Ala	Val	Gly	Ala	Asp	Pro	Val	Gly	Ala	Val	Ala	Ile	Phe	
			90					95						100		

ccc	cat	gg	gaa	aat	aca	caa	cct	gca	cca	ccc	aca	g	gat	ttt	gac	451
Pro	His	Gly	Glu	Asn	Thr	Gln	Pro	Ala	Pro	Pro	Thr	Val	Asp	Phe	Asp	
			105					110					115			

gat	gaa	ctt	gat	ttc	tcg	gct	gca	cta	acc	gag	tcc	ggg	att	gcg	gat	499
Asp	Glu	Leu	Asp	Phe	Ser	Ala	Ala	Leu	Thr	Glu	Ser	Gly	Ile	Ala	Asp	
		120					125					130				

ccc	g	gca	ctg	gcc	gg	gtc	caa	gac	aaa	gcc	tct	gca	cgc	acc	atc	547
Pro	Val	Ala	Leu	Ala	Gly	Val	Gln	Asp	Lys	Ala	Ser	Ala	Arg	Thr	Ile	
	135					140					145					

gcg	gtc	ccc	g	gca	agc	gat	gcc	atc	ttg	aaa	ctc	tcc	ccg	cct	gaa	595
Ala	Val	Pro	Val	Ala	Ser	Asp	Ala	Ile	Leu	Lys	Leu	Ser	Pro	Pro	Glu	
150					155				160						165	

tac	cct	tac	ttg	gtg	gaa	aac	gaa	gca	gct	tgt	tac	cag	ttg	ctg	acc	643
Tyr	Pro	Tyr	Leu	Val	Glu	Asn	Glu	Ala	Ala	Cys	Tyr	Gln	Leu	Leu	Thr	
			170					175						180		

aaa	aat	aag	ctt	cgc	att	gaa	ctg	tcc	aaa	gta	gaa	g	ctc	cat	gac	691
Lys	Asn	Lys	Leu	Arg	Ile	Glu	Leu	Ser	Lys	Val	Glu	Val	Leu	His	Asp	

185	190	195	
aaa cac ggc agg tcc gga ctc tta gtt cac cgc ttt gac cgc aca ccc			739
Lys His Gly Arg Ser Gly Leu Leu Val His Arg Phe Asp Arg Thr Pro			
200	205	210	
aaa ggc aaa atc ccc gtc gag gat gca gga cag gtc ttg gga atc tgg			787
Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln Val Leu Gly Ile Trp			
215	220	225	
cct gca gat aaa tac tta gtg agc tac gag gac atc gca caa gcc ctc			835
Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp Ile Ala Gln Ala Leu			
230	235	240	245
act aaa gtg tgc gcc tcc ccc atc ttg gcg atg cgc aat ctc gcc ttc			883
Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met Arg Asn Leu Ala Phe			
250	255	260	
caa atc gca gtc gcg tgg ctc agc ggc aat ggt gat ctt cat gcc aag			931
Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly Asp Leu His Ala Lys			
265	270	275	
aac atc tcc att atc aac aaa ggc cgc gga ttt gag atc agc ccc atc			979
Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe Glu Ile Ser Pro Ile			
280	285	290	
tat gac atc cct gcc acc gca gta tat ggc gac acc acg atg gca tta			1027
Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp Thr Thr Met Ala Leu			
295	300	305	
gaa atc cag gga tcc aaa aag gat ctc agc caa aag aaa ttc cta aaa			1075
Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln Lys Lys Phe Leu Lys			
310	315	320	325
ttc tgt aca tcc atc gga cta cca gaa aaa aca gcc atg tcg gtt gcg			1123
Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr Ala Met Ser Val Ala			
330	335	340	
aac gct gca ctg ttg gca aca gaa aat gcc gca gag aca att ctt gct			1171
Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala Glu Thr Ile Leu Ala			
345	350	355	
tcg gga aat ttt gat aca cgg atg aat cga gat ctg gcc agg gtt ctc			1219
Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp Leu Ala Arg Val Leu			
360	365	370	
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Lys His Arg Arg Ser Ala Trp Gly Ala			
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tcg			1269

<210> 140

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

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 35 40 45
 Ile Thr Arg Ser Gly Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro
 50 55 60
 Glu Gly Arg Arg Leu Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala
 65 70 75 80
 Asp Asp Glu Leu Ser Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly
 85 90 95
 Ala Val Ala Ile Phe Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro
 100 105 110
 Thr Val Asp Phe Asp Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu
 115 120 125
 Ser Gly Ile Ala Asp Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala
 130 135 140
 Ser Ala Arg Thr Ile Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys
 145 150 155 160
 Leu Ser Pro Pro Glu Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys
 165 170 175
 Tyr Gln Leu Leu Thr Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val
 180 185 190
 Glu Val Leu His Asp Lys His Gly Arg Ser Gly Leu Leu Val His Arg
 195 200 205
 Phe Asp Arg Thr Pro Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln
 210 215 220
 Val Leu Gly Ile Trp Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp
 225 230 235 240
 Ile Ala Gln Ala Leu Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met
 245 250 255
 Arg Asn Leu Ala Phe Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly
 260 265 270
 Asp Leu His Ala Lys Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe
 275 280 285
 Glu Ile Ser Pro Ile Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp
 290 295 300
 Thr Thr Met Ala Leu Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln
 305 310 315 320
 Lys Lys Phe Leu Lys Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr
 325 330 335

Ala Met Ser Val Ala Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala
 340 345 350

Glu Thr Ile Leu Ala Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp
 355 360 365

Leu Ala Arg Val Leu Lys His Arg Arg Ser Ala Trp Gly Ala
 370 375 380

<210> 141

<211> 1269

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1246)

<223> FRXA00222

<400> 141

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                                         Met Thr Pro Thr Ala
                                         1                     5

gat atc tgg ttt aaa gat act ttg gct gct cat ttc aca cgc gac ggc 163
Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His Phe Thr Arg Asp Gly
                        10                     15                     20

gac cag acc aca ttc tcc tac aca gct gat tac gca ggt cca ccg att 211
Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr Ala Gly Pro Pro Ile
                        25                     30                     35

gcc acg tcc ctg ccc atc aat tct gaa ccc gtg att acg cgc tct gga 259
Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val Ile Thr Arg Ser Gly
                        40                     45                     50

gcg atc cca cca ttt ttc gcg gga tta ctc ccc gaa ggt cgt cgc tta 307
Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro Glu Gly Arg Arg Leu
                        55                     60                     65

agt tca ctc cgg aga aac att aaa gcc tct gcc gat gat gaa ctt tca 355
Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala Asp Asp Glu Leu Ser
                        70                     75                     80                     85

ctc ctt cta gca gtg gga gct gat cct gtt ggt gca gtc gct atc ttc 403
Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly Ala Val Ala Ile Phe
                        90                     95                     100

ccc cat ggt gaa aat aca caa cct gca cca ccc aca gtt gat ttt gac 451
Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro Thr Val Asp Phe Asp
                        105                     110                     115

gat gaa ctt gat ttc tcg gct gca cta acc gag tcc ggg att gcg gat 499
Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu Ser Gly Ile Ala Asp
                        120                     125                     130

ccc gtt gca ctg gcc ggt gtc caa gac aaa gcc tct gca cgc acc atc 547
Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala Ser Ala Arg Thr Ile
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aaa aat aag ctt cgc att gaa ctg tcc aaa gta gaa gtt ctc cat gac Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val Glu Val Leu His Asp 185 190 195			691
aaa cac ggc agg tcc gga ctc tta gtt cac cgc ttt gac cgc aca ccc Lys His Gly Arg Ser Gly Leu Leu Val His Arg Phe Asp Arg Thr Pro 200 205 210			739
aaa ggc aaa atc ccc gtc gag gat gca gga cag gtc ttg gga atc tgg Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln Val Leu Gly Ile Trp 215 220 225			787
cct gca gat aaa tac tta gtg agc tac gag gac atc gca caa gcc ctc Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp Ile Ala Gln Ala Leu 230 235 240 245			835
act aaa gtg tgc gcc tcc ccc atc ttg gcg atg cgc aat ctc gcc ttc Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met Arg Asn Leu Ala Phe 250 255 260			883
caa atc gca gtc gcg tgg ctc agc ggc aat ggt gat ctt cat gcc aag Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly Asp Leu His Ala Lys 265 270 275			931
aac atc tcc att atc aac aaa ggc cgc gga ttt gag atc agc ccc atc Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe Glu Ile Ser Pro Ile 280 285 290			979
tat gac atc cct gcc acc gca gta tat ggc gac acc acg atg gca tta Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp Thr Thr Met Ala Leu 295 300 305			1027
gaa atc cag gga tcc aaa aag gat ctc agc caa aag aaa ttc cta aaa Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln Lys Lys Phe Leu Lys 310 315 320 325			1075
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aac gct gca ctg ttg gca aca gaa aat gcc gca gag aca att ctt gct Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala Glu Thr Ile Leu Ala 345 350 355			1171
tcg gga aat ttt gat aca cgg atg aat cga gat ctg gcc agg gtt ctc Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp Leu Ala Arg Val Leu 360 365 370			1219
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tcg

1269

<210> 142

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

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35 40 45

Ile Thr Arg Ser Gly Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro
50 55 60

Glu Gly Arg Arg Leu Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala
65 70 75 80

Asp Asp Glu Leu Ser Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly
85 90 95

Ala Val Ala Ile Phe Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro
100 105 110

Thr Val Asp Phe Asp Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu
115 120 125

Ser Gly Ile Ala Asp Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala
130 135 140

Ser Ala Arg Thr Ile Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys
145 150 155 160

Leu Ser Pro Pro Glu Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys
165 170 175

Tyr Gln Leu Leu Thr Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val
180 185 190

Glu Val Leu His Asp Lys His Gly Arg Ser Gly Leu Leu Val His Arg
195 200 205

Phe Asp Arg Thr Pro Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln
210 215 220

Val Leu Gly Ile Trp Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp
225 230 235 240

Ile Ala Gln Ala Leu Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met
245 250 255

Arg Asn Leu Ala Phe Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly
260 265 270

Asp Leu His Ala Lys Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe
 275 280 285
 Glu Ile Ser Pro Ile Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp
 290 295 300
 Thr Thr Met Ala Leu Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln
 305 310 315 320
 Lys Lys Phe Leu Lys Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr
 325 330 335
 Ala Met Ser Val Ala Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala
 340 345 350
 Glu Thr Ile Leu Ala Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp
 355 360 365
 Leu Ala Arg Val Leu Lys His Arg Arg Ser Ala Trp Gly Ala
 370 375 380

<210> 143

<211> 633

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(610)

<223> RXN00232

<400> 143

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 Met Asn Asp Arg Ala
 1 5
 cac caa cga ata ggc gac atc gag cga tcc caa gcc ctc gac cga ctt 163
 His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln Ala Leu Asp Arg Leu
 10 15 20
 ggg tca tat ttt gca gac gga tac ctc gac atc gac gaa ttc gat acc 211
 Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile Asp Glu Phe Asp Thr
 25 30 35
 cga acc ggc gcc gca gca atc gca cgc aca gcc ggt gaa ata gat gtc 259
 Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala Gly Glu Ile Asp Val
 40 45 50
 ttg ttc aca gat ctt ccc gaa caa cag gca agc acc gcc gtg aca ccc 307
 Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser Thr Ala Val Thr Pro
 55 60 65
 gtg caa gac gat acc gag aaa gaa tta gac ctg gtc cta cag cga gga 355
 Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu Val Leu Gln Arg Gly
 70 75 80 85
 aag aag ctc aag cag atc gac tcc gcc att tgg gct gtc gtg atg gtc 403
 Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp Ala Val Val Met Val

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Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val Pro Tyr Phe Trp Val						
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gtg ttc atc ctt ggc gga gcg gcc tcc gcg ggt gcg cga ttc ttg ctc						499
Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly Ala Arg Phe Leu Leu						
	120		125		130	
aaa gta gat gac gcc gat gaa aaa ctc ttt gag gaa ctc cac agc aag						547
Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu Glu Leu His Ser Lys						
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gaa caa agc gaa cgc gaa gca cgc cta cgc att gcg gca caa cgt cga						595
Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile Ala Ala Gln Arg Arg						
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Arg Glu Leu Glu Gln						
	170					

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<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

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Asp	Glu	Phe	Asp	Thr	Arg	Thr	Gly	Ala	Ala	Ala	Ile	Ala	Arg	Thr	Ala
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Gly	Glu	Ile	Asp	Val	Leu	Phe	Thr	Asp	Leu	Pro	Glu	Gln	Gln	Ala	Ser
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Thr	Ala	Val	Thr	Pro	Val	Gln	Asp	Asp	Thr	Glu	Lys	Glu	Leu	Asp	Leu
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Val	Leu	Gln	Arg	Gly	Lys	Lys	Leu	Lys	Gln	Ile	Asp	Ser	Ala	Ile	Trp
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Ala	Val	Val	Met	Val	Ser	Phe	Phe	Leu	Gly	Leu	Phe	Val	Phe	Asn	Val
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Pro	Tyr	Phe	Trp	Val	Val	Phe	Ile	Leu	Gly	Gly	Ala	Ala	Ser	Ala	Gly
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Ala	Arg	Phe	Leu	Leu	Lys	Val	Asp	Asp	Ala	Asp	Glu	Lys	Leu	Phe	Glu
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Glu	Leu	His	Ser	Lys	Glu	Gln	Ser	Glu	Arg	Glu	Ala	Arg	Leu	Arg	Ile
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Ala	Ala	Gln	Arg	Arg	Arg	Glu	Leu	Glu	Gln
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Arg Glu Leu Glu Gln

170

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<400> 146
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 35 40 45
 Gly Glu Ile Asp Val Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser
 50 55 60
 Thr Ala Val Thr Pro Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu
 65 70 75 80
 Val Leu Gln Arg Gly Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp
 85 90 95
 Ala Val Val Met Val Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val
 100 105 110
 Pro Tyr Phe Trp Val Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly
 115 120 125
 Ala Arg Phe Leu Leu Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu
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 Glu Leu His Ser Lys Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile
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 Ala Ala Gln Arg Arg Arg Glu Leu Glu Gln
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 <222> (101)..(826)
 <223> RXN00236

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 Met Val Ile Ser Phe
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<213> Corynebacterium glutamicum

<400> 148
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35 40 45
Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
50 55 60
Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
65 70 75 80
Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
85 90 95
Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
100 105 110
Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
115 120 125
Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
130 135 140
Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
145 150 155 160
Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
165 170 175
Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
180 185 190
Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
195 200 205
Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
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Ala Ile

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                                         Met Val Ile Ser Phe
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Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
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Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
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ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt 259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
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Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
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Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
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Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
                        90                        95                        100

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Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu
                        105                        110                        115

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Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
                        120                        125                        130

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Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
                        135                        140                        145

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Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
                        150                        155                        160                        165

ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta 643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
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gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg 691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
                        185                        190                        195

ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca 739

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 215 220 225

gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa 836
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<211> 242

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
 50 55 60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65 70 75 80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
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Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
 100 105 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
 115 120 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
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Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
 145 150 155 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
 165 170 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
 180 185 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
 195 200 205

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Ala Ile

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN00242

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 Val Asn Glu Trp Arg
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 Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr Val Ile Ile Ser Val
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 gcc gtg ttt act tct gct gtg gct ctg ctc gga gtt gtg aaa aag cgc 211
 Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly Val Val Lys Lys Arg
 25 30 35
 tct cgg tgg cgg gtt ctc gga gct ctc atc tcc tca gca gtt ctc acc 259
 Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser Ser Ala Val Leu Thr
 40 45 50
 agt ggc gca tgg gtg gtt att gaa aag ctg tgg aag cct ttc ccc gac 307
 Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp Lys Pro Phe Pro Asp
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 Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly Leu Ala Val Phe Pro
 70 75 80 85
 ctg ttg agc atc ttg ttc cgc act ggt cgt aca aga ata ctg atg gct 403
 Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr Arg Ile Leu Met Ala
 90 95 100
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 Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala Ala Val Ile Asn Val
 105 110 115
 atc tac cag cca tac ccg acg ttg ggt tct ttc aat ccc gtg cca acg 499
 Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe Asn Pro Val Pro Thr
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 gct gtg tcc atg tcg tat gca gat ttt gaa tct cag acc act gcc ccg 547
 Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser Gln Thr Thr Ala Pro
 135 140 145

acg atg gat gac cgt gaa gtc ggt gcc ctt gtg cag gtg ccg cta gct	595
Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val Gln Val Pro Leu Ala	
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Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp Ala Arg Asp Ala Tyr	
170 175 180	
gcc tat att ccg cct gcg tat tgg gat aat cct tcc cta caa ctg cca	691
Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro Ser Leu Gln Leu Pro	
185 190 195	
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Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln Pro Asp Gln Trp Phe	
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Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn Phe Gln Ala Thr His	
215 220 225	
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Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp Gly Thr Gly Ser Phe	
230 235 240 245	
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Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala Gln Ser Val Met Thr	
250 255 260	
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Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys Gln Lys Phe Arg Val	
265 270 275	
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Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly Leu Ser Tyr Gly Gly	
280 285 290	
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Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro Glu Ala Tyr Gly Ser	
295 300 305	
ttc ctt gac ttc tcg ggc cag gaa gaa cca aca ctt ggc aca cgc cag	1075
Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr Leu Gly Thr Arg Gln	
310 315 320 325	
caa act gtt gat cag ctt ttc ggc ggc gat gaa gac gca ttc aaa gcc	1123
Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu Asp Ala Phe Lys Ala	
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Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile Ser Ser Gly Ala His	
345 350 355	
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Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala Gly Ser Asn Asp Lys	
360 365 370	
agt gca gtg agc gcg ctg tct cat ctt gat aat ttg agc aat cag gcg	1267
Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn Leu Ser Asn Gln Ala	
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 390 395 400 405

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 Val Trp Arg Val Ala Leu Ala Asn Thr Phe Asp Trp Val Ala Lys Arg
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<210> 152
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 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30

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 35 40 45

Ser Ala Val Leu Thr Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp
 50 55 60

Lys Pro Phe Pro Asp Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly
 65 70 75 80

Leu Ala Val Phe Pro Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr
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Arg Ile Leu Met Ala Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala
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Ala Val Ile Asn Val Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe
 115 120 125

Asn Pro Val Pro Thr Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser
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Gln Thr Thr Ala Pro Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val
 145 150 155 160

Gln Val Pro Leu Ala Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp
 165 170 175

Ala Arg Asp Ala Tyr Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro
 180 185 190

Ser Leu Gln Leu Pro Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln
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 210 215 220

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<223> FRXA00242
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aca gtc tcg ctt gta gat tcc acg gcg ctg acc gtg atc atc agt gtg 163
Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr Val Ile Ile Ser Val
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Pro	Asn	Pro	Trp	Thr	Ile	Tyr	Leu	Ser	Ala	Gly	Leu	Ala	Val	Phe	Pro		
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Thr	Leu	Thr	Val	Ile	Ala	Leu	Val	Asn	Thr	Ala	Ala	Val	Ile	Asn	Val		
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Ala	Val	Ser	Met	Ser	Tyr	Ala	Asp	Phe	Glu	Ser	Gln	Thr	Thr	Ala	Pro		
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Gly	Thr	Thr	Asp	Asp	Ser	Thr	Ser	Gly	Phe	Asp	Ala	Arg	Asp	Ala	Tyr		
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Val	Leu	Val	Leu	Met	Pro	Gly	Asn	Pro	Gly	Gln	Pro	Asp	Gln	Trp	Phe		
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Ser	Ser	Gly	Asn	Ala	Asp	Gln	Thr	Ala	Asp	Asn	Phe	Gln	Ala	Thr	His		
	215					220					225						
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Asp	Gly	Ile	Ser	Pro	Ile	Val	Ile	Ser	Val	Asp	Gly	Thr	Gly	Ser	Phe		
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Ser	Gly	Asn	Pro	Ala	Cys	Val	Asp	Ser	Asp	Ala	Gln	Ser	Val	Met	Thr		
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tat	cta	tcc	cac	gat	gtc	ccc	atg	ttg	atc	aaa	cag	aaa	ttc	cga	gtc	931	
Tyr	Leu	Ser	His	Asp	Val	Pro	Met	Leu	Ile	Lys	Gln	Lys	Phe	Arg	Val		

265	270	275	
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280	285	290	
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Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro Glu Ala Tyr Gly Ser			
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ttc ctt gac ttc tcg ggc cag gaa gaa cca aca ctt ggc aca cgc cag			1075
Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr Leu Gly Thr Arg Gln			
310	315	320	325
caa act gtt gat cag ctt ttc ggc ggc gat gaa gac gca ttc aaa gcc			1123
Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu Asp Ala Phe Lys Ala			
330	335	340	
gtt aat ccg gaa gat ctg ctc aat caa gca atc agc tca gga gcg cat			1171
Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile Ser Ser Gly Ala His			
345	350	355	
acc tac agc ggg att tcg ggc agg ttt att gct ggt agc aac gat aaa			1219
Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala Gly Ser Asn Asp Lys			
360	365	370	
agt gca gtg agc gcg ctg tct cat ctt gat aat ttg agc aat cag gcg			1267
Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn Leu Ser Asn Gln Ala			
375	380	385	
ggc atg tcc acc acc ttt gat acc gtg gcc ggt gga			1303
Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly Gly			
390	395	400	

<210> 154

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Val Asn Glu Trp Arg Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr
1 5 10 15

Val Ile Ile Ser Val Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly
20 25 30

Val Val Lys Lys Arg Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser
35 40 45

Ser Ala Val Leu Thr Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp
50 55 60

Lys Pro Phe Pro Asp Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly
65 70 75 80

Leu Ala Val Phe Pro Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr
85 90 95

Arg Ile Leu Met Ala Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala
100 105 110

Ala Val Ile Asn Val Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe
115 120 125

Asn Pro Val Pro Thr Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser
130 135 140

Gln Thr Thr Ala Pro Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val
145 150 155 160

Gln Val Pro Leu Ala Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp
165 170 175

Ala Arg Asp Ala Tyr Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro
180 185 190

Ser Leu Gln Leu Pro Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln
195 200 205

Pro Asp Gln Trp Phe Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn
210 215 220

Phe Gln Ala Thr His Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp
225 230 235 240

Gly Thr Gly Ser Phe Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala
245 250 255

Gln Ser Val Met Thr Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys
260 265 270

Gln Lys Phe Arg Val Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly
275 280 285

Leu Ser Tyr Gly Gly Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro
290 295 300

Glu Ala Tyr Gly Ser Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr
305 310 315 320

Leu Gly Thr Arg Gln Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu
325 330 335

Asp Ala Phe Lys Ala Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile
340 345 350

Ser Ser Gly Ala His Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala
355 360 365

Gly Ser Asn Asp Lys Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn
370 375 380

Leu Ser Asn Gln Ala Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly
385 390 395 400

Gly

<210> 155

<211> 1050

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1027)

<223> RXN00247

<400> 155

aaccctaac tactgacctc gcaccacttg ttgcagcccg ttaccacgct gcattgagcg 60

cactgctggc	acatatctaa	gaccgctaag	gaaatcagct	atg	cag	aca	tta	atc	115
				Met	Gln	Thr	Leu	Ile	
				1				5	

ttt	atc	gcc	att	gca	ggc	gtc	gca	gca	cag	ctt	gtt	gat	ggc	ggc	ctc	163
Phe	Ile	Ala	Ile	Ala	Gly	Val	Ala	Ala	Gln	Leu	Val	Asp	Gly	Gly	Leu	
			10						15						20	

ggc	atg	ggg	ttc	ggc	gtc	acc	tca	acc	acc	atc	ctc	atc	atg	ctc	gca	211
Gly	Met	Gly	Phe	Gly	Val	Thr	Ser	Thr	Thr	Ile	Leu	Ile	Met	Leu	Ala	
			25					30					35			

ggt	tta	ggc	cct	gcg	cag	gca	tcc	gcc	gtc	gtg	cac	acc	gca	gag	gtt	259
Gly	Leu	Gly	Pro	Ala	Gln	Ala	Ser	Ala	Val	Val	His	Thr	Ala	Glu	Val	
			40				45					50				

gga	acc	acc	tta	gtt	tct	ggt	tta	agc	cac	tgg	aaa	ttt	ggc	aac	gtg	307
Gly	Thr	Thr	Leu	Val	Ser	Gly	Leu	Ser	His	Trp	Lys	Phe	Gly	Asn	Val	
	55					60					65					

gat	tgg	aaa	gta	gtt	gtc	cgg	ctc	ggt	atc	ccc	ggc	gct	atc	ggc	gca	355
Asp	Trp	Lys	Val	Val	Val	Arg	Leu	Gly	Ile	Pro	Gly	Ala	Ile	Gly	Ala	
	70					75				80					85	

ttt	gct	ggc	gct	acc	ttc	ttg	tcc	aat	att	tcc	acc	gaa	gca	gca	gca	403
Phe	Ala	Gly	Ala	Thr	Phe	Leu	Ser	Asn	Ile	Ser	Thr	Glu	Ala	Ala	Ala	
				90					95					100		

ccg	atc	acc	tcc	ctg	att	ctt	gcc	ctg	atc	ggc	atg	aac	cta	gtc	tgg	451
Pro	Ile	Thr	Ser	Leu	Ile	Leu	Ala	Leu	Ile	Gly	Met	Asn	Leu	Val	Trp	
			105					110					115			

cga	ttc	agc	aag	gga	cgc	atc	cgc	cgc	gac	tat	tcc	gat	cgc	ccg	cac	499
Arg	Phe	Ser	Lys	Gly	Arg	Ile	Arg	Arg	Asp	Tyr	Ser	Asp	Arg	Pro	His	
		120				125						130				

agc	agg	gga	ttc	ctc	ggc	gga	ctc	ggt	att	gtc	ggt	ggt	ttc	gtt	gac	547
Ser	Arg	Gly	Phe	Leu	Gly	Gly	Leu	Gly	Ile	Val	Gly	Gly	Phe	Val	Asp	
	135					140					145					

gca	tcc	ggt	ggc	ggc	gga	tgg	ggt	cca	gtg	acc	acc	tct	acg	ctg	ctg	595
Ala	Ser	Gly	Gly	Gly	Gly	Trp	Gly	Pro	Val	Thr	Thr	Ser	Thr	Leu	Leu	
	150				155				160						165	

tct	ttg	gga	cgc	acc	gaa	ccc	cgc	aaa	gta	gtc	ggc	acc	gtc	aac	acc	643
Ser	Leu	Gly	Arg	Thr	Glu	Pro	Arg	Lys	Val	Val	Gly	Thr	Val	Asn	Thr	
			170					175						180		

gca	gaa	ttc	tta	gtc	tcc	cta	gcc	gca	aca	ttg	ggc	ttc	gtc	gtg	gga	691
Ala	Glu	Phe	Leu	Val	Ser	Leu	Ala	Ala	Thr	Leu	Gly	Phe	Val	Val	Gly	

185	190	195	
ctg tgg gat gac cta gta gct aac	ctc tct gca gtt ctc gcg ttg ctc	739	
Leu Trp Asp Asp Leu Val Ala Asn	Leu Ser Ala Val Leu Ala Leu Leu		
200	210		
atc ggc ggc gca atc gca gca cca	atc ggc gcc tgg atg atc tct cgc	787	
Ile Gly Gly Ala Ile Ala Ala Pro	Ile Gly Ala Trp Met Ile Ser Arg		
215	225		
gtt aat gca acc gtc ctc ggt ggc	ttc gtg ggc acc ctg att gtc aca	835	
Val Asn Ala Thr Val Leu Gly Gly	Phe Val Gly Thr Leu Ile Val Thr		
230	240	245	
ctg aac ctg cca aag gtg ctc aac	gtg gtt ggc ctt gat ttc atc ccc	883	
Leu Asn Leu Pro Lys Val Leu Asn	Val Val Gly Leu Asp Phe Ile Pro		
250	255	260	
acc ggc ctc atc cag gtc acc gtc	ctc ctc atc ggc ctg ccg ctg acg	931	
Thr Gly Leu Ile Gln Val Thr Val	Leu Leu Ile Gly Leu Pro Leu Thr		
265	270	275	
tac ctc ggc ttc cgc cgc tac cgc	aaa aat ctc ctc aac gag acc atc	979	
Tyr Leu Gly Phe Arg Arg Tyr Arg	Lys Asn Leu Leu Asn Glu Thr Ile		
280	285	290	
tcc agc gaa gtt gtc tcc gaa cca	aag ggc caa aag att aaa agc act	1027	
Ser Ser Glu Val Val Ser Glu Pro	Lys Gly Gln Lys Ile Lys Ser Thr		
295	300	305	
taaaacacgc ttttcgacgc cca		1050	

<210> 156

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Gln Thr Leu Ile Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu
1 5 10 15

Val Asp Gly Gly Leu Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile
20 25 30

Leu Ile Met Leu Ala Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val
35 40 45

His Thr Ala Glu Val Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp
50 55 60

Lys Phe Gly Asn Val Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro
65 70 75 80

Gly Ala Ile Gly Ala Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser
85 90 95

Thr Glu Ala Ala Ala Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly
100 105 110

Met Asn Leu Val Trp Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr

115	120	125
Ser Asp Arg Pro His Ser	Arg Gly Phe Leu Gly	Gly Leu Gly Ile Val
130	135	140
Gly Gly Phe Val Asp Ala Ser	Gly Gly Gly Gly Trp Gly Pro Val Thr	
145	150	155
Thr Ser Thr Leu Leu Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val		
	165	170
Gly Thr Val Asn Thr Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu		
	180	185
Gly Phe Val Val Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala		
	195	200
Val Leu Ala Leu Leu Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala		
	210	215
Trp Met Ile Ser Arg Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly		
	225	230
Thr Leu Ile Val Thr Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly		
	245	250
Leu Asp Phe Ile Pro Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile		
	260	265
Gly Leu Pro Leu Thr Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu		
	275	280
Leu Asn Glu Thr Ile Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln		
	290	295
Lys Ile Lys Ser Thr		
305		

<210> 157
 <211> 1050
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1027)
 <223> FRXA00247

<400> 157
 aaccctaac tactgacctc gcaccacttg ttgcagcccg ttaccacgct gcattgagcg 60
 cactgctggc acatatctaa gaccgctaag gaaatcagct atg cag aca tta atc 115
 Met Gln Thr Leu Ile
 1 5
 ttt atc gcc att gca ggc gtc gca gca cag ctt gtt gat ggc ggc ctc 163
 Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu Val Asp Gly Gly Leu
 10 15 20
 ggc atg ggg ttc ggc gtc acc tca acc acc atc ctc atc atg ctc gca 211

Gly	Met	Gly	Phe	Gly	Val	Thr	Ser	Thr	Thr	Ile	Leu	Ile	Met	Leu	Ala		
			25					30					35				
ggt	tta	ggc	cct	gcg	cag	gca	tcc	gcc	gtc	gtg	cac	acc	gca	gag	gtt	259	
Gly	Leu	Gly	Pro	Ala	Gln	Ala	Ser	Ala	Val	Val	His	Thr	Ala	Glu	Val		
		40					45					50					
gga	acc	acc	tta	gtt	tct	ggt	tta	agc	cac	tgg	aaa	ttt	ggc	aac	gtg	307	
Gly	Thr	Thr	Leu	Val	Ser	Gly	Leu	Ser	His	Trp	Lys	Phe	Gly	Asn	Val		
	55					60					65						
gat	tgg	aaa	gta	gtt	gtc	cgg	ctc	ggt	atc	ccc	ggc	gct	atc	ggc	gca	355	
Asp	Trp	Lys	Val	Val	Val	Arg	Leu	Gly	Ile	Pro	Gly	Ala	Ile	Gly	Ala		
	70					75				80					85		
ttt	gct	ggc	gct	acc	ttc	ttg	tcc	aat	att	tcc	acc	gaa	gca	gca	gca	403	
Phe	Ala	Gly	Ala	Thr	Phe	Leu	Ser	Asn	Ile	Ser	Thr	Glu	Ala	Ala	Ala		
				90					95					100			
ccg	atc	acc	tcc	ctg	att	ctt	gcc	ctg	atc	ggc	atg	aac	cta	gtc	tgg	451	
Pro	Ile	Thr	Ser	Leu	Ile	Leu	Ala	Leu	Ile	Gly	Met	Asn	Leu	Val	Trp		
			105					110					115				
cga	ttc	agc	aag	gga	cgc	atc	cgc	cgc	gac	tat	tcc	gat	cgc	ccg	cac	499	
Arg	Phe	Ser	Lys	Gly	Arg	Ile	Arg	Arg	Asp	Tyr	Ser	Asp	Arg	Pro	His		
		120					125					130					
agc	agg	gga	ttc	ctc	ggc	gga	ctc	ggt	att	gtc	ggt	ggt	ttc	gtt	gac	547	
Ser	Arg	Gly	Phe	Leu	Gly	Gly	Leu	Gly	Ile	Val	Gly	Gly	Phe	Val	Asp		
	135					140					145						
gca	tcc	ggt	ggc	ggc	gga	tgg	ggt	cca	gtg	acc	acc	tct	acg	ctg	ctg	595	
Ala	Ser	Gly	Gly	Gly	Gly	Trp	Gly	Pro	Val	Thr	Thr	Ser	Thr	Leu	Leu		
	150					155				160					165		
tct	ttg	gga	cgc	acc	gaa	ccc	cgc	aaa	gta	gtc	ggc	acc	gtc	aac	acc	643	
Ser	Leu	Gly	Arg	Thr	Glu	Pro	Arg	Lys	Val	Val	Gly	Thr	Val	Asn	Thr		
				170					175					180			
gca	gaa	ttc	tta	gtc	tcc	cta	gcc	gca	aca	ttg	ggc	ttc	gtc	gtg	gga	691	
Ala	Glu	Phe	Leu	Val	Ser	Leu	Ala	Ala	Thr	Leu	Gly	Phe	Val	Val	Gly		
			185					190					195				
ctg	tgg	gat	gac	cta	gta	gct	aac	ctc	tct	gca	gtt	ctc	gcg	ttg	ctc	739	
Leu	Trp	Asp	Asp	Leu	Val	Ala	Asn	Leu	Ser	Ala	Val	Leu	Ala	Leu	Leu		
		200					205					210					
atc	ggc	ggc	gca	atc	gca	gca	cca	atc	ggc	ggc	tgg	atg	atc	tct	cgc	787	
Ile	Gly	Gly	Ala	Ile	Ala	Ala	Pro	Ile	Gly	Ala	Trp	Met	Ile	Ser	Arg		
	215					220					225						
gtt	aat	gca	acc	gtc	ctc	ggt	ggc	ttc	gtg	ggc	acc	ctg	att	gtc	aca	835	
Val	Asn	Ala	Thr	Val	Leu	Gly	Gly	Phe	Val	Gly	Thr	Leu	Ile	Val	Thr		
	230				235					240				245			
ctg	aac	ctg	cca	aag	gtg	ctc	aac	gtg	gtt	ggc	ctt	gat	ttc	atc	ccc	883	
Leu	Asn	Leu	Pro	Lys	Val	Leu	Asn	Val	Val	Gly	Leu	Asp	Phe	Ile	Pro		
				250				255						260			
acc	ggc	ctc	atc	cag	gtc	acc	gtc	ctc	ctc	atc	ggc	ctg	ccg	ctg	acg	931	
Thr	Gly	Leu	Ile	Gln	Val	Thr	Val	Leu	Leu	Ile	Gly	Leu	Pro	Leu	Thr		

265	270	275	
tac ctc ggc ttc cgc cgc tac cgc	aaa aat ctc ctc aac gag acc atc		979
Tyr Leu Gly Phe Arg Arg Tyr Arg	Lys Asn Leu Leu Asn Glu Thr Ile		
280	285	290	
tcc agc gaa gtt gtc tcc gaa cca aag ggc caa aag att aaa agc act			1027
Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln Lys Ile Lys Ser Thr			
295	300	305	
taaaacacgc ttttcgacgc cca			1050

<210> 158
 <211> 309
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 158
 Met Gln Thr Leu Ile Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu
 1 5 10 15
 Val Asp Gly Gly Leu Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile
 20 25 30
 Leu Ile Met Leu Ala Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val
 35 40 45
 His Thr Ala Glu Val Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp
 50 55 60
 Lys Phe Gly Asn Val Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro
 65 70 75 80
 Gly Ala Ile Gly Ala Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser
 85 90 95
 Thr Glu Ala Ala Ala Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly
 100 105 110
 Met Asn Leu Val Trp Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr
 115 120 125
 Ser Asp Arg Pro His Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val
 130 135 140
 Gly Gly Phe Val Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
 145 150 155 160
 Thr Ser Thr Leu Leu Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val
 165 170 175
 Gly Thr Val Asn Thr Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu
 180 185 190
 Gly Phe Val Val Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala
 195 200 205
 Val Leu Ala Leu Leu Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala
 210 215 220

Trp Met Ile Ser Arg Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly
225 230 235 240

Thr Leu Ile Val Thr Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly
245 250 255

Leu Asp Phe Ile Pro Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile
260 265 270

Gly Leu Pro Leu Thr Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu
275 280 285

Leu Asn Glu Thr Ile Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln
290 295 300

Lys Ile Lys Ser Thr
305

<210> 159

<211> 894

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(871)

<223> RXN00256

<400> 159

aattaatcaa tcagaaaaac atattgaata cttataaatt tctgacatac tcattaatga 60

gatattcgaa gtctttatca aaatgattaa caaaaggagt atg ttt atg tcg cta 115
Met Phe Met Ser Leu
1 5

aaa act cgc cga ata ttc ggc gca ctt gct gtt tcg cta tca atc tct 163
Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val Ser Leu Ser Ile Ser
10 15 20

ttc tca gcc att gct aca cct gca gca tcc gca caa gaa cta gtg gtg 211
Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala Gln Glu Leu Val Val
25 30 35

agc aca tca gca gta aac gaa ttt ggt gta gtt acc agt gac atc acg 259
Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val Thr Ser Asp Ile Thr
40 45 50

gct gag caa att ctt cag gcg caa gat cta atc gct gag atg aaa cag 307
Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile Ala Glu Met Lys Gln
55 60 65

tca gag gac ata tat gag tat ttc ggt gcc ttg tct gac gtt gaa cag 355
Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu Ser Asp Val Glu Gln
70 75 80 85

aga tcc atc att gca gct gta aag gaa aat cca tat ctc att gag aac 403
Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro Tyr Leu Ile Glu Asn
90 95 100

gaa tca ccc cgt atg aga gtc caa agt gaa aca ccc gac gag gaa aca 451

Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr Pro Asp Glu Glu Thr
 105 110 115
 cct gat aag aaa aag ccg agc aaa acc tac aag ctc tat atg agc att 499
 Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys Leu Tyr Met Ser Ile
 120 125 130
 ctc gaa atg atg tca tgt atc aat ctt gtt gat gtt ccg tca tgt gcc 547
 Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp Val Pro Ser Cys Ala
 135 140 145
 caa gcc ctt aaa gcg gca aat ata gct gaa cgc gag gcc aag gcc cgt 595
 Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg Glu Ala Lys Ala Arg
 150 155 160 165
 tac ccc gat tcg gtc act aat ggt aaa ggc gat gcc ctt cgt cat tgt 643
 Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp Ala Leu Arg His Cys
 170 175 180
 gca tgg agc gct ctc atg act att cga atc gga aaa gat gca gcc gaa 691
 Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly Lys Asp Ala Ala Glu
 185 190 195
 aga att ggt aac gct cat gaa acc gtt gtg aga ggt gaa ccc gaa gaa 739
 Arg Ile Gly Asn Ala His Glu Thr Val Val Arg Gly Glu Pro Glu Glu
 200 205 210
 aga gaa atg gat ctc atc aat aac gcg ctg ggt aga gac atc ggc gaa 787
 Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly Arg Asp Ile Gly Glu
 215 220 225
 aga ttc atc atc aat ggc gat gaa acg ggt gcg ctc agt act tgt gta 835
 Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala Leu Ser Thr Cys Val
 230 235 240 245
 tcc atg gct aat atc ggg cta ctt cat act ctg ttg taaacaaagg 881
 Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu Leu
 250 255
 aagtttctat cat 894

<210> 160

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Phe Met Ser Leu Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val
 1 5 10 15

Ser Leu Ser Ile Ser Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala
 20 25 30

Gln Glu Leu Val Val Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val
 35 40 45

Thr Ser Asp Ile Thr Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile
 50 55 60

Ala Glu Met Lys Gln Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu

65	70	75	80
Ser Asp Val Glu Gln Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro	85	90	95
Tyr Leu Ile Glu Asn Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr	100	105	110
Pro Asp Glu Glu Thr Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys	115	120	125
Leu Tyr Met Ser Ile Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp	130	135	140
Val Pro Ser Cys Ala Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg	145	150	155
Glu Ala Lys Ala Arg Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp	165	170	175
Ala Leu Arg His Cys Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly	180	185	190
Lys Asp Ala Ala Glu Arg Ile Gly Asn Ala His Glu Thr Val Val Arg	195	200	205
Gly Glu Pro Glu Glu Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly	210	215	220
Arg Asp Ile Gly Glu Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala	225	230	235
Leu Ser Thr Cys Val Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu	245	250	255

Leu

<210> 161
 <211> 894
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(871)
 <223> FRXA00256

<400> 161
 aattaatcaa tcagaaaaac atattgaata cttataaatt tctgacatac tcattaatga 60
 gatattcgaa gtctttatca aaatgattaa caaaaggagt atg ttt atg tcg cta 115
 Met Phe Met Ser Leu 5
 aaa act cgc cga ata ttc ggc gca ctt gct gtt tcg cta tca atc tct 163
 Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val Ser Leu Ser Ile Ser 20
 ttc tca gcc att gct aca cct gca gca tcc gca caa gaa cta gtg gtg 211

Phe	Ser	Ala	Ile	Ala	Thr	Pro	Ala	Ala	Ser	Ala	Gln	Glu	Leu	Val	Val	
			25					30					35			
agc	aca	tca	gca	gta	aac	gaa	ttt	ggt	gta	ggt	acc	agt	gac	atc	acg	259
Ser	Thr	Ser	Ala	Val	Asn	Glu	Phe	Gly	Val	Val	Thr	Ser	Asp	Ile	Thr	
		40					45					50				
gct	gag	caa	att	ctt	cag	gcg	caa	gat	cta	atc	gct	gag	atg	aaa	cag	307
Ala	Glu	Gln	Ile	Leu	Gln	Ala	Gln	Asp	Leu	Ile	Ala	Glu	Met	Lys	Gln	
	55					60					65					
tca	gag	gac	ata	tat	gag	tat	ttc	ggt	gcc	ttg	tct	gac	ggt	gaa	cag	355
Ser	Glu	Asp	Ile	Tyr	Glu	Tyr	Phe	Gly	Ala	Leu	Ser	Asp	Val	Glu	Gln	
	70				75				80						85	
aga	tcc	atc	att	gca	gct	gta	aag	gaa	aat	cca	tat	ctc	att	gag	aac	403
Arg	Ser	Ile	Ile	Ala	Ala	Val	Lys	Glu	Asn	Pro	Tyr	Leu	Ile	Glu	Asn	
				90					95					100		
gaa	tca	ccc	cgt	atg	aga	gtc	caa	agt	gaa	aca	ccc	gac	gag	gaa	aca	451
Glu	Ser	Pro	Arg	Met	Arg	Val	Gln	Ser	Glu	Thr	Pro	Asp	Glu	Glu	Thr	
			105					110					115			
cct	gat	aag	aaa	aag	ccg	agc	aaa	acc	tac	aag	ctc	tat	atg	agc	att	499
Pro	Asp	Lys	Lys	Lys	Pro	Ser	Lys	Thr	Tyr	Lys	Leu	Tyr	Met	Ser	Ile	
		120					125					130				
ctc	gaa	atg	atg	tca	tgt	atc	aat	ctt	gtt	gat	gtt	ccg	tca	tgt	gcc	547
Leu	Glu	Met	Met	Ser	Cys	Ile	Asn	Leu	Val	Asp	Val	Pro	Ser	Cys	Ala	
	135				140						145					
caa	gcc	ctt	aaa	gcg	gca	aat	ata	gct	gaa	cgc	gag	gcc	aag	gcc	cgt	595
Gln	Ala	Leu	Lys	Ala	Ala	Asn	Ile	Ala	Glu	Arg	Glu	Ala	Lys	Ala	Arg	
	150			155					160						165	
tac	ccc	gat	tcg	gtc	act	aat	ggt	aaa	ggc	gat	gcc	ctt	cgt	cat	tgt	643
Tyr	Pro	Asp	Ser	Val	Thr	Asn	Gly	Lys	Gly	Asp	Ala	Leu	Arg	His	Cys	
			170					175						180		
gca	tgg	agc	gct	ctc	atg	act	att	cga	atc	gga	aaa	gat	gca	gcc	gaa	691
Ala	Trp	Ser	Ala	Leu	Met	Thr	Ile	Arg	Ile	Gly	Lys	Asp	Ala	Ala	Glu	
			185					190					195			
aga	att	ggt	aac	gct	cat	gaa	acc	gtt	gtg	aga	ggt	gaa	ccc	gaa	gaa	739
Arg	Ile	Gly	Asn	Ala	His	Glu	Thr	Val	Val	Arg	Gly	Glu	Pro	Glu	Glu	
		200					205					210				
aga	gaa	atg	gat	ctc	atc	aat	aac	gcg	ctg	ggt	aga	gac	atc	ggc	gaa	787
Arg	Glu	Met	Asp	Leu	Ile	Asn	Asn	Ala	Leu	Gly	Arg	Asp	Ile	Gly	Glu	
	215					220					225					
aga	ttc	atc	atc	aat	ggc	gat	gaa	acg	ggt	gcg	ctc	agt	act	tgt	gta	835
Arg	Phe	Ile	Ile	Asn	Gly	Asp	Glu	Thr	Gly	Ala	Leu	Ser				

<210> 162
 <211> 257
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 162
 Met Phe Met Ser Leu Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val
 1 5 10 15
 Ser Leu Ser Ile Ser Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala
 20 25 30
 Gln Glu Leu Val Val Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val
 35 40 45
 Thr Ser Asp Ile Thr Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile
 50 55 60
 Ala Glu Met Lys Gln Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu
 65 70 75 80
 Ser Asp Val Glu Gln Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro
 85 90 95
 Tyr Leu Ile Glu Asn Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr
 100 105 110
 Pro Asp Glu Glu Thr Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys
 115 120 125
 Leu Tyr Met Ser Ile Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp
 130 135 140
 Val Pro Ser Cys Ala Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg
 145 150 155 160
 Glu Ala Lys Ala Arg Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp
 165 170 175
 Ala Leu Arg His Cys Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly
 180 185 190
 Lys Asp Ala Ala Glu Arg Ile Gly Asn Ala His Glu Thr Val Val Arg
 195 200 205
 Gly Glu Pro Glu Glu Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly
 210 215 220
 Arg Asp Ile Gly Glu Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala
 225 230 235 240
 Leu Ser Thr Cys Val Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu
 245 250 255
 Leu

<210> 163
 <211> 501

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXN00264

<400> 163

aaaccggaag ggcccgttta ctcccctact tggcgcagaa atccacatca atccaggtga 60

agcagtcatc tttgatgttg atcccacggt tgaacacggt ttg ctt gtc gat tcc 115
 Leu Leu Val Asp Ser
 1 5

ggc gac gtc caa cta gaa ggc gtc acc gtc gag ccc acc cag ctg gcc 163
 Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu Pro Thr Gln Leu Ala
 10 15 20

tac acc ggc atc aat gaa acc caa ctc cga atc cgt aac atc ggc acc 211
 Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile Arg Asn Ile Gly Thr
 25 30 35

aca ccg gcg cgt act gta ctg cta ggt ggc gaa cca ttt acc gaa gac 259
 Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu Pro Phe Thr Glu Asp
 40 45 50

atc gtg atg tgg tgg aac ttc att ggc cgc agc cat gaa gaa att gcc 307
 Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser His Glu Glu Ile Ala
 55 60 65

gag tac cgt aaa cag tgg cag gcc gaa gct gat cgt ttt ggt atc acc 355
 Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp Arg Phe Gly Ile Thr
 70 75 80 85

cac gga tat atc agc cac cac aaa gat ggg ctc acc agg ctt cca gca 403
 His Gly Tyr Ile Ser His His Lys Asp Gly Leu Thr Arg Leu Pro Ala
 90 95 100

ccc gag ctt ccc aac gct gct atc aag gca cgt aaa aac cca gca cca 451
 Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg Lys Asn Pro Ala Pro
 105 110 115

act gca cga cca gaa acg aga att gat taaatgcgct ccgctcacgg 498
 Thr Ala Arg Pro Glu Thr Arg Ile Asp
 120 125

ccc 501

<210> 164

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Leu Leu Val Asp Ser Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu
 1 5 10 15

Pro Thr Gln Leu Ala Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile
 20 25 30

ccc gag ctt ccc aac gct gct atc aag gca cgt aaa aac cca gca cca 451
 Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg Lys Asn Pro Ala Pro
 105 110 115

act gca cga cca gaa acg aga att gat taaatgcgct ccgctcacgg 498
 Thr Ala Arg Pro Glu Thr Arg Ile Asp
 120 125

ccc 501

<210> 166
 <211> 126
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 166
 Leu Leu Val Asp Ser Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu
 1 5 10 15
 Pro Thr Gln Leu Ala Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile
 20 25 30
 Arg Asn Ile Gly Thr Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu
 35 40 45
 Pro Phe Thr Glu Asp Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser
 50 55 60
 His Glu Glu Ile Ala Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp
 65 70 75 80
 Arg Phe Gly Ile Thr His Gly Tyr Ile Ser His His Lys Asp Gly Leu
 85 90 95
 Thr Arg Leu Pro Ala Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg
 100 105 110
 Lys Asn Pro Ala Pro Thr Ala Arg Pro Glu Thr Arg Ile Asp
 115 120 125

<210> 167
 <211> 441
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(418)
 <223> RXN00267

<400> 167
 gtcgtactta tcttttaaag tcatgcctta aaggatacgg agatcactcc ggcttggtt 60
 ggggtggcggg gttatcaaag tagtcgtagc gttgagaact atg cga aac tct aag 115
 Met Arg Asn Ser Lys
 1 5
 tct ggc ctg gcc ttt tcc gca gct gca cta ttt tgt gtc gtc gcg gta 163
 Ser Gly Leu Ala Phe Ser Ala Ala Ala Leu Phe Cys Val Val Ala Val

	10	15	20	
atc act cgt att gca agt tcc cca tca ttt atc gct att gtg gcg atc				211
Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile Ala Ile Val Ala Ile				
	25	30	35	
atc gtg gct gcg atc gca ctt ttt gtg ggt ctg aac agt cgt gtg gga				259
Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu Asn Ser Arg Val Gly				
	40	45	50	
aca aag ctt gtt gat cag cca gtg gtg ttc acc cag gaa caa att gat				307
Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr Gln Glu Gln Ile Asp				
	55	60	65	
caa ttg aaa gag ttg aaa tcc cgc gac cag gag gcg gca gcg atc cgt				355
Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu Ala Ala Ala Ile Arg				
	70	75	80	85
cag gcg cag ctg tgg agt agg gga tcg tcc agc gaa gcg gtc gca gag				403
Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser Glu Ala Val Ala Glu				
	90	95	100	
gct gtg agg aag ctc taagtcgact taagtgcgcg aag				441
Ala Val Arg Lys Leu				
	105			

<210> 168

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Met	Arg	Asn	Ser	Lys	Ser	Gly	Leu	Ala	Phe	Ser	Ala	Ala	Ala	Leu	Phe
1				5					10					15	

Cys	Val	Val	Ala	Val	Ile	Thr	Arg	Ile	Ala	Ser	Ser	Pro	Ser	Phe	Ile
			20					25					30		

Ala	Ile	Val	Ala	Ile	Ile	Val	Ala	Ala	Ile	Ala	Leu	Phe	Val	Gly	Leu
		35					40					45			

Asn	Ser	Arg	Val	Gly	Thr	Lys	Leu	Val	Asp	Gln	Pro	Val	Val	Phe	Thr
	50					55					60				

Gln	Glu	Gln	Ile	Asp	Gln	Leu	Lys	Glu	Leu	Lys	Ser	Arg	Asp	Gln	Glu
65					70					75					80

Ala	Ala	Ala	Ile	Arg	Gln	Ala	Gln	Leu	Trp	Ser	Arg	Gly	Ser	Ser	Ser
				85				90						95	

Glu	Ala	Val	Ala	Glu	Ala	Val	Arg	Lys	Leu
		100						105	

<210> 169

<211> 358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (66)..(335)
 <223> FRXA00267

<400> 169

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cgtacggttg agaactatgc gaaactctaa gtctggcctg gccttttccg cagctgcact 60

atattt gtg tct gtc gcg gta atc act cgt att gca agt tcc cca tca ttt 110
Val Ser Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe
      1             5             10             15

atc gct att gtg gcg atc atc gtg gct gcg atc gca ctt ttt gtg ggt 158
Ile Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly
      20             25             30

ctg aac agt cgt gtg gga aca aag ctt gtt gat cag cca gtg gtg ttc 206
Leu Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe
      35             40             45

acc cag gaa caa att gat caa ttg aaa gag ttg aaa tcc cgc gac cag 254
Thr Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln
      50             55             60

gag gcg gca gcg atc cgt cag gcg cag ctg tgg agt agg gga tcg tcc 302
Glu Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser
      65             70             75

agc gaa gcg gtc gca gag gct gtg agg aag ctg taagtcgact taagtgcgcg 355
Ser Glu Ala Val Ala Glu Ala Val Arg Lys Leu
      80             85             90

aag 358

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<210> 170
 <211> 90
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 170

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Val Ser Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile
      1             5             10             15

Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu
      20             25             30

Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr
      35             40             45

Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu
      50             55             60

Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser
      65             70             75             80

Glu Ala Val Ala Glu Ala Val Arg Lys Leu
      85             90

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<210> 171
 <211> 1113

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1090)

<223> RXN00271

<400> 171

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tagttttaa at catgagacat ttcacatatg gttctttatc cgagacatgt gttgacgctg 60
tctgccccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
                                         Met Phe Ser Ser Arg
                                         1                               5
tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
                        10                        15                        20
tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
                        25                        30                        35
ggg ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
                        40                        45                        50
gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
                        55                        60                        65
ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
                        70                        75                        80                        85
act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
                        90                        95                        100
gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
                        105                        110                        115
act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
                        120                        125                        130
gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act 547
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
                        135                        140                        145
tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg 595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
                        150                        155                        160                        165
gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
                        170                        175                        180
aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg 691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu

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185	190	195	
ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln 200 205 210			739
cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr 215 220 225			787
gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu 230 235 240 245			835
cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly 250 255 260			883
ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln 265 270 275			931
act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala 280 285 290			979
acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu 295 300 305			1027
gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp 310 315 320 325			1075
aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga Lys Ala Glu Arg Val 330			1113

<210> 172
 <211> 330
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 172
 Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly
 1 5 10 15
 Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
 20 25 30
 Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
 35 40 45
 Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
 50 55 60
 Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
 65 70 75 80
 Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser

85										90					95				
Asp	Asn	Leu	Asp	Leu	Val	Leu	Ala	Val	Ala	Thr	Pro	Ala	Ala	Gln	Ala				
			100						105					110					
Thr	Ala	Gln	Asn	Ile	Thr	Asp	Ile	Pro	Val	Leu	Phe	Thr	Ala	Val	Thr				
		115					120						125						
Asp	Ala	Val	Ser	Ala	Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly				
		130					135					140							
Asn	Val	Thr	Gly	Thr	Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu				
		145				150				155					160				
Leu	Leu	Gln	Gln	Leu	Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr				
				165					170					175					
Ala	Ser	Gly	Glu	Val	Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys				
			180					185					190						
Ala	Ala	Glu	Pro	Leu	Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr				
		195						200					205						
Val	Asn	Glu	Ile	Gln	Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val				
		210				215					220								
Ile	Tyr	Val	Pro	Thr	Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu				
		225			230					235					240				
Val	Gln	Val	Ala	Glu	Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser				
				245					250					255					
Gly	Thr	Val	Glu	Gly	Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr				
			260					265						270					
Glu	Leu	Gly	Arg	Gln	Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp				
		275					280					285							
Gly	Glu	Asp	Pro	Ala	Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr				
		290				295					300								
Tyr	Val	Ile	Asn	Glu	Asp	Ala	Ala	Glu	Arg	Gln	Gly	Val	Glu	Ile	Pro				
		305			310					315					320				
Gln	Glu	Ile	Leu	Asp	Lys	Ala	Glu	Arg	Val										
			325					330											

<210> 173

<211> 1113

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1090)

<223> FRXA00271

<400> 173

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tctgccccctt tttgaaaata acactttaag gagatgtgcc	atg ttt tct tcc cgt	115
	Met Phe Ser Ser Arg	
	1 5	
tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct	163	
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala		
10 15 20		
tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca	211	
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala		
25 30 35		
ggg ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct	259	
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro		
40 45 50		
gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca	307	
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala		
55 60 65		
ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc	355	
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly		
70 75 80 85		
act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc	403	
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu		
90 95 100		
gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc	451	
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile		
105 110 115		
act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca	499	
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala		
120 125 130		
gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act	547	
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr		
135 140 145		
tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg	595	
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu		
150 155 160 165		
gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc	643	
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val		
170 175 180		
aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg	691	
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu		
185 190 195		
ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag	739	
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln		
200 205 210		
cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act	787	
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr		
215 220 225		
gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag	835	

Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu
 230 235 240 245
 cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt 883
 Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly
 250 255 260
 ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag 931
 Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln
 265 270 275
 act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca 979
 Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala
 280 285 290
 acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa 1027
 Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu
 295 300 305
 gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat 1075
 Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp
 310 315 320 325
 aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga 1113
 Lys Ala Glu Arg Val
 330

<210> 174

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly
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 20 25 30
 Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
 35 40 45
 Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
 50 55 60
 Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
 65 70 75 80
 Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
 85 90 95
 Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
 100 105 110
 Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
 115 120 125
 Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
 130 135 140

Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
 145 150 155 160
 Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
 165 170 175
 Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
 180 185 190
 Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
 195 200 205
 Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
 210 215 220
 Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
 225 230 235 240
 Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser
 245 250 255
 Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr
 260 265 270
 Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp
 275 280 285
 Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr
 290 295 300
 Tyr Val Ile Asn Glu Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro
 305 310 315 320
 Gln Glu Ile Leu Asp Lys Ala Glu Arg Val
 325 330

<210> 175
 <211> 495
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(472)
 <223> RXN00272

<400> 175
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 tccagtgggt ggccatctgc cacaaccagg tgcagggcac atg ccg gaa cca gaa 115
 Met Pro Glu Pro Glu
 1 5
 acc tcc acg atg ggc tcc atc caa aag tcc ggt gaa tgg ctc gtt cct 163
 Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly Glu Trp Leu Val Pro
 10 15 20
 gca tat tcg gca tac aag ctc aac ggt gct gac ctt ttc tta gat atc 211
 Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp Leu Phe Leu Asp Ile
 25 30 35

cgc cat gcc acc gcg gct gct cct gtc att acc ttt gat gtc aac atg 259
 Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr Phe Asp Val Asn Met
 40 45 50
 acc atg ggt tct atg acg ctg att gtt cca ccg ggt gtg tat gtg gaa 307
 Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro Gly Val Tyr Val Glu
 55 60 65
 gtg cag atg gct tcc aag aac tgg tcg gat ttc aag gtt caa aca acc 355
 Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe Lys Val Gln Thr Thr
 70 75 80 85
 aat cct ctc ccc ggt gct ccc cga gtg ttc atc act ggt gtt gca cgc 403
 Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile Thr Gly Val Ala Arg
 90 95 100
 gca tca ggg ttg aag gtt ttc acc aag cat cct cat gag cct ttt ggg 451
 Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro His Glu Pro Phe Gly
 105 110 115
 ttc tgg cag aaa atg ttt gag tagcctcggg ccacgcccga acc 495
 Phe Trp Gln Lys Met Phe Glu
 120

<210> 176
 <211> 124
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 176
 Met Pro Glu Pro Glu Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly
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 Glu Trp Leu Val Pro Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp
 20 25 30
 Leu Phe Leu Asp Ile Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr
 35 40 45
 Phe Asp Val Asn Met Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro
 50 55 60
 Gly Val Tyr Val Glu Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe
 65 70 75 80
 Lys Val Gln Thr Thr Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile
 85 90 95
 Thr Gly Val Ala Arg Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro
 100 105 110
 His Glu Pro Phe Gly Phe Trp Gln Lys Met Phe Glu
 115 120

<210> 177
 <211> 495
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(472)

<223> FRXA00272

<400> 177

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tccagtgggt ggccatctgc cacaaccagg tgcagggcac atg ccg gaa cca gaa 115
                                         Met Pro Glu Pro Glu
                                         1 5

acc tcc acg atg ggc tcc atc caa aag tcc ggt gaa tgg ctc gtt cct 163
Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly Glu Trp Leu Val Pro
              10              15              20

gca tat tcg gca tac aag ctc aac ggt gct gac ctt ttc tta gat atc 211
Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp Leu Phe Leu Asp Ile
              25              30              35

cgc cat gcc acc gcg gct gct cct gtc att acc ttt gat gtc aac atg 259
Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr Phe Asp Val Asn Met
              40              45              50

acc atg ggt tct atg acg ctg att gtt cca ccg ggt gtg tat gtg gaa 307
Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro Gly Val Tyr Val Glu
              55              60              65

gtg cag atg gct tcc aag aac tgg tcg gat ttc aag gtt caa aca acc 355
Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe Lys Val Gln Thr Thr
              70              75              80              85

aat cct ctc ccc ggt gct ccc cga gtg ttc atc act ggt gtt gca cgc 403
Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile Thr Gly Val Ala Arg
              90              95              100

gca tca ggg ttg aag gtt ttc acc aag cat cct cat gag cct ttt ggg 451
Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro His Glu Pro Phe Gly
              105              110              115

ttc tgg cag aaa atg ttt gag tagcctcggg ccacgcccga acc 495
Phe Trp Gln Lys Met Phe Glu
              120

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<210> 178

<211> 124

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

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Met Pro Glu Pro Glu Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly
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Glu Trp Leu Val Pro Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp
  20              25              30

Leu Phe Leu Asp Ile Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr
  35              40              45

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Phe	Asp	Val	Asn	Met	Thr	Met	Gly	Ser	Met	Thr	Leu	Ile	Val	Pro	Pro
	50					55					60				
Gly	Val	Tyr	Val	Glu	Val	Gln	Met	Ala	Ser	Lys	Asn	Trp	Ser	Asp	Phe
65					70					75					80
Lys	Val	Gln	Thr	Thr	Asn	Pro	Leu	Pro	Gly	Ala	Pro	Arg	Val	Phe	Ile
				85					90					95	
Thr	Gly	Val	Ala	Arg	Ala	Ser	Gly	Leu	Lys	Val	Phe	Thr	Lys	His	Pro
			100					105					110		
His	Glu	Pro	Phe	Gly	Phe	Trp	Gln	Lys	Met	Phe	Glu				
		115					120								

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<210> 179
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1132)
<223> RXN00283
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<400> 179																	
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tggactgtcg gatttatgac atggcgcgca cgataccgcc																	115
<div>Val Ala Ser Ala Thr</div> <div>1 5</div>																	
gca tcg gat tcg cac ttg tcg aca tgc tgc tcc tcg tct ggc cga tcg																	163
<div>Ala Ser Asp Ser His Leu Ser Thr Cys Cys Ser Ser Ser Gly Arg Ser</div> <div>10 15 20</div>																	
gct tcg cct tcg tcg cct gga ctg gcg cca agc tgg ctc act acc ggc																	211
<div>Ala Ser Pro Ser Ser Pro Gly Leu Ala Pro Ser Trp Leu Thr Thr Gly</div> <div>25 30 35</div>																	
gaa ctc ttt gcc caa ttc acc tcc aca gac ggc aac gct gcg atc atc																	259
<div>Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly Asn Ala Ala Ile Ile</div> <div>40 45 50</div>																	
gca gca tcc ggc ggc ggc gcc ata ggg ccc caa gcg ctt ttc gac gcc																	307
<div>Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln Ala Leu Phe Asp Ala</div> <div>55 60 65</div>																	
tcc gtc cgc acc ttc ctc atc tcc cca gct ctc cta ctc gtc gca gta																	355
<div>Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu Leu Leu Val Ala Val</div> <div>70 75 80 85</div>																	
gtt gca gtc ttt ttt gct tat cga cgc cgc gac ccc gaa ccc atc atc																	403
<div>Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp Pro Glu Pro Ile Ile</div> <div>90 95 100</div>																	
ccc tta gct ctc atc ggc tct gtg gtg ttc ttc caa atc att acc tac																	451
<div>Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe Gln Ile Ile Thr Tyr</div> <div>105 110 115</div>																	

tca ctt gga tct acc ttc ggc ctg ctg cgc ttt ttc ctc acc gcc ctg	499
Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe Phe Leu Thr Ala Leu	
120 125 130	
ccg ctc acc att atc ttg ctg ttc caa att atc ccg ccc cgc cac cga	547
Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile Pro Pro Arg His Arg	
135 140 145	
ttc ccc tca ctg cga cca ggt gcg tgc tac cgc gat cgc gtc acc ggc	595
Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg Asp Arg Val Thr Gly	
150 155 160 165	
aag tac gtg ccc aaa aca atc acc ggt gtt tta gtt ctc gcg atc ttc	643
Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu Val Leu Ala Ile Phe	
170 175 180	
ggc ggc acc ggc atc acc ctg tac ggc atg agc agt gct aac tgg gcg	691
Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser Ser Ala Asn Trp Ala	
185 190 195	
ccc cag gaa tat gcc atc caa gaa cta gtt ttc aac atg gga tcg cca	739
Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe Asn Met Gly Ser Pro	
200 205 210	
tcg cag gac gcc gtc cac acc ctg aac acc ttc tcc act gaa atg gat	787
Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe Ser Thr Glu Met Asp	
215 220 225	
gtc gcc gat ttc gtc gac tcc cta aac ctt gga gac ggc gaa gtc ctt	835
Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly Asp Gly Glu Val Leu	
230 235 240 245	
ctc tcc acc acc tac ggc ttc gcc gtc ctc acc gca tca aac aac caa	883
Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr Ala Ser Asn Asn Gln	
250 255 260	
aag caa ttc atc atc ccc tcc gac gaa gac ttc atc acc acc ctc aac	931
Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe Ile Thr Thr Leu Asn	
265 270 275	
gaa ccc gct gag cac ggc gtt aag tac atc ctc gcc ctc cca cgc gaa	979
Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu Ala Leu Pro Arg Glu	
280 285 290	
ggt cgc ggc gcc acc gac ccg atc aac ctg cgc tac cca gac atg tat	1027
Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg Tyr Pro Asp Met Tyr	
295 300 305	
gaa acc ggc agc cac atc gcc acg atg gaa atc gaa ttc atc aat caa	1075
Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile Glu Phe Ile Asn Gln	
310 315 320 325	
ggc caa gga caa cca aat tgg cgc ctc tat cgg gtg ctc acc aca cct	1123
Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg Val Leu Thr Thr Pro	
330 335 340	
gaa cag tcg tagactcttt gtaactaccg ttg	1155
Glu Gln Ser	

<210> 180

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Val	Ala	Ser	Ala	Thr	Ala	Ser	Asp	Ser	His	Leu	Ser	Thr	Cys	Cys	Ser
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Ser	Ser	Gly	Arg	Ser	Ala	Ser	Pro	Ser	Ser	Pro	Gly	Leu	Ala	Pro	Ser
		20					25						30		

Trp	Leu	Thr	Thr	Gly	Glu	Leu	Phe	Ala	Gln	Phe	Thr	Ser	Thr	Asp	Gly
		35					40					45			

Asn	Ala	Ala	Ile	Ile	Ala	Ala	Ser	Gly	Gly	Gly	Ala	Ile	Gly	Pro	Gln
	50					55					60				

Ala	Leu	Phe	Asp	Ala	Ser	Val	Arg	Thr	Phe	Leu	Ile	Ser	Pro	Ala	Leu
65					70					75					80

Leu	Leu	Val	Ala	Val	Val	Ala	Val	Phe	Phe	Ala	Tyr	Arg	Arg	Arg	Asp
				85					90					95	

Pro	Glu	Pro	Ile	Ile	Pro	Leu	Ala	Leu	Ile	Gly	Ser	Val	Val	Phe	Phe
			100					105					110		

Gln	Ile	Ile	Thr	Tyr	Ser	Leu	Gly	Ser	Thr	Phe	Gly	Leu	Leu	Arg	Phe
		115					120					125			

Phe	Leu	Thr	Ala	Leu	Pro	Leu	Thr	Ile	Ile	Leu	Leu	Phe	Gln	Ile	Ile
	130					135					140				

Pro	Pro	Arg	His	Arg	Phe	Pro	Ser	Leu	Arg	Pro	Gly	Ala	Cys	Tyr	Arg
145					150					155					160

Asp	Arg	Val	Thr	Gly	Lys	Tyr	Val	Pro	Lys	Thr	Ile	Thr	Gly	Val	Leu
				165					170					175	

Val	Leu	Ala	Ile	Phe	Gly	Gly	Thr	Gly	Ile	Thr	Leu	Tyr	Gly	Met	Ser
			180					185					190		

Ser	Ala	Asn	Trp	Ala	Pro	Gln	Glu	Tyr	Ala	Ile	Gln	Glu	Leu	Val	Phe
		195				200						205			

Asn	Met	Gly	Ser	Pro	Ser	Gln	Asp	Ala	Val	His	Thr	Leu	Asn	Thr	Phe
	210					215					220				

Ser	Thr	Glu	Met	Asp	Val	Ala	Asp	Phe	Val	Asp	Ser	Leu	Asn	Leu	Gly
225					230					235					240

Asp	Gly	Glu	Val	Leu	Leu	Ser	Thr	Thr	Tyr	Gly	Phe	Ala	Val	Leu	Thr
				245					250					255	

Ala	Ser	Asn	Asn	Gln	Lys	Gln	Phe	Ile	Ile	Pro	Ser	Asp	Glu	Asp	Phe
			260					265					270		

Ile	Thr	Thr	Leu	Asn	Glu	Pro	Ala	Glu	His	Gly	Val	Lys	Tyr	Ile	Leu
		275					280						285		

Ala	Leu	Pro	Arg	Glu	Gly	Arg	Gly	Ala	Thr	Asp	Pro	Ile	Asn	Leu	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

290		295		300
Tyr Pro Asp Met Tyr Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile				
305		310		315
Glu Phe Ile Asn Gln Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg				
	325		330	335
Val Leu Thr Thr Pro Glu Gln Ser				
	340			

<210> 181
 <211> 1251
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1228)
 <223> FRXA00283

<400> 181
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 acggaaaacg tccacagacc tcattacctg tggttttgcg ttg gca ttg gcg ttt 115
 Leu Ala Leu Ala Phe
 1 5
 tta gcg cgc tat gac gcc ctc atc atg gcc ttc gta gcc atg tgg act 163
 Leu Ala Arg Tyr Asp Ala Leu Ile Met Ala Phe Val Ala Met Trp Thr
 10 15 20
 gtc gga ttt atg aca tgg cgc gca cga tac cgc cgt ggc ttc cgc gac 211
 Val Gly Phe Met Thr Trp Arg Ala Arg Tyr Arg Arg Gly Phe Arg Asp
 25 30 35
 cgc atc gga ttc gca ctt gtc gac atg ctg ctc ctc gtc tgg ccg atc 259
 Arg Ile Gly Phe Ala Leu Val Asp Met Leu Leu Leu Val Trp Pro Ile
 40 45 50
 ggc ttc gcc ttc gtc gcc tgg act ggc gcc agc tgg ctc act acc ggc 307
 Gly Phe Ala Phe Val Ala Trp Thr Gly Ala Ser Trp Leu Thr Thr Gly
 55 60 65
 gaa ctc ttt gcc caa ttc acc tcc aca gac ggc aac gct gcg atc atc 355
 Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly Asn Ala Ala Ile Ile
 70 75 80 85
 gca gca tcc ggc ggc ggc gcc ata ggg ccc caa gcg ctt ttc gac gcc 403
 Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln Ala Leu Phe Asp Ala
 90 95 100
 tcc gtc cgc acc ttc ctc atc tcc cca gct ctc cta ctc gtc gca gta 451
 Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu Leu Leu Val Ala Val
 105 110 115
 gtt gca gtc ttt ttt gct tat cga cgc cgc gac ccc gaa ccc atc atc 499
 Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp Pro Glu Pro Ile Ile
 120 125 130

ccc tta gct ctc atc ggc tct gtg gtg ttc ttc caa atc att acc tac	547
Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe Gln Ile Ile Thr Tyr	
135 140 145	
tca ctt gga tct acc ttc ggc ctg ctg cgc ttt ttc ctc acc gcc ctg	595
Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe Phe Leu Thr Ala Leu	
150 155 160 165	
ccg ctc acc att atc ttg ctg ttc caa att atc ccg ccc cgc cac cga	643
Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile Pro Pro Arg His Arg	
170 175 180	
ttc ccc tca ctg cga cca ggt gcg tgc tac cgc gat cgc gtc acc ggc	691
Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg Asp Arg Val Thr Gly	
185 190 195	
aag tac gtg ccc aaa aca atc acc ggt gtt tta gtt ctc gcg atc ttc	739
Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu Val Leu Ala Ile Phe	
200 205 210	
ggc ggc acc ggc atc acc ctg tac ggc atg agc agt gct aac tgg gcg	787
Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser Ser Ala Asn Trp Ala	
215 220 225	
ccc cag gaa tat gcc atc caa gaa cta gtt ttc aac atg gga tcg cca	835
Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe Asn Met Gly Ser Pro	
230 235 240 245	
tcg cag gac gcc gtc cac acc ctg aac acc ttc tcc act gaa atg gat	883
Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe Ser Thr Glu Met Asp	
250 255 260	
gtc gcc gat ttc gtc gac tcc cta aac ctt gga gac ggc gaa gtc ctt	931
Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly Asp Gly Glu Val Leu	
265 270 275	
ctc tcc acc acc tac ggc ttc gcc gtc ctc acc gca tca aac aac caa	979
Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr Ala Ser Asn Asn Gln	
280 285 290	
aag caa ttc atc atc ccc tcc gac gaa gac ttc atc acc acc ctc aac	1027
Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe Ile Thr Thr Leu Asn	
295 300 305	
gaa ccc gct gag cac ggc gtt aag tac atc ctc gcc ctc cca cgc gaa	1075
Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu Ala Leu Pro Arg Glu	
310 315 320 325	
ggg cgc ggc gcc acc gac ccg atc aac ctg cgc tac cca gac atg tat	1123
Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg Tyr Pro Asp Met Tyr	
330 335 340	
gaa acc ggc agc cac atc gcc acg atg gaa atc gaa ttc atc aat caa	1171
Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile Glu Phe Ile Asn Gln	
345 350 355	
ggc caa gga caa cca aat tgg cgc ctc tat cgg gtg ctc acc aca cct	1219
Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg Val Leu Thr Thr Pro	
360 365 370	
gaa cag tcg tagactcttt gtaactaccg ttg	1251

Glu Gln Ser
375

<210> 182
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 182
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Val Ala Met Trp Thr Val Gly Phe Met Thr Trp Arg Ala Arg Tyr Arg
20 25 30
Arg Gly Phe Arg Asp Arg Ile Gly Phe Ala Leu Val Asp Met Leu Leu
35 40 45
Leu Val Trp Pro Ile Gly Phe Ala Phe Val Ala Trp Thr Gly Ala Ser
50 55 60
Trp Leu Thr Thr Gly Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly
65 70 75 80
Asn Ala Ala Ile Ile Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln
85 90 95
Ala Leu Phe Asp Ala Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu
100 105 110
Leu Leu Val Ala Val Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp
115 120 125
Pro Glu Pro Ile Ile Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe
130 135 140
Gln Ile Ile Thr Tyr Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe
145 150 155 160
Phe Leu Thr Ala Leu Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile
165 170 175
Pro Pro Arg His Arg Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg
180 185 190
Asp Arg Val Thr Gly Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu
195 200 205
Val Leu Ala Ile Phe Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser
210 215 220
Ser Ala Asn Trp Ala Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe
225 230 235 240
Asn Met Gly Ser Pro Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe
245 250 255
Ser Thr Glu Met Asp Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly
260 265 270

90 95 100
 cac tac cgc agc gtg agc gcg gag cta caa aga taaaaatgct ttctgacgtc 456
 His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
 105 110

cac 459

<210> 184
 <211> 112
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 184
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 Phe Glu Ala Gly Gly Arg Thr Asn Trp His Thr His Pro Val Gly Gln
 20 25 30
 Asn Ile Ile Val Leu Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu
 35 40 45
 Pro Ala Arg Leu Leu Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly
 50 55 60
 Val Arg His Trp His Gly Ala Val Ser Gly Ala Pro Met Phe His Val
 65 70 75 80
 Val Val Asn Leu Lys Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu
 85 90 95
 Pro Val Asp Glu Glu His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
 100 105 110

<210> 185
 <211> 459
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(436)
 <223> FRXA00334

<400> 185
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 taatccagcg cctgcacagt ggttttctgg cgaggtccat atg gcc aag ctt gat 115
 Met Ala Lys Leu Asp
 1 5
 gac aac gtg cag att gag act gtg aac gtg tct ttt gag gca ggc ggt 163
 Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser Phe Glu Ala Gly Gly
 10 15 20
 cgc acc aat tgg cac act cac cca gtc ggt caa aac ata att gtg ctg 211
 Arg Thr Asn Trp His Thr His Pro Val Gly Gln Asn Ile Ile Val Leu
 25 30 35

```

tcg ggc ttg ggc att tat gag gcg gag ggg gag cct gct cga ctc ctg 259
Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu Pro Ala Arg Leu Leu
      40                      45                      50

gag cct ggc gat gtt gtt ttc gca gcc gcc ggg gtt cgc cac tgg cac 307
Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly Val Arg His Trp His
      55                      60                      65

ggc gcc gtg tct ggt gca ccg atg ttc cac gtg gtg gtt aac ctc aaa 355
Gly Ala Val Ser Gly Ala Pro Met Phe His Val Val Val Asn Leu Lys
      70                      75                      80                      85

ggc atc gac ggc gag acc gtc gat tgg gag gag ccg gtc gac gag gag 403
Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu Pro Val Asp Glu Glu
                        90                      95                      100

cac tac cgc agc gtg agc gcg gag cta caa aga taaaaatgct tttcgacgtc 456
His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
      105                      110

cac 459

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<210> 186
 <211> 112
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 186
Met Ala Lys Leu Asp Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser
  1                      5                      10                      15

Phe Glu Ala Gly Gly Arg Thr Asn Trp His Thr His Pro Val Gly Gln
      20                      25                      30

Asn Ile Ile Val Leu Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu
      35                      40                      45

Pro Ala Arg Leu Leu Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly
      50                      55                      60

Val Arg His Trp His Gly Ala Val Ser Gly Ala Pro Met Phe His Val
      65                      70                      75                      80

Val Val Asn Leu Lys Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu
      85                      90                      95

Pro Val Asp Glu Glu His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
      100                      105                      110

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<210> 187
 <211> 1263
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1240)
 <223> RXN00338

tcttagaagg	cgtagtcaca	ccattaacct	tgccagaatt	tttcaaggct	tggctagact	60										
tgggaaacga	acatgcggta	ccaaccaggg	gagttaatgc	gtg Val 1	agt Ser gat Asp gta Val acc Thr 5	115										
gtt Val	ggc Gly	gat Asp	att Ile	cgc Arg 10	cgc Arg att Ile ttg Leu gat Asp 15	gag Glu gct Ala tat Tyr ccg Pro ccg Pro gcg Ala ttg Leu 20	163									
gcg Ala	gaa Glu	agc Ser	tgg Trp	gac Asp 25	aaa Lys gtg Val ggg Gly ctg Leu 30	atc Ile tgc Cys ggg Gly gat Asp cca Pro aca Thr gag Glu 35	211									
tgc Ser	gtg Val	aag Lys	cgt Arg	gtc Val	ggg Gly	tta Leu	gca Ala 45	ctc Leu	gat Asp	tgc Cys	acc Thr	cag Gln	gca Ala	gtg Val	gcc Ala	259
gac Asp	aag Lys 55	gct Ala	gtg Val	gac Asp	atg Met	ggg Gly 60	ttg Leu	gac Asp	atg Met	ctg Leu	atc Ile 65	att Ile	cac His	cac His	cca Pro	307
ttg Leu 70	ctg Leu	ctg Leu	cgt Arg	ggg Gly	gtg Val 75	acg Thr	tct Ser	gtt Val	gct Ala	gcg Ala 80	gat Asp	gag Glu	cca Pro	aaa Lys	ggc Gly 85	355
aag Lys	gtc Val	att Ile	cac His	acc Thr 90	cta Leu	att Ile	cgc Arg	ggc Gly	ggg Gly 95	gtg Val	gca Ala	ctg Leu	ttt Phe	tcc Ser	gcg Ala 100	403
cac His	act Thr	aat Asn	gcg Ala	gat Asp	tcc Ser	gcg Ala	cgc Arg	cca Pro 110	ggt Gly	gtc Val	aac Asn	gat Asp	aaa Lys 115	ctc Leu	gcc Ala	451
gag Glu	ctc Leu	gtc Val	ggc Gly	atc Ile	acg Thr	gcc Ala	ggg Gly 125	cga Arg	ccc Pro	atc Ile	gcg Ala	aca Thr	cgg Arg	ctt Leu	tta Leu 130	499
ggc Gly	ggc Gly	atg Met	gac Asp	aaa Lys	tgg Trp	ggc Gly 140	gtg Val	cac His	gtt Val	ctg Leu	ccc Pro 145	aag Lys	gat Asp	gca Ala	gcg Ala 150	547
tac Tyr 150	cta Leu	aag Lys	aag Lys	atg Met	ctt Leu	ttc Phe	gac Asp	gca Ala	ggt Gly	gcc Ala	ggt Gly	gcg Ala	atc Ile	ggc Gly	gac Asp 165	595
tac Tyr	cga Arg	gag Glu	tgt Cys	gcc Ala 170	ttt Phe	gag Glu	atc Ile	gaa Glu	gga Gly 175	acc Thr	ggg Gly	cag Gln	ttt Phe	agg Arg	ccc Pro 180	643
gtg Val	gag Glu	ggg Gly	gcg Ala	aat Asn	ccg Pro	gca Ala	gag Glu	ggg Gly 190	gac Asp	gtc Val	gat Asp	aag Lys	ctt Leu	ttt Phe	aaa Lys 195	691
tcc Ser	ctt Leu	gag Glu	ctg Leu	cgc Arg	atc Ile	gag Glu	ttt Phe 205	gtt Val	gca Ala	ccg Pro	cgc Arg	aac Asn	ctg Leu	cgc Arg	gcc Ala 210	739
cgg	ctc	acg	tgc	gtg	ctg	cgg	gag	gct	cat	ccg	tat	gag	gag	cct	gcc	787

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Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala
 215                      220                      225

ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc 835
Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr
230                      235                      240                      245

gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat 883
Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp
                      250                      255                      260

ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg 931
Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val
                      265                      270                      275

cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca 979
Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser
                      280                      285                      290

tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg 1027
Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val
                      295                      300                      305

gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat 1075
Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr
310                      315                      320                      325

ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc 1123
Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser
                      330                      335                      340

gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc 1171
Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
                      345                      350                      355

cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc 1219
Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
                      360                      365                      370

atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag 1263
Met Ser Ala Arg Ala Val Asn
                      375                      380

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<210> 188

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala
 1                      5                      10                      15

```

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Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
 20                      25                      30

```

```

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
 35                      40                      45

```

```

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
 50                      55                      60

```

Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala
65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
85 90 95

Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
100 105 110

Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
115 120 125

Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
130 135 140

Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
145 150 155 160

Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
165 170 175

Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
180 185 190

Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
195 200 205

Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
210 215 220

Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser
225 230 235 240

Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro
245 250 255

Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val
260 265 270

Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser
275 280 285

Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val
290 295 300

Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His
305 310 315 320

Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr
325 330 335

Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile
340 345 350

Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg
355 360 365

Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn
370 375 380

<210> 189
 <211> 806
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(783)
 <223> FRXA00338

<400> 189

gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta ggc ggc	48
Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu Gly Gly	
1 5 10 15	
atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg tac cta	96
Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala Tyr Leu	
20 25 30	
aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac tac cga	144
Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp Tyr Arg	
35 40 45	
gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc gtg gag	192
Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro Val Glu	
50 55 60	
ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa tcc ctt	240
Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys Ser Leu	
65 70 75 80	
gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc cgg ctc	288
Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala Arg Leu	
85 90 95	
acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc ttc gat	336
Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala Phe Asp	
100 105 110	
att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc gga ttg	384
Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr Gly Leu	
115 120 125	
ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat ttc gtg	432
Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp Phe Val	
130 135 140	
caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg cgc gct	480
Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val Arg Ala	
145 150 155 160	
acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca tca ggg	528
Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser Ser Gly	
165 170 175	
tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg gac gtt	576
Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val Asp Val	
180 185 190	
tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat ctc cga	624

Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr Leu Arg
 195 200 205

gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc gaa ttt 672
 Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser Glu Phe
 210 215 220

cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc cca cag 720
 Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala Pro Gln
 225 230 235 240

gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc atg tct 768
 Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr Met Ser
 245 250 255

gcg cga gca gtg aac taaattcttg agaactaaaa aag 806
 Ala Arg Ala Val Asn
 260

<210> 190

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu Gly Gly
 1 5 10 15

Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala Tyr Leu
 20 25 30

Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp Tyr Arg
 35 40 45

Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro Val Glu
 50 55 60

Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys Ser Leu
 65 70 75 80

Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala Arg Leu
 85 90 95

Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala Phe Asp
 100 105 110

Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr Gly Leu
 115 120 125

Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp Phe Val
 130 135 140

Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val Arg Ala
 145 150 155 160

Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser Ser Gly
 165 170 175

Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val Asp Val
 180 185 190

Val Ser Asp Val Thr Val Gly Asp Ile Leu Arg Ile Leu Asp Glu Ala
 1 5 10 15
 Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Val Leu Ile Cys
 20 25 30
 Val Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
 35 40 45
 Thr Gln Ala Leu Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
 50 55 60
 Ile Ile His His Pro Leu
 65 70

<210> 193
 <211> 552
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(529)
 <223> RXN00342

<400> 193
 cggtaatgtg caattcggat atatcaatag cccgcggtt tcatgttgaa tccatgtaat 60
 cgaaaaaacac atcggggccc acacgaggag gattattaaa gtg gcc gac gct ccg 115
 Val Ala Asp Ala Pro
 1 5
 ggc gca gtc aag caa ggt gcc cag gat tat gct caa cta ctc ggc att 163
 Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala Gln Leu Leu Gly Ile
 10 15 20
 caa tcg ggt cat atc gtt caa gaa att gga tgg gat gaa gat tcc gac 211
 Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp Asp Glu Asp Ser Asp
 25 30 35
 acg ctg atc agc gag tcc atc gaa gat gca atc ggt gag gaa cta ctc 259
 Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile Gly Glu Glu Leu Leu
 40 45 50
 gat gaa gaa acc gac gag ctg tgc gat gtc gtg ctg ctc tgg tgg cgc 307
 Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val Leu Leu Trp Trp Arg
 55 60 65
 gag gat gac ggc gat ctc gtc gac gga ctt gtg gat tcc atc cgc tcc 355
 Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val Asp Ser Ile Arg Ser
 70 75 80 85
 ctc gct gag aat ggt cgt atc tgg gtg ttg act cct ggc att ggt aaa 403
 Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr Pro Gly Ile Gly Lys
 90 95 100
 gaa gga gcc ctg gct cct gga gtt atc tct gaa tca gct caa ctg gca 451
 Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu Ser Ala Gln Leu Ala
 105 110 115

ggt ctc gtg cag acc aag gca gaa cgt ctc ggt aat tgg caa ggt tct 499
 Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly Asn Trp Gln Gly Ser
 120 125 130

tgc ctc gtc cag cgt gga aac aag aag cct taacaatcgc taatttcac 549
 Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
 135 140

ggc 552

<210> 194

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala
 1 5 10 15

Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp
 20 25 30

Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile
 35 40 45

Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val
 50 55 60

Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val
 65 70 75 80

Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr
 85 90 95

Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu
 100 105 110

Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly
 115 120 125

Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
 130 135 140

<210> 195

<211> 524

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (73)..(501)

<223> FRXA00342

<400> 195

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agaattatta aa gtg gcc gac gct ccg ggc gca gtc aag caa ggt gcc cag 111
 1 5 10
 Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln

gat tat gct caa cta ctc ggc att caa tcg ggt cat atc gtt caa gaa 159
Asp Tyr Ala Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu
15 20 25

att gga tgg gat gaa gat tcc gac acg ctg atc agc gag tcc atc gaa 207
Ile Gly Trp Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu
30 35 40 45

gat gca atc ggt gag gaa cta ctc gat gaa gaa acc gac gag ctg tgc 255
Asp Ala Ile Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys
50 55 60

gat gtc gtg ctg ctc tgg tgg cgc gag gat gac ggc gat ctc gtc gac 303
Asp Val Val Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp
65 70 75

gga ctt gtg gat tcc atc cgc tcc ctc gct gag aat ggt cgt atc tgg 351
Gly Leu Val Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp
80 85 90

gtg ttg act cct ggc att ggt aaa gaa gga gcc ctg gct cct gga gtt 399
Val Leu Thr Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val
95 100 105

atc tct gaa tca gct caa ctg gca ggt ctc gtg cag acc aag gca gaa 447
Ile Ser Glu Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu
110 115 120 125

cgt ctc ggt aat tgg caa ggt tct tgc ctc gtc cag cgt gga aac aag 495
Arg Leu Gly Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys
130 135 140

aag cct taacaatcgc taatttccac ggc 524
Lys Pro

<210> 196
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala
1 5 10 15

Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp
20 25 30

Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile
35 40 45

Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val
50 55 60

Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val
65 70 75 80

Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr
85 90 95


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Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val Val
 135          140          145

agc gcc gtg gtg att ttc tgg cgc ccg ctg ctt ttc gcc agc gcc gat 595
Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala Asp
150          155          160          165

ccg atc atg gcg cag gcc tcc gga gta aac gtc cga ttc atc gcc gtt 643
Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala Val
          170          175          180

gcc ttc gca gtt ctg gtt ggc ctc acc acg tcc cag tcc gtg cag att 691
Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln Ile
          185          190          195

gtc ggt gcg ctg ctg gtc atg gca ttg ctg atc act ccc ggc gcg gcc 739
Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala Ala
          200          205          210

gct gtg gcg gtg acc gcc aat cca gtg aaa gcc gtg gtg ctg gca gtc 787
Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala Val
          215          220          225

atc ttc gcg gaa gta tcg gct gtc ggt ggc ctg cta ttg tcg cta gcg 835
Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu Ala
230          235          240          245

cct ggt ttg ccg gtg agt gtt ttt gtc acc acc atc tct ttt gtg att 883
Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val Ile
          250          255          260

tac ctg gtc tgc cgc ctg atc ggt tgg ctc cgc ggc cgt gga gct cag 931
Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala Gln
          265          270          275

cgt gac gaa gat gct tat cga cgc cgc cag cac gat cac cac cct cac 979
Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro His
          280          285          290

taggcgtttc gaagtcctat ttc 1002

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<210> 198

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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Val Asp Leu Ser Thr Trp Leu Ser Asp Thr Gln Tyr Leu Ile Ser Val
 1          5          10          15

Asp Phe Val Gln His Ala Leu Ile Ala Ser Ala Leu Leu Gly Leu Leu
          20          25          30

Ser Gly Val Ile Ala Pro Leu Ile Val Val Arg Gln Gln Ser Phe Ala
          35          40          45

Val His Gly Thr Ala Glu Leu Ala Leu Met Gly Ala Ala Ala Ala Leu
          50          55          60

Leu Phe Gly Leu Asn Val Gly Gly Gly Ala Val Ile Gly Ser Val Val

```

65	70	75	80
Ala Ala Ile Leu Leu Ala Leu Leu Gly Met Lys Gln Gln Asp Ser Ala	85	90	95
Val Gly Ala Val Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile	100	105	110
His Leu Tyr Pro Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly	115	120	125
Gln Ile Val Gly Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val	130	135	140
Thr Val Ile Val Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu	145	150	155
Phe Ala Ser Ala Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val	165	170	175
Arg Phe Ile Ala Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser	180	185	190
Gln Ser Val Gln Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile	195	200	205
Thr Pro Gly Ala Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala	210	215	220
Val Val Leu Ala Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu	225	230	235
Leu Leu Ser Leu Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr	245	250	255
Ile Ser Phe Val Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg	260	265	270
Gly Arg Gly Ala Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His	275	280	285
Asp His His Pro His	290		

<210> 199
 <211> 594
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(579)
 <223> FRXA00344

<400> 199	
atg agt ttc gga ctc ggt ctg tcc gtg ctg ttc att cac ctc tac ccc	48
Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile His Leu Tyr Pro	
1 5 10 15	
ggc cga agc tcc acc gcg ttc tcc ctg ctc aca ggg caa atc gtt ggt	96

Gly	Arg	Ser	Ser	Thr	Ala	Phe	Ser	Leu	Leu	Thr	Gly	Gln	Ile	Val	Gly		
			20					25					30				
gtt	tcc	tca	tca	tcg	ctg	tgg	atc	ctt	gtg	gca	gtc	acc	gtg	atc	gtg	144	
Val	Ser	Ser	Ser	Ser	Leu	Trp	Ile	Leu	Val	Ala	Val	Thr	Val	Ile	Val		
		35					40					45					
gtt	agc	gcc	gtg	gtg	att	ttc	tgg	cgc	ccg	ctg	ctt	ttc	gcc	agc	gcc	192	
Val	Ser	Ala	Val	Val	Ile	Phe	Trp	Arg	Pro	Leu	Leu	Phe	Ala	Ser	Ala		
		50				55					60						
gat	ccg	atc	atg	gcg	cag	gcc	tcc	gga	gta	aac	gtc	cga	ttc	atc	gcc	240	
Asp	Pro	Ile	Met	Ala	Gln	Ala	Ser	Gly	Val	Asn	Val	Arg	Phe	Ile	Ala		
		65			70				75						80		
gtt	gcc	ttc	gca	gtt	ctg	gtt	ggc	ctc	acc	acg	tcc	cag	tcc	gtg	cag	288	
Val	Ala	Phe	Ala	Val	Leu	Val	Gly	Leu	Thr	Thr	Ser	Gln	Ser	Val	Gln		
				85				90						95			
att	gtc	ggc	gcg	ctg	ctg	gtc	atg	gca	ttg	ctg	atc	act	ccc	ggc	gcg	336	
Ile	Val	Gly	Ala	Leu	Leu	Val	Met	Ala	Leu	Leu	Ile	Thr	Pro	Gly	Ala		
			100					105					110				
gcc	gct	gtg	gcg	gtg	acc	gcc	aat	cca	gtg	aaa	gcc	gtg	gtg	ctg	gca	384	
Ala	Ala	Val	Ala	Val	Thr	Ala	Asn	Pro	Val	Lys	Ala	Val	Val	Leu	Ala		
			115				120					125					
gtc	atc	ttc	gcg	gaa	gta	tcg	gct	gtc	ggc	ggc	ctg	cta	ttg	tcg	cta	432	
Val	Ile	Phe	Ala	Glu	Val	Ser	Ala	Val	Gly	Gly	Leu	Leu	Leu	Ser	Leu		
		130				135					140						
gcg	cct	ggc	ttg	ccg	gtg	agt	gtt	ttt	gtc	acc	acc	atc	tct	ttt	gtg	480	
Ala	Pro	Gly	Leu	Pro	Val	Ser	Val	Phe	Val	Thr	Thr	Ile	Ser	Phe	Val		
					145		150			155					160		
att	tac	ctg	gtc	tgc	cgc	ctg	atc	ggc	tgg	ctc	cgc	ggc	cgt	gga	gct	528	
Ile	Tyr	Leu	Val	Cys	Arg	Leu	Ile	Gly	Trp	Leu	Arg	Gly	Arg	Gly	Ala		
				165					170					175			
cag	cgt	gac	gaa	gat	gct	tat	cga	cgc	cgc	cag	cac	gat	cac	cac	cct	576	
Gln	Arg	Asp	Glu	Asp	Ala	Tyr	Arg	Arg	Arg	Gln	His	Asp	His	His	Pro		
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His																	

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<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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Gly	Arg	Ser	Ser	Thr	Ala	Phe	Ser	Leu	Leu	Thr	Gly	Gln	Ile	Val	Gly
			20					25					30		

Val	Ser	Ser	Ser	Ser	Leu	Trp	Ile	Leu	Val	Ala	Val	Thr	Val	Ile	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala 50 55 60		
Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala 65 70 75 80		
Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln 85 90 95		
Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala 100 105 110		
Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala 115 120 125		
Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu 130 135 140		
Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val 145 150 155 160		
Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala 165 170 175		
Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro 180 185 190		

His

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 <213> Corynebacterium glutamicum

<220>
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 <223> RXN00353

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 Val Gly Arg Ser Phe
 1 5
 acc aac agg act ttt gat ccg ttg ccg ttc atg gtg gtt tat ccg gat 163
 Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met Val Val Tyr Pro Asp
 10 15 20
 ggg gtg gat cag cat tgg aat gat gcg cgg ttg ggt ttg gat gaa aat 211
 Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu Gly Leu Asp Glu Asn
 25 30 35
 acc cgc cat tta ggc att gat gat gtg ggg ttc ttt gta aaa ctc gcc 259
 Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe Phe Val Lys Leu Ala
 40 45 50

acg cac ttg ggc aac acg tat ggc atc aag agg atc ttt att gtt ggc 307
 Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg Ile Phe Ile Val Gly
 55 60 65
 tat tcc aac ggt ggg cag atg gtg ttg cgg ctc atg cat gag gtt ccc 355
 Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu Met His Glu Val Pro
 70 75 80 85
 aag atg ctc agt ggc gct gca acc att gca tcc aac atg cca gtt gca 403
 Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser Asn Met Pro Val Ala
 90 95 100
 gag aat acg ctg ccg cag gtg aaa acc ttc aag aca cat ccg gtg cct 451
 Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys Thr His Pro Val Pro
 105 110 115
 tat ttg gcg atg gct gga act gcc gat act ttt tca ccg tat gag ggt 499
 Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe Ser Pro Tyr Glu Gly
 120 125 130
 ggc gat gcc ggt att ggt cgc gaa cac cgc cgt ggc gtg ggc atg tcc 547
 Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg Gly Val Gly Met Ser
 135 140 145
 gcc ttt gat tca gct gcc tat att gcc gcc cga aac gga ctg acc gaa 595
 Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg Asn Gly Leu Thr Glu
 150 155 160 165
 cac cgc cac gac gtg att gat gat gtg gtg tcg atc gat acc tgg gat 643
 His Arg His Asp Val Ile Asp Asp Val Val Ser Ile Asp Thr Trp Asp
 170 175 180
 gga gaa aat ccc gtt gag ttt tgg aca ctc aac ggg atc ggc cac ttg 691
 Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn Gly Ile Gly His Leu
 185 190 195
 gta cca agt ggg aaa act tat cca gaa ttt cta ggc ccc tca acc aca 739
 Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu Gly Pro Ser Thr Thr
 200 205 210
 tca gtg ata gcg gct gag gag att ggg aag ttc ttt gat ggg gtc agg 787
 Ser Val Ile Ala Ala Glu Ile Gly Lys Phe Phe Asp Gly Val Arg
 215 220 225
 cgt cga taagctcaag ctttaaaaac gca 816
 Arg Arg
 230

<210> 202

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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Val Val Tyr Pro Asp Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu
 20 25 30

Gly	Leu	Asp 35	Glu	Asn	Thr	Arg	His 40	Leu	Gly	Ile	Asp	Asp 45	Val	Gly	Phe
Phe	Val 50	Lys	Leu	Ala	Thr	His 55	Leu	Gly	Asn	Thr	Tyr 60	Gly	Ile	Lys	Arg
Ile 65	Phe	Ile	Val	Gly	Tyr 70	Ser	Asn	Gly	Gly	Gln 75	Met	Val	Leu	Arg	Leu 80
Met	His	Glu	Val	Pro 85	Lys	Met	Leu	Ser	Gly 90	Ala	Ala	Thr	Ile	Ala 95	Ser
Asn	Met	Pro 100	Val	Ala	Glu	Asn	Thr 105	Leu	Pro	Gln	Val	Lys 110	Thr	Phe	Lys
Thr	His 115	Pro	Val	Pro	Tyr	Leu	Ala 120	Met	Ala	Gly	Thr	Ala 125	Asp	Thr	Phe
Ser 130	Pro	Tyr	Glu	Gly	Gly	Asp 135	Ala	Gly	Ile	Gly	Arg 140	Glu	His	Arg	Arg
Gly 145	Val	Gly	Met	Ser 150	Ala	Phe	Asp	Ser	Ala	Ala 155	Tyr	Ile	Ala	Ala 160	Arg
Asn	Gly	Leu	Thr 165	Glu	His	Arg	His	Asp 170	Val	Ile	Asp	Asp	Val	Val 175	Ser
Ile	Asp	Thr 180	Trp	Asp	Gly	Glu	Asn 185	Pro	Val	Glu	Phe	Trp 190	Thr	Leu	Asn
Gly	Ile 195	Gly	His	Leu	Val	Pro	Ser 200	Gly	Lys	Thr	Tyr 205	Pro	Glu	Phe	Leu
Gly 210	Pro	Ser	Thr	Thr	Ser	Val 215	Ile	Ala	Ala	Glu	Glu 220	Ile	Gly	Lys	Phe
Phe 225	Asp	Gly	Val	Arg	Arg	Arg 230									

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<212> DNA
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<223> FRXA00353
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                                         Val Gly Arg Ser Phe
                                         1                               5

acc aac agg act ttt gat ccg ttg ccg ttc atg gtg gtt tat ccg gat 163
Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met Val Val Tyr Pro Asp
                        10                        15                        20

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ggg gtg gat cag cat tgg aat gat gcg cgg ttg ggt ttg gat gaa aat 211
 Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu Gly Leu Asp Glu Asn
 25 30 35

acc cgc cat tta ggc att gat gat gtg ggg ttc ttt gta aaa ctc gcc 259
 Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe Phe Val Lys Leu Ala
 40 45 50

acg cac ttg ggc aac acg tat ggc atc aag agg atc ttt att gtt ggc 307
 Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg Ile Phe Ile Val Gly
 55 60 65

tat tcc aac ggt ggg cag atg gtg ttg cgg ctc atg cat gag gtt ccc 355
 Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu Met His Glu Val Pro
 70 75 80 85

aag atg ctc agt ggc gct gca acc att gca tcc aac atg cca gtt gca 403
 Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser Asn Met Pro Val Ala
 90 95 100

gag aat acg ctg ccg cag gtg aaa acc ttc aag aca cat ccg gtg cct 451
 Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys Thr His Pro Val Pro
 105 110 115

tat ttg gcg atg gct gga act gcc gat act ttt tca ccg tat gag ggt 499
 Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe Ser Pro Tyr Glu Gly
 120 125 130

ggc gat gcc ggt att ggt cgc gaa cac cgc cgt ggc gtg ggc atg tcc 547
 Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg Gly Val Gly Met Ser
 135 140 145

gcc ttt gat tca gct gcc tat att gcc gcc cga aac gga ctg acc gaa 595
 Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg Asn Gly Leu Thr Glu
 150 155 160 165

cac cgc cac gac gtg att gat gat gtg gtg tgc atc gat acc tgg gat 643
 His Arg His Asp Val Ile Asp Asp Val Val Ser Ile Asp Thr Trp Asp
 170 175 180

gga gaa aat ccc gtt gag ttt tgg aca ctc aac ggg atc ggc cac ttg 691
 Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn Gly Ile Gly His Leu
 185 190 195

gta cca agt ggg aaa act tat cca gaa ttt cta ggc ccc tca acc aca 739
 Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu Gly Pro Ser Thr Thr
 200 205 210

tca gtg ata gcg gct gag gag att ggg aag ttc ttt gat ggg gtc agg 787
 Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe Phe Asp Gly Val Arg
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 Arg Arg
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Val Val Tyr Pro Asp Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu
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Gly Leu Asp Glu Asn Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe
35 40 45

Phe Val Lys Leu Ala Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg
50 55 60

Ile Phe Ile Val Gly Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu
65 70 75 80

Met His Glu Val Pro Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser
85 90 95

Asn Met Pro Val Ala Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys
100 105 110

Thr His Pro Val Pro Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe
115 120 125

Ser Pro Tyr Glu Gly Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg
130 135 140

Gly Val Gly Met Ser Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg
145 150 155 160

Asn Gly Leu Thr Glu His Arg His Asp Val Ile Asp Asp Val Val Ser
165 170 175

Ile Asp Thr Trp Asp Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn
180 185 190

Gly Ile Gly His Leu Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu
195 200 205

Gly Pro Ser Thr Thr Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe
210 215 220

Phe Asp Gly Val Arg Arg Arg
225 230

<210> 205

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(913)

<223> RXN00354

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ttctcgatta tgtacctcat ttacgcgtaa agtttggggc	atg gga aag tta ctt	115
	Met Gly Lys Leu Leu	
	1 5	
ttc gta gac atc ggt ggc aca ctg ctg gat tac tca aat gaa gtt ccg	163	
Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr Ser Asn Glu Val Pro		
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cgt tcg gcc gtt gac gcg atc cgt aag gca cgc gcc aaa gga cac cgc	211	
Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg Ala Lys Gly His Arg		
25 30 35		
gtg tac ttg agc tct ggt cga agc agc gct gag gtg act tct cag ttg	259	
Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu Val Thr Ser Gln Leu		
40 45 50		
tgg gat atc gga gtg gat ggc ctc att ggc gca aat ggt gga tat gtg	307	
Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala Asn Gly Gly Tyr Val		
55 60 65		
gaa agc gca cag gag tct gtg ttc cac cgc cgt ttg tcg ggt gag gag	355	
Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg Leu Ser Gly Glu Glu		
70 75 80 85		
acc cgc cac att gtg gag tgg ctc tac aac cgt ggt ttg gag ttt tat	403	
Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg Gly Leu Glu Phe Tyr		
90 95 100		
ctc gag tcc aac aac ggt ttg tat gca agc cgt ggt ttc cgt gag gct	451	
Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg Gly Phe Arg Glu Ala		
105 110 115		
tct aag cca gtg ctg tct cgc ctt tcg gag aag acc gac gtg aca gtc	499	
Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys Thr Asp Val Thr Val		
120 125 130		
gat agc atg tac ccg gat atg ttc tgg ggc gcg agc ctt gat cgt gac	547	
Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala Ser Leu Asp Arg Asp		
135 140 145		
gat gtg aac aag atc agt tac atc ttc aat tct cag gaa gat ttg gac	595	
Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser Gln Glu Asp Leu Asp		
150 155 160 165		
gca gcg cgt gag gcg ttc cct aac ctg gag cac acc acg tgg ggt ggt	643	
Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His Thr Thr Trp Gly Gly		
170 175 180		
cag acg ggt gcg ttg ttc ggc acg atc ggt gtg tct gtc aac aag aag	691	
Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val Ser Val Asn Lys Lys		
185 190 195		
atc ggc gtg gat cgc ctg ctg aag tac ctg aac gca gat cgc gca aac	739	
Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn Ala Asp Arg Ala Asn		
200 205 210		
acc att gcg ttc ggc gac agc gat gag gat ctc tcc cta ttt gag gcg	787	
Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu Ser Leu Phe Glu Ala		
215 220 225		

agc gct tac ggc gtc gcg atg ggc gag gcc acc gaa tcg ctc aag gct 835
 Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr Glu Ser Leu Lys Ala
 230 235 240 245

gct gct gac ctg gtc acg gat gct gtt ggg cag gac ggc ttg cgc aat 883
 Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln Asp Gly Leu Arg Asn
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gcg ttt tta aag ctt gag ctt atc gac gcc tgaccccatc aaagaacttc 933
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 265 270

cca 936

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<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

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 20 25 30

Ala Lys Gly His Arg Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu
 35 40 45

Val Thr Ser Gln Leu Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala
 50 55 60

Asn Gly Gly Tyr Val Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg
 65 70 75 80

Leu Ser Gly Glu Glu Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg
 85 90 95

Gly Leu Glu Phe Tyr Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg
 100 105 110

Gly Phe Arg Glu Ala Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys
 115 120 125

Thr Asp Val Thr Val Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala
 130 135 140

Ser Leu Asp Arg Asp Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser
 145 150 155 160

Gln Glu Asp Leu Asp Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His
 165 170 175

Thr Thr Trp Gly Gly Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val
 180 185 190

Ser Val Asn Lys Lys Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn
 195 200 205

Ala Asp Arg Ala Asn Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu

210	215	220
Ser Leu Phe Glu Ala	Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr	
225	230	235 240
Glu Ser Leu Lys Ala Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln		
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Asp Gly Leu Arg Asn Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala		
	260	265 270

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1447)
 <223> RXN00362

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 Met Gly Ile Ile Ala
 1 5
 ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa 163
 Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
 10 15 20
 cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt 211
 Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
 25 30 35
 gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat 259
 Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
 40 45 50
 gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg 307
 Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
 55 60 65
 ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc 355
 Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
 70 75 80 85
 ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc 403
 Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
 90 95 100
 act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga 451
 Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
 105 110 115
 aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg 499
 Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
 120 125 130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc	547
Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly	
135 140 145	
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Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala	
150 155 160 165	
ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg	643
Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu	
170 175 180	
gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt	691
Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe	
185 190 195	
tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg	739
Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg	
200 205 210	
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Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile	
215 220 225	
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Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser	
230 235 240 245	
gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg	883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met	
250 255 260	
tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att	931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile	
265 270 275	
gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag	979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln	
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Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe	
295 300 305	
tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg	1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro	
310 315 320 325	
cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg	1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met	
330 335 340	
gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg	1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser	
345 350 355	
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Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu	
360 365 370	
gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg	1267

Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu
 375 380 385

tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac 1315
 Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr
 390 395 400 405

ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca 1363
 Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro
 410 415 420

ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt 1411
 Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val
 425 430 435

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta 1457
 Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
 440 445

aaaatgaact caa 1470

<210> 208
 <211> 449
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 208
 Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu
 1 5 10 15

Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu
 20 25 30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile
 35 40 45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met
 50 55 60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
 65 70 75 80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
 85 90 95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
 100 105 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
 115 120 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
 130 135 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met
 145 150 155 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
 165 170 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
180 185 190
Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
195 200 205
Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
210 215 220
Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
225 230 235 240
Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
245 250 255
Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr
260 265 270
Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala
275 280 285
His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val
290 295 300
Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu
305 310 315 320
Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu
325 330 335
Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val
340 345 350
Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro
355 360 365
Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile
370 375 380
Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val
385 390 395 400
Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr
405 410 415
Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu
420 425 430
Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr
435 440 445

Gly

<210> 209

<211> 983

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(960)

<223> FRXA00362

<400> 209

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Asp Glu Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala	
1 5 10 15	
ggc aac tct ggc ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc	96
Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe	
20 25 30	
atc att ttg gca ttg cca gct gca gca gct tct tcg gcc tct cag gtg	144
Ile Ile Leu Ala Leu Pro Ala Ala Ala Ser Ser Ala Ser Gln Val	
35 40 45	
tac att gct ttg gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta	192
Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu	
50 55 60	
gcg gtc gtc ttt tac tgg aca cgt aaa gat aaa att cct gcc acc cct	240
Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro	
65 70 75 80	
gat gat caa cgg gtg tca ttc ggt gag gca atg aag act gga tgg cgt	288
Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg	
85 90 95	
tca ccg ttg atc ttc ctt gga att ttg atc ccc gta atc ctc aca atc	336
Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile	
100 105 110	
ggc cca ttg tct gaa tgg tta aag aca cat gga gtt ggg gag tct ggt	384
Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly	
115 120 125	
gtt aaa tcg atg tcg atc atc gtg tgg gtg cca att ctg att acg gca	432
Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala	
130 135 140	
att gct ctg att gaa ggg cgt aaa cga att gct aac aac atg gca cac	480
Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His	
145 150 155 160	
ttt agg gtt cag atc tcc aag gac ttg cca caa ttt gcc acc gta gga	528
Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly	
165 170 175	
att tcg ttg ttt tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg	576
Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu	
180 185 190	
ggt gtt ggc ccg cag ttg tct aac tgg ctt gat tcc atg gac cta cct	624
Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro	
195 200 205	
aag tct gtc atg gtg atc att gtc tgc atc atg tgc att gtg gtg gca	672
Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala	
210 215 220	

acg cca ctg tcg tca aca gca acc gcg gct gcg att ggt gct ccc gct 720
 Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala
 225 230 235 240
 gtc gct gcg ttg gct gcg gta ggt att gat cca act gtg gcg atc gta 768
 Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val
 245 250 255
 gtg atc ttg ctg tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc 816
 Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly
 260 265 270
 gcg ccg att tac ctt tct gct gcg atc gcc gat gca aac cca acg aaa 864
 Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys
 275 280 285
 atg ttc gta cca ctg att acg tac ttt gtt gtc ccc atg att ctg ctt 912
 Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu
 290 295 300
 gct tgg cta gtt gga atg gga ttc tta cca gtg att gtt cct acg ggt 960
 Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
 305 310 315 320
 taaaggggta aaaatgaact caa 983

<210> 210

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

Asp Glu Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala
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 Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe
 20 25 30
 Ile Ile Leu Ala Leu Pro Ala Ala Ala Ser Ser Ala Ser Gln Val
 35 40 45
 Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu
 50 55 60
 Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro
 65 70 75 80
 Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg
 85 90 95
 Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile
 100 105 110
 Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly
 115 120 125
 Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala
 130 135 140
 Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His

145		150		155		160
Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly						
		165		170		175
Ile Ser Leu Phe Ser Ala Leu Ala Ala Asn Ile Met Glu Glu Leu						
		180		185		190
Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro						
		195		200		205
Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala						
		210		215		220
Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala						
		225		230		235
Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val						
		245		250		255
Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly						
		260		265		270
Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys						
		275		280		285
Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu						
		290		295		300
Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly						
		305		310		315
						320

<210> 211

<211> 439

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(439)

<223> RXN00373

<400> 211

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cacgtggcgg atctgcgcgc taagggcgag ctgccgccgc cgaggaagaa acgcaggcgt 60
cgaaaagcgt cttaaaaggt ttttcactag ggtgttgtcc atg gac atc cag cag 115
                                         Met Asp Ile Gln Gln
                                         1           5

cta gac gcc gaa aca aca gca tgg aaa gac agc ctc ctg cgc gcc gca 163
Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser Leu Leu Arg Ala Ala
                        10                        15                        20

cag gag gct ggt ttt cat ttt gag cca ccg aaa ctc ttc gag gat ttt 211
Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys Leu Phe Glu Asp Phe
                        25                        30                        35

gag acc atg gtg gag cag tac aag cag gca gct gcg agc gac ccg gac 259
Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala Ala Ser Asp Pro Asp
                        40                        45                        50

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att gat gtc act gat att cag caa atg tgg ggc atc gtg gtg ggg gag 307
Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly Ile Val Val Gly Glu
55 60 65

tac ctg cgc gaa aaa atg ggc atg gaa tgg gtc gtc atc acc gat gac 355
Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val Val Ile Thr Asp Asp
70 75 80 85

tac ggc act gac ctc gcg att cta gcc acg gca ccc aac ggg gac cac 403
Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala Pro Asn Gly Asp His
90 95 100

gta tat tcc tgc ccc atc atc gtg gtg ggc aag cgc 439
Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys Arg
105 110

<210> 212

<211> 113

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

Met Asp Ile Gln Gln Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser
1 5 10 15

Leu Leu Arg Ala Ala Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys
20 25 30

Leu Phe Glu Asp Phe Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala
35 40 45

Ala Ser Asp Pro Asp Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly
50 55 60

Ile Val Val Gly Glu Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val
65 70 75 80

Val Ile Thr Asp Asp Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala
85 90 95

Pro Asn Gly Asp His Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys
100 105 110

Arg

<210> 213

<211> 439

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(439)

<223> FRXA00373

<400> 213

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<210>	216
<211>	135
<212>	PRT

<213> Corynebacterium glutamicum

<400> 216

Met Ser Thr Thr Arg Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu
 1 5 10 15

Gly Val Ile Leu Ile Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly
 20 25 30

Leu Glu Gly Val Thr Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala
 35 40 45

Gly Ile Ala Ala Ile Ala Ala Val Val Glu Leu Leu Gly Gly Ile
 50 55 60

Leu Ile Ile Leu Gly Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala
 65 70 75 80

Ile Asp Met Leu Phe Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile
 85 90 95

Phe Val Thr Asn Asn Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly
 100 105 110

Ala Leu Leu Leu Ile Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly
 115 120 125

Val Leu Ala Lys Arg Lys Ala
 130 135

<210> 217

<211> 528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(505)

<223> FRXA00390

<400> 217

ggaaatagac cgtaaatagc tggctctttac atttgccaga aagctccgac gaaaccccaa 60

tagttgacac ggaaactaat tcattctagc tttagtgacc atg tca act acc agg 115
 Met Ser Thr Thr Arg
 1 5

gaa att gca ttc ctc atc gca cgt atc ctc ttg ggc gtc atc ctc atc 163
 Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu Gly Val Ile Leu Ile
 10 15 20

gcc cac ggc tgg gac aag ttc gcc atc aca gga ctt gaa ggc gtc acc 211
 Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly Leu Glu Gly Val Thr
 25 30 35

ggc ttc ttc gat tca ctc ggc atc cca gca gcc ggc atc gcc gca ata 259
 Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala Gly Ile Ala Ala Ile
 40 45 50

gct gct gca gtc gtc gag ctc cta gga gga atc ctt atc atc cta gga 307

Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile Leu Ile Ile Leu Gly
 55 60 65

gta ttt acc cgc atc gtt gcc gcc ttc gtt gcc ata gac atg ctc ttc 355
 Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala Ile Asp Met Leu Phe
 70 75 80 85

gca gca ctg ttt gcg cac gtc tcc tcc ggc atc ttt gtc acc aac aat 403
 Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile Phe Val Thr Asn Asn
 90 95 100

ggg tgg gaa ctc acc ggc gca atc ggc gct ggc gcg ctg ctt ctc atc 451
 Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly Ala Leu Leu Leu Ile
 105 110 115

gca gtt ggc gca agt gca tgg agc atc gac ggg gtt ctg gca aaa cgc 499
 Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly Val Leu Ala Lys Arg
 120 125 130

aag gcc taaatctagc gccacaactc cga 528
 Lys Ala
 135

<210> 218
 <211> 135
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 218
 Met Ser Thr Thr Arg Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu
 1 5 10 15

Gly Val Ile Leu Ile Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly
 20 25 30

Leu Glu Gly Val Thr Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala
 35 40 45

Gly Ile Ala Ala Ile Ala Ala Val Val Glu Leu Leu Gly Gly Ile
 50 55 60

Leu Ile Ile Leu Gly Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala
 65 70 75 80

Ile Asp Met Leu Phe Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile
 85 90 95

Phe Val Thr Asn Asn Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly
 100 105 110

Ala Leu Leu Leu Ile Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly
 115 120 125

Val Leu Ala Lys Arg Lys Ala
 130 135

<210> 219
 <211> 438
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(415)

<223> RXN00399

<400> 219

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ggacattgct atgtcgtgag ttgtagtaac cccaaagccc acggattaat caatagtga 60
attcaatgat tttcttttcc cacaggccta aacttaaadc atg agc cac aac gac 115
                                         Met Ser His Asn Asp
                                         1 5

agc cca aac ttt gct cgc cga gcg ctc aat tgg ctc cgc caa ggt tat 163
Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp Leu Arg Gln Gly Tyr
                        10 15 20

cca acc ggt gtt ccg cgg cac gat act ttc gct ctg ttt tac gtt ttg 211
Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala Leu Phe Tyr Val Leu
                        25 30 35

gag cgc gaa ctt act gag gaa gat ctc aat gag ctc gca gag ctt ctc 259
Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu Leu Ala Glu Leu Leu
                        40 45 50

atc gcg gaa ggt gag aac aat ggg ctg cac gat aat ccc att acg cgt 307
Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp Asn Pro Ile Thr Arg
                        55 60 65

gaa aaa atc ggc aag ctg atc acg cat gtt cac agt cag cca cct gag 355
Glu Lys Ile Gly Lys Leu Ile Thr His Val His Ser Gln Pro Pro Glu
                        70 75 80 85

gat gaa gac atc gat cga att cag aaa aag ctg cag gct gag ggc ttc 403
Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu Gln Ala Glu Gly Phe
                        90 95 100

ccc acc cgc aat taattaattg gagttttgtt gtt 438
Pro Thr Arg Asn
                        105

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<210> 220

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Met Ser His Asn Asp Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp
  1 5 10 15

Leu Arg Gln Gly Tyr Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala
  20 25 30

Leu Phe Tyr Val Leu Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu
  35 40 45

Leu Ala Glu Leu Leu Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp
  50 55 60

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Asn Pro Ile Thr Arg Glu Lys Ile Gly Lys Leu Ile Thr His Val His
65 70 75 80

Ser Gln Pro Pro Glu Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu
85 90 95

Gln Ala Glu Gly Phe Pro Thr Arg Asn
100 105

<210> 221

<211> 438

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(415)

<223> FRXA00399

<400> 221

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attcaatgat tttcttttcc cacaggccta aacttaaata atg agc cac aac gac 115
Met Ser His Asn Asp
1 5

agc cca aac ttt gct cgc cga gcg ctc aat tgg ctc cgc caa ggt tat 163
Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp Leu Arg Gln Gly Tyr
10 15 20

cca acc ggt gtt ccg cgg cac gat act ttc gct ctg ttt tac gtt ttg 211
Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala Leu Phe Tyr Val Leu
25 30 35

gag cgc gaa ctt act gag gaa gat ctc aat gag ctc gca gag ctt ctc 259
Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu Leu Ala Glu Leu Leu
40 45 50

atc gcg gaa ggt gag aac aat ggg ctg cac gat aat ccc att acg cgt 307
Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp Asn Pro Ile Thr Arg
55 60 65

gaa aaa atc ggc aag ctg atc acg cat gtt cac agt cag cca cct gag 355
Glu Lys Ile Gly Lys Leu Ile Thr His Val His Ser Gln Pro Pro Glu
70 75 80 85

gat gaa gac atc gat cga att cag aaa aag ctg cag gct gag ggc ttc 403
Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu Gln Ala Glu Gly Phe
90 95 100

ccc acc cgc aat taattaattg gagttttgtt gtt 438
Pro Thr Arg Asn
105

<210> 222

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Met Ser His Asn Asp Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp
 1 5 10 15
 Leu Arg Gln Gly Tyr Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala
 20 25 30
 Leu Phe Tyr Val Leu Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu
 35 40 45
 Leu Ala Glu Leu Leu Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp
 50 55 60
 Asn Pro Ile Thr Arg Glu Lys Ile Gly Lys Leu Ile Thr His Val His
 65 70 75 80
 Ser Gln Pro Pro Glu Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu
 85 90 95
 Gln Ala Glu Gly Phe Pro Thr Arg Asn
 100 105

<210> 223

<211> 1673

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1650)

<223> RXN00416

<400> 223

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 Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15
 att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac 96
 Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30
 cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc 144
 Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45
 ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga 192
 Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60
 tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt 240
 Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80
 tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct 288
 Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95
 tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg 336
 Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110

gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn 115 120 125	384
tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met 130 135 140	432
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala 145 150 155 160	480
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe 165 170 175	528
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala 180 185 190	576
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu 195 200 205	624
ggg ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu 210 215 220	672
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His 225 230 235 240	720
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser 245 250 255	768
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val 260 265 270	816
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val 275 280 285	864
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn 290 295 300	912
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320	960
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335	1008
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350	1056

aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa 1104
 Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln
 355 360 365

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat 1152
 Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
 370 375 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca 1200
 Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
 385 390 395 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag 1248
 Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
 405 410 415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac 1296
 Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
 420 425 430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg 1344
 Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
 435 440 445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc 1392
 Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
 450 455 460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg 1440
 Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
 465 470 475 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc 1488
 Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
 485 490 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg 1536
 Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
 500 505 510

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg 1584
 Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
 515 520 525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg 1632
 Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
 530 535 540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa 1673
 Val Val Thr His Asn Glu
 545 550

<210> 224

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30
 Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45
 Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60
 Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80
 Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95
 Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110
 Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125
 Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
 130 135 140
 Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
 145 150 155 160
 Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
 165 170 175
 Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
 180 185 190
 Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
 195 200 205
 Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
 210 215 220
 Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
 225 230 235 240
 Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
 245 250 255
 Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
 260 265 270
 Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
 275 280 285
 Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
 290 295 300
 Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
 305 310 315 320
 Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
 325 330 335

Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
 340 345 350
 Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln
 355 360 365
 Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
 370 375 380
 Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
 385 390 395 400
 Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
 405 410 415
 Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
 420 425 430
 Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
 435 440 445
 Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
 450 455 460
 Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
 465 470 475 480
 Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
 485 490 495
 Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
 500 505 510
 Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
 515 520 525
 Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
 530 535 540
 Val Val Thr His Asn Glu
 545 550

<210> 225
 <211> 350
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(327)
 <223> FRXA00416

<400> 225
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 Thr Ser His Tyr Ala Asn Pro Leu Gly Glu Phe Gly Asn Arg Asn Ala
 1 5 10 15
 ttc atc gaa gat ctc gcg atc cga agc tgg aat gag ttg gct gat cct 96
 Phe Ile Glu Asp Leu Ala Ile Arg Ser Trp Asn Glu Leu Ala Asp Pro
 20 25 30

caa caa ttc agc gac gcc ttg aac acc tct cca tgg acg atc cct gag 144
 Gln Gln Phe Ser Asp Ala Leu Asn Thr Ser Pro Trp Thr Ile Pro Glu
 35 40 45

 gtg ttc atc ttc cgt ggc tcc atc gat gat cct gac gcc ggt tgg aaa 192
 Val Phe Ile Phe Arg Gly Ser Ile Asp Asp Pro Asp Ala Gly Trp Lys
 50 55 60

 tac gat gtg gct gaa gat ctg tac ccg aac aat cca aac gtg cgc ttc 240
 Tyr Asp Val Ala Glu Asp Leu Tyr Pro Asn Asn Pro Asn Val Arg Phe
 65 70 75 80

 cgc ggc gtg tac ttt aac ccg gag tca ttt gat cag atg tgg cag acc 288
 Arg Gly Val Tyr Phe Asn Pro Glu Ser Phe Asp Gln Met Trp Gln Thr
 85 90 95

 aag caa gtg gga cct ttc gtg gtg gta acg cac aat gag taattcctca 337
 Lys Gln Val Gly Pro Phe Val Val Val Thr His Asn Glu
 100 105

 ccaaacgacc caa 350

<210> 226
 <211> 109
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 226
 Thr Ser His Tyr Ala Asn Pro Leu Gly Glu Phe Gly Asn Arg Asn Ala
 1 5 10 15

 Phe Ile Glu Asp Leu Ala Ile Arg Ser Trp Asn Glu Leu Ala Asp Pro
 20 25 30

 Gln Gln Phe Ser Asp Ala Leu Asn Thr Ser Pro Trp Thr Ile Pro Glu
 35 40 45

 Val Phe Ile Phe Arg Gly Ser Ile Asp Asp Pro Asp Ala Gly Trp Lys
 50 55 60

 Tyr Asp Val Ala Glu Asp Leu Tyr Pro Asn Asn Pro Asn Val Arg Phe
 65 70 75 80

 Arg Gly Val Tyr Phe Asn Pro Glu Ser Phe Asp Gln Met Trp Gln Thr
 85 90 95

 Lys Gln Val Gly Pro Phe Val Val Val Thr His Asn Glu
 100 105

<210> 227
 <211> 1065
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1065)
 <223> FRXA00418

<400> 227

ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct	48
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala	
1 5 10 15	
att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac	96
Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp	
20 25 30	
cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc	144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly	
35 40 45	
ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga	192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly	
50 55 60	
tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt	240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly	
65 70 75 80	
tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct	288
Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala	
85 90 95	
tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg	336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val	
100 105 110	
gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat	384
Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn	
115 120 125	
tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg	432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met	
130 135 140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc	480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala	
145 150 155 160	
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc	528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe	
165 170 175	
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg	576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala	
180 185 190	
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg	624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu	
195 200 205	
ggg ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt	672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu	
210 215 220	
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac	720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His	
225 230 235 240	

tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca 768
 Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
 245 250 255
 agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg 816
 Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
 260 265 270
 cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg 864
 Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
 275 280 285
 ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac 912
 Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
 290 295 300
 acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc 960
 Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
 305 310 315 320
 acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat 1008
 Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
 325 330 335
 cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc 1056
 Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
 340 345 350
 aat cta att 1065
 Asn Leu Ile
 355

<210> 228
 <211> 355
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 228
 Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15
 Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30
 Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45
 Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60
 Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80
 Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95
 Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
115 120 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
130 135 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145 150 155 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
165 170 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
180 185 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
195 200 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
210 215 220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225 230 235 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
245 250 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
260 265 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
275 280 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
290 295 300

Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305 310 315 320

Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
325 330 335

Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
340 345 350

Asn Leu Ile
355

<210> 229

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXN00422

<400> 229

aagcgccggg cgcggaaggc gctggctgag gccttcggcg cggaggtcca gccactgccg 60

cttgacaccg aataggacaa atgggtctat cctggggcgc atg ccc acg aat tat	115
Met Pro Thr Asn Tyr	
1 5	
gca cgc gac aac gtc att tcc ttg gcg tct gcc cgc gag cag cgt tcc	163
Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala Arg Glu Gln Arg Ser	
10 15 20	
ggg aaa ccc gag ccc aaa ccc gaa cta aca ctc atc gtc cgc gcc acc	211
Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu Ile Val Arg Ala Thr	
25 30 35	
aac gtg caa gcg gac ggc gag gtc cac agg caa att ggg ttg aac tcg	259
Asn Val Gln Ala Asp Gly Glu Val His Arg Gln Ile Gly Leu Asn Ser	
40 45 50	
gcg atg agc ctg gac gag ctg cac aat gta ctc aac atc gtt ttc ggt	307
Ala Met Ser Leu Asp Glu Leu His Asn Val Leu Asn Ile Val Phe Gly	
55 60 65	
gtt ggc ggc gag cag tca ccc tgg cgt ttc gaa gac caa ttc cac caa	355
Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu Asp Gln Phe His Gln	
70 75 80 85	
ccc agc gcc ccc gac acc aac ctc ggc gaa ctc ctg ccc gaa ccc ggc	403
Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu Leu Pro Glu Pro Gly	
90 95 100	
gac ttc ctg ttt tac ttc tgg ggc ctg tgg caa ttc aac ctg caa tgc	451
Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln Phe Asn Leu Gln Cys	
105 110 115	
gtg gaa atg tac ccg cgc gac aac ggc acc ccg cgc gcg ctg tgc atc	499
Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro Arg Ala Leu Cys Ile	
120 125 130	
ggc ggc tcc ggc ggc ctc ggc gac gac ttc gac caa gcc acc atc aac	547
Gly Gly Ser Gly Gly Leu Gly Asp Asp Phe Asp Gln Ala Thr Ile Asn	
135 140 145	
gcc gaa ctc acc ggc acc gac acc atc cgc gac gtc ctc tcc ggc gtg	595
Ala Glu Leu Thr Gly Thr Asp Thr Ile Arg Asp Val Leu Ser Gly Val	
150 155 160 165	
cgc ccc gaa gtc atc gac ctc gtc gac cgc acc ggc gtc ttc gac ttc	643
Arg Pro Glu Val Ile Asp Leu Val Asp Arg Thr Gly Val Phe Asp Phe	
170 175 180	
atc cca ctg ctc caa gcg ctc gac ctc aaa aga gaa ccg ctt atc gac	691
Ile Pro Leu Leu Gln Ala Leu Asp Leu Lys Arg Glu Pro Leu Ile Asp	
185 190 195	
gcc acc cgc tac cac acc tgc cgc acg ctg cca gtg gaa aac agc gcc	739
Ala Thr Arg Tyr His Thr Cys Arg Thr Leu Pro Val Glu Asn Ser Ala	
200 205 210	
gaa gcc tcc gac gca ttc tgg tcc tgc gta ctc gcc ctg tcc tgc ctc	787
Glu Ala Ser Asp Ala Phe Trp Ser Cys Val Leu Ala Leu Ser Cys Leu	
215 220 225	

gga aac gac gaa ctt ttc atc gaa gtg atc gaa tcc aca atg agc acc 835
 Gly Asn Asp Glu Leu Phe Ile Glu Val Ile Glu Ser Thr Met Ser Thr
 230 235 240 245

 ctc ggc tgg gtc gcc gac gac ggc tcc cca cta cgt gca cca gag atc 883
 Leu Gly Trp Val Ala Asp Asp Gly Ser Pro Leu Arg Ala Pro Glu Ile
 250 255 260

 acc agc gcc tgc gaa gcc tcc ctg aag ata ctc gcg gaa ctc ggt ggc 931
 Thr Ser Ala Cys Glu Ala Ser Leu Lys Ile Leu Ala Glu Leu Gly Gly
 265 270 275

 tac ggc cca gag cgg ctt gcc ccc gtg gat cgc ctg gac att tat agg 979
 Tyr Gly Pro Glu Arg Leu Ala Pro Val Asp Arg Leu Asp Ile Tyr Arg
 280 285 290

 gag ctg ctg tgt ttc taggtattgt gtaacctcgt gtc 1017
 Glu Leu Cys Phe
 295

<210> 230
 <211> 298
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 230
 Met Pro Thr Asn Tyr Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala
 1 5 10 15

 Arg Glu Gln Arg Ser Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu
 20 25 30

 Ile Val Arg Ala Thr Asn Val Gln Ala Asp Gly Glu Val His Arg Gln
 35 40 45

 Ile Gly Leu Asn Ser Ala Met Ser Leu Asp Glu Leu His Asn Val Leu
 50 55 60

 Asn Ile Val Phe Gly Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu
 65 70 75 80

 Asp Gln Phe His Gln Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu
 85 90 95

 Leu Pro Glu Pro Gly Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln
 100 105 110

 Phe Asn Leu Gln Cys Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro
 115 120 125

 Arg Ala Leu Cys Ile Gly Gly Ser Gly Gly Leu Gly Asp Asp Phe Asp
 130 135 140

 Gln Ala Thr Ile Asn Ala Glu Leu Thr Gly Thr Asp Thr Ile Arg Asp
 145 150 155 160

 Val Leu Ser Gly Val Arg Pro Glu Val Ile Asp Leu Val Asp Arg Thr
 165 170 175

 Gly Val Phe Asp Phe Ile Pro Leu Leu Gln Ala Leu Asp Leu Lys Arg

180	185	190
Glu Pro Leu Ile Asp Ala Thr Arg Tyr His Thr Cys Arg Thr Leu Pro		
195	200	205
Val Glu Asn Ser Ala Glu Ala Ser Asp Ala Phe Trp Ser Cys Val Leu		
210	215	220
Ala Leu Ser Cys Leu Gly Asn Asp Glu Leu Phe Ile Glu Val Ile Glu		
225	230	235
Ser Thr Met Ser Thr Leu Gly Trp Val Ala Asp Asp Gly Ser Pro Leu		
245	250	255
Arg Ala Pro Glu Ile Thr Ser Ala Cys Glu Ala Ser Leu Lys Ile Leu		
260	265	270
Ala Glu Leu Gly Gly Tyr Gly Pro Glu Arg Leu Ala Pro Val Asp Arg		
275	280	285
Leu Asp Ile Tyr Arg Glu Leu Leu Cys Phe		
290	295	

<210> 231
 <211> 523
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(523)
 <223> FRXA00422

<400> 231
 aagcgccggg cgcggaaggc gctggctgag gccttcggcg cggaggtcca gccactgccg 60
 cttgacaccg aataggacaa atgggtctat cctggggcgc atg ccc acg aat tat 115
 Met Pro Thr Asn Tyr
 1 5
 gca cgc gac aac gtc att tcc ttg gcg tct gcc cgc gag cag cgt tcc 163
 Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala Arg Glu Gln Arg Ser
 10 15 20
 ggg aaa ccc gag ccc aaa ccc gaa cta aca ctc atc gtc cgc gcc acc 211
 Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu Ile Val Arg Ala Thr
 25 30 35
 aac gtg caa gcg gac ggc gag gtc cac agg caa att ggg ttg aac tcg 259
 Asn Val Gln Ala Asp Gly Glu Val His Arg Gln Ile Gly Leu Asn Ser
 40 45 50
 gcg atg agc ctg gac gag ctg cac aat gta ctc aac atc gtt ttc ggt 307
 Ala Met Ser Leu Asp Glu Leu His Asn Val Leu Asn Ile Val Phe Gly
 55 60 65
 gtt ggc ggc gag cag tca ccc tgg cgt ttc gaa gac caa ttc cac caa 355
 Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu Asp Gln Phe His Gln
 70 75 80 85

ccc agc gcc ccc gac acc aac ctc ggc gaa ctc ctg ccc gaa ccc ggc 403
Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu Leu Pro Glu Pro Gly
90 95 100

gac ttc ctg ttt tac ttc tgg ggc ctg tgg caa ttc aac ctg caa tgc 451
Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln Phe Asn Leu Gln Cys
105 110 115

gtg gaa atg tac ccg cgc gac aac ggc acc ccg cgc gcg ctg tgc atc 499
Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro Arg Ala Leu Cys Ile
120 125 130

ggc ggc tcc ggc ggc ctc ggc gac 523
Gly Gly Ser Gly Gly Leu Gly Asp
135 140

<210> 232

<211> 141

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Pro Thr Asn Tyr Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala
1 5 10 15

Arg Glu Gln Arg Ser Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu
20 25 30

Ile Val Arg Ala Thr Asn Val Gln Ala Asp Gly Glu Val His Arg Gln
35 40 45

Ile Gly Leu Asn Ser Ala Met Ser Leu Asp Glu Leu His Asn Val Leu
50 55 60

Asn Ile Val Phe Gly Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu
65 70 75 80

Asp Gln Phe His Gln Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu
85 90 95

Leu Pro Glu Pro Gly Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln
100 105 110

Phe Asn Leu Gln Cys Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro
115 120 125

Arg Ala Leu Cys Ile Gly Gly Ser Gly Gly Leu Gly Asp
130 135 140

<210> 233

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXN00447

Lys Pro Val Leu Lys Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu
 65 70 75 80
 Gly Leu Phe Ser Leu Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu
 85 90 95
 Tyr Val Ser Asp Leu Ile Gly Phe Gly Leu Arg Ile Glu Thr Phe Gly
 100 105 110
 Ala Ala Phe Trp Gly Ala Ile Val Leu Ala Leu Val Asn Trp Val Leu
 115 120 125
 Gly Pro Ile Thr Gly Leu Leu Gly Ala Lys Lys Asp
 130 135 140

<210> 235
 <211> 400
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(400)
 <223> FRXA00447

<400> 235
 gagcacggca tcgtgattcg cgcgttcccc gaggggtgcgc gcatttcggt gaccaacgcc 60
 gaggaactg acaagctgct gcgcgcgtgg gaggccatca atg ctg ggt agt ctt 115
 Met Leu Gly Ser Leu
 1 5
 tgg cgt ttt gcg gtg cgc acc gca gca ggc gcg gtg gcg ttg tgg gtg 163
 Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala Val Ala Leu Trp Val
 10 15 20
 gtt att aag ctt atc gac ggc atc tcc ctg agt ttt ccc acc aca cct 211
 Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser Phe Pro Thr Thr Pro
 25 30 35
 ctc tat cag gac ggt cag cac gac aat ctg ctg aca ttc ctg gcg gtg 259
 Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu Thr Phe Leu Ala Val
 40 45 50
 gca gca atc att gtc gtg ttg aat gcc acg gtg aaa ccc gtc ttg aag 307
 Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val Lys Pro Val Leu Lys
 55 60 65
 ctg ctt ggt ttg ccg ttg aca atc atc acc ttg ggt ctg ttc tcg ctg 355
 Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu Gly Leu Phe Ser Leu
 70 75 80 85
 gtc atc aac gcg gta atc atg ctg ctg gcg gag tat gtg tca gat 400
 Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu Tyr Val Ser Asp
 90 95 100

<210> 236
 <211> 100

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

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 1 5 10 15

Val Ala Leu Trp Val Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser
 20 25 30

Phe Pro Thr Thr Pro Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu
 35 40 45

Thr Phe Leu Ala Val Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val
 50 55 60

Lys Pro Val Leu Lys Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu
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Gly Leu Phe Ser Leu Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu
 85 90 95

Tyr Val Ser Asp
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<210> 237

<211> 873

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(850)

<223> RXN00455

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 Met Val Val Asp Val
 1 5

caa aat caa tca cac acc cca gaa acc cag cct caa cct ggg cag ggc 163
 Gln Asn Gln Ser His Thr Pro Glu Thr Gln Pro Gln Pro Gly Gln Gly
 10 15 20

gca gcc aag aaa acc ccc gtt gcg tcc gga aac tcc acg ttc att cac 211
 Ala Ala Lys Lys Thr Pro Val Ala Ser Gly Asn Ser Thr Phe Ile His
 25 30 35

att cag cca agc ttg tac ccc att ttg ctg gcg ctg ttt gtt gca gtc 259
 Ile Gln Pro Ser Leu Tyr Pro Ile Leu Leu Ala Leu Phe Val Ala Val
 40 45 50

ttt cta att tca aat atc acc gca acc aag ggc gta gaa atc ggc ccg 307
 Phe Leu Ile Ser Asn Ile Thr Ala Thr Lys Gly Val Glu Ile Gly Pro
 55 60 65

ttg gtg aca gac ggt gcg ttc ttc ctc ttc ccc atc tca tat gtg ttg 355
 Leu Val Thr Asp Gly Ala Phe Phe Leu Phe Pro Ile Ser Tyr Val Leu

70	75	80	85	
ggc gat gtt cta gcc gaa tgt tac ggc ttc aaa tcc act cgt cgt gcc				403
Gly Asp Val Leu Ala Glu Cys Tyr Gly Phe Lys Ser Thr Arg Arg Ala				
	90	95	100	
att ctt act ggt ttt ggc atc acg atg ctc gcg gcg ctg tct ttc tac				451
Ile Leu Thr Gly Phe Gly Ile Thr Met Leu Ala Ala Leu Ser Phe Tyr				
	105	110	115	
att tcc atc tgg ctg cct ggc gca agt ttc tgg gaa ggc caa gaa gct				499
Ile Ser Ile Trp Leu Pro Gly Ala Ser Phe Trp Glu Gly Gln Glu Ala				
	120	125	130	
ttc gaa gca acg ctc ggc ctt gtt cca cag atc atc gtg gca tca ctg				547
Phe Glu Ala Thr Leu Gly Leu Val Pro Gln Ile Ile Val Ala Ser Leu				
	135	140	145	
gcg ggc tat att gtg ggt cag ctg ctc aac gcc aaa gtt ctg gtg gct				595
Ala Gly Tyr Ile Val Gly Gln Leu Leu Asn Ala Lys Val Leu Val Ala				
	150	155	160	165
atc aaa aag cgc acg ggt gaa aag tcc ctg tgg gcg cgc ctg att ggt				643
Ile Lys Lys Arg Thr Gly Glu Lys Ser Leu Trp Ala Arg Leu Ile Gly				
	170	175	180	
tcc acc gtt gtc gga gaa ttt gtc gat acc ctg ctg ttt tgc gcc atc				691
Ser Thr Val Val Gly Glu Phe Val Asp Thr Leu Leu Phe Cys Ala Ile				
	185	190	195	
gca gcg cca gtg atc ggt att gcc acc gcc ccg gat ttc atc aac tac				739
Ala Ala Pro Val Ile Gly Ile Ala Thr Ala Pro Asp Phe Ile Asn Tyr				
	200	205	210	
gtt gtg gtg ggc ttc gtg tgg aaa acc ctt cta gag gtc atc ctc atg				787
Val Val Val Gly Phe Val Trp Lys Thr Leu Leu Glu Val Ile Leu Met				
	215	220	225	
ccc atc acc tac gca gtc att agg tgg gtg aaa cgc cgc gaa ggt tat				835
Pro Ile Thr Tyr Ala Val Ile Arg Trp Val Lys Arg Arg Glu Gly Tyr				
	230	235	240	245
gaa acc ttc gac gcg tagtaccggc ctaagaattc ttc				873
Glu Thr Phe Asp Ala				
	250			

<210> 238

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

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Gln	Pro	Gly	Gln	Gly	Ala	Ala	Lys	Lys	Thr	Pro	Val	Ala	Ser	Gly	Asn
		20						25					30		

Ser	Thr	Phe	Ile	His	Ile	Gln	Pro	Ser	Leu	Tyr	Pro	Ile	Leu	Leu	Ala
		35					40					45			

Leu Phe Val Ala Val Phe Leu Ile Ser Asn Ile Thr Ala Thr Lys Gly
 50 55 60
 Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe Phe Leu Phe Pro
 65 70 75 80
 Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys Tyr Gly Phe Lys
 85 90 95
 Ser Thr Arg Arg Ala Ile Leu Thr Gly Phe Gly Ile Thr Met Leu Ala
 100 105 110
 Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly Ala Ser Phe Trp
 115 120 125
 Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu Val Pro Gln Ile
 130 135 140
 Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln Leu Leu Asn Ala
 145 150 155 160
 Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu Lys Ser Leu Trp
 165 170 175
 Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe Val Asp Thr Leu
 180 185 190
 Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile Ala Thr Ala Pro
 195 200 205
 Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp Lys Thr Leu Leu
 210 215 220
 Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile Arg Trp Val Lys
 225 230 235 240
 Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
 245 250

<210> 239

<211> 641

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(618)

<223> FRXA00455

<400> 239

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 1 5 10 15

gca acc aag ggc gta gaa atc ggc ccg ttg gtg aca gac ggt gcg ttc 96
 Ala Thr Lys Gly Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe
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ttc ctc ttc ccc atc tca tat gtg ttg ggc gat gtt cta gcc gaa tgt 144

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<210> 240
<211> 206
<212> PRT
<213> Corynebacterium glutamicum
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<400> 240
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Ala Thr Lys Gly Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe
                20                      25                      30
Phe Leu Phe Pro Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys
    35                      40                      45

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Ser	Ala	Glu	Gln	Lys	Gln	Asp	Ser	Leu	Ala	Glu	Lys	Gln	Asp	Ile	Val		
55						60					65						
gca	ggt	cct	tcc	gct	ttt	tct	gat	ctt	ttc	cct	ggg	gat	ggg	ttg	ccg	355	
Ala	Val	Pro	Ser	Ala	Phe	Ser	Asp	Leu	Phe	Pro	Gly	Asp	Gly	Leu	Pro		
70					75				80						85		
cgt	cgt	gcg	gtt	act	caa	ttg	gtt	gaa	cag	cca	ctt	gtg	gtg	gtg	gac	403	
Arg	Arg	Ala	Val	Thr	Gln	Leu	Val	Glu	Gln	Pro	Leu	Val	Val	Val	Asp		
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ttc	ctg	gct	cat	att	act	gcc	cag	ggg	gga	cac	gct	gcg	gtg	att	ggg	451	
Phe	Leu	Ala	His	Ile	Thr	Ala	Gln	Gly	Gly	His	Ala	Ala	Val	Ile	Gly		
			105					110					115				
tgg	aag	gat	tta	gcc	tac	gcc	ggg	gtg	att	gat	tcc	gga	ggg	gtg	tgc	499	
Trp	Lys	Asp	Leu	Ala	Tyr	Ala	Gly	Val	Ile	Asp	Ser	Gly	Gly	Val	Cys		
		120					125					130					
gag	aac	atc	att	gct	att	cca	aat	cct	ggg	acg	gag	cca	ctg	aat	gtg	547	
Glu	Asn	Ile	Ile	Ala	Ile	Pro	Asn	Pro	Gly	Thr	Glu	Pro	Leu	Asn	Val		
	135					140					145						
gca	gcg	gtg	ctg	tgt	gag	ggg	ttg	gat	gtg	gtc	gtg	tac	aaa	ggc	ccg	595	
Ala	Ala	Val	Leu	Cys	Glu	Gly	Leu	Asp	Val	Val	Val	Tyr	Lys	Gly	Pro		
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gag	att	tcc	ctg	tcg	cca	acc	aga	gcg	agg	ccg	ttg	ctg	gga	aag	ctg	643	
Glu	Ile	Ser	Leu	Ser	Pro	Thr	Arg	Ala	Arg	Pro	Leu	Leu	Gly	Lys	Leu		
				170					175					180			
agg	cag	ggg	act	gct	gcc	ttg	gtg	atg	ggt	ggc	acg	aaa	gta	agc	tca	691	
Arg	Gln	Gly	Thr	Ala	Ala	Leu	Val	Met	Val	Gly	Thr	Lys	Val	Ser	Ser		
			185					190					195				
ccg	gcg	ctg	tcg	gtg	gat	gca	gag	atc	act	gat	tat	ggt	ggc	att	ggg	739	
Pro	Ala	Leu	Ser	Val	Asp	Ala	Glu	Ile	Thr	Asp	Tyr	Val	Gly	Ile	Gly		
		200					205					210					
gca	ggg	agt	ggg	cgt	att	cgt	ggc	ggt	gag	atg	cag	gtg	cgg	gct	gtg	787	
Ala	Gly	Ser	Gly	Arg	Ile	Arg	Gly	Val	Glu	Met	Gln	Val	Arg	Ala	Val		
	215					220					225						
tcg	aaa	act	cac	ggg	gtg	cgc	agc	gga	aaa	gtc	ctg	atc	agt	agg	cct	835	
Ser	Lys	Thr	His	Gly	Val	Arg	Ser	Gly	Lys	Val	Leu	Ile	Ser	Arg	Pro		
230					235					240					245		
cag	gat	gca	gca	ttg	ctt	gag	cct	gaa	cag	cca	aca	acg	ttg	cgg	gcg	883	
Gln	Asp	Ala	Ala	Leu	Leu	Glu	Pro	Glu	Gln	Pro	Thr	Thr	Leu	Arg	Ala		
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Val	Pro																

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<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

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35 40 45

Pro Ser Val Glu Glu Ser Ala Glu Gln Lys Gln Asp Ser Leu Ala Glu
50 55 60

Lys Gln Asp Ile Val Ala Val Pro Ser Ala Phe Ser Asp Leu Phe Pro
65 70 75 80

Gly Asp Gly Leu Pro Arg Arg Ala Val Thr Gln Leu Val Glu Gln Pro
85 90 95

Leu Val Val Val Asp Phe Leu Ala His Ile Thr Ala Gln Gly Gly His
100 105 110

Ala Ala Val Ile Gly Trp Lys Asp Leu Ala Tyr Ala Gly Val Ile Asp
115 120 125

Ser Gly Gly Val Cys Glu Asn Ile Ile Ala Ile Pro Asn Pro Gly Thr
130 135 140

Glu Pro Leu Asn Val Ala Ala Val Leu Cys Glu Gly Leu Asp Val Val
145 150 155 160

Val Tyr Lys Gly Pro Glu Ile Ser Leu Ser Pro Thr Arg Ala Arg Pro
165 170 175

Leu Leu Gly Lys Leu Arg Gln Gly Thr Ala Ala Leu Val Met Val Gly
180 185 190

Thr Lys Val Ser Ser Pro Ala Leu Ser Val Asp Ala Glu Ile Thr Asp
195 200 205

Tyr Val Gly Ile Gly Ala Gly Ser Gly Arg Ile Arg Gly Val Glu Met
210 215 220

Gln Val Arg Ala Val Ser Lys Thr His Gly Val Arg Ser Gly Lys Val
225 230 235 240

Leu Ile Ser Arg Pro Gln Asp Ala Ala Leu Leu Glu Pro Glu Gln Pro
245 250 255

Thr Thr Leu Arg Ala Val Pro
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<210> 243

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> FRXA00473

<400> 243

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                                   Leu Trp Gly Asp Gly
                                   1       5

act ccg gtg tcg ctc cct gac ctt tca gga tta agt aga gcg gag cgc 163
Thr Pro Val Ser Leu Pro Asp Leu Ser Gly Leu Ser Arg Ala Glu Arg
              10              15              20

att gat gcg ttg cgt tca cgc atg tcc acc atg ggt gct gcg gtg cca 211
Ile Asp Ala Leu Arg Ser Arg Met Ser Thr Met Gly Ala Ala Val Pro
              25              30              35

aag ttt gag ccg tcg gtg gaa gaa agt gct gaa caa aag cag gat tct 259
Lys Phe Glu Pro Ser Val Glu Glu Ser Ala Glu Gln Lys Gln Asp Ser
              40              45              50

ctc gcc gaa aaa cag gac ata gtt gca gtt cct tcc gct ttt tct gat 307
Leu Ala Glu Lys Gln Asp Ile Val Ala Val Pro Ser Ala Phe Ser Asp
              55              60              65

ctt ttc cct ggg gat ggt ttg ccg cgt cgt gcg gtt act caa ttg gtt 355
Leu Phe Pro Gly Asp Gly Leu Pro Arg Arg Ala Val Thr Gln Leu Val
              70              75              80              85

gaa cag cca ctt gtg gtg gtg gac ttc ctg gct cat att act gcc cag 403
Glu Gln Pro Leu Val Val Val Asp Phe Leu Ala His Ile Thr Ala Gln
              90              95              100

ggg gga cac gct gcg gtg att ggg tgg aag gat tta gcc tac gcc ggg 451
Gly Gly His Ala Ala Val Ile Gly Trp Lys Asp Leu Ala Tyr Ala Gly
              105              110              115

gtg att gat tcc gga ggt gtg tgc gag aac atc att gct att cca aat 499
Val Ile Asp Ser Gly Gly Val Cys Glu Asn Ile Ile Ala Ile Pro Asn
              120              125              130

cct ggt acg gag cca ctg aat gtg gca gcg gtg ctg tgt gag ggg ttg 547
Pro Gly Thr Glu Pro Leu Asn Val Ala Ala Val Leu Cys Glu Gly Leu
              135              140              145

gat gtg gtc gtg tac aaa ggc ccg gag att tcc ctg tcg cca acc aga 595
Asp Val Val Val Tyr Lys Gly Pro Glu Ile Ser Leu Ser Pro Thr Arg
              150              155              160              165

gcg agg ccg ttg ctg gga aag ctg agg cag ggg act gct gcc ttg gtg 643
Ala Arg Pro Leu Leu Gly Lys Leu Arg Gln Gly Thr Ala Ala Leu Val
              170              175              180

atg gtt ggc acg aaa gta agc tca ccg gcg ctg tcg gtg gat gca gag 691
Met Val Gly Thr Lys Val Ser Ser Pro Ala Leu Ser Val Asp Ala Glu
              185              190              195

atc act gat tat gtt ggc att ggt gca ggt agt ggg cgt att cgt ggc 739
Ile Thr Asp Tyr Val Gly Ile Gly Ala Gly Ser Gly Arg Ile Arg Gly
              200              205              210

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gtt gag atg cag gtg cgg gct gtg tcg aaa act cac ggt gtg cgc agc 787
 Val Glu Met Gln Val Arg Ala Val Ser Lys Thr His Gly Val Arg Ser
 215 220 225

gga aaa gtc ctg atc agt agg cct cag gat gca gca ttg ctt gag cct 835
 Gly Lys Val Leu Ile Ser Arg Pro Gln Asp Ala Ala Leu Leu Glu Pro
 230 235 240 245

gaa cag cca aca acg ttg cgg gcg gtc cca tgacgcgggt gatggcattg 885
 Glu Gln Pro Thr Thr Leu Arg Ala Val Pro
 250 255

tgg 888

<210> 244

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

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Gly Ala Ala Val Pro Lys Phe Glu Pro Ser Val Glu Glu Ser Ala Glu
 35 40 45

Gln Lys Gln Asp Ser Leu Ala Glu Lys Gln Asp Ile Val Ala Val Pro
 50 55 60

Ser Ala Phe Ser Asp Leu Phe Pro Gly Asp Gly Leu Pro Arg Arg Ala
 65 70 75 80

Val Thr Gln Leu Val Glu Gln Pro Leu Val Val Val Asp Phe Leu Ala
 85 90 95

His Ile Thr Ala Gln Gly Gly His Ala Ala Val Ile Gly Trp Lys Asp
 100 105 110

Leu Ala Tyr Ala Gly Val Ile Asp Ser Gly Gly Val Cys Glu Asn Ile
 115 120 125

Ile Ala Ile Pro Asn Pro Gly Thr Glu Pro Leu Asn Val Ala Ala Val
 130 135 140

Leu Cys Glu Gly Leu Asp Val Val Val Tyr Lys Gly Pro Glu Ile Ser
 145 150 155 160

Leu Ser Pro Thr Arg Ala Arg Pro Leu Leu Gly Lys Leu Arg Gln Gly
 165 170 175

Thr Ala Ala Leu Val Met Val Gly Thr Lys Val Ser Ser Pro Ala Leu
 180 185 190

Ser Val Asp Ala Glu Ile Thr Asp Tyr Val Gly Ile Gly Ala Gly Ser
 195 200 205

Gly Arg Ile Arg Gly Val Glu Met Gln Val Arg Ala Val Ser Lys Thr

210	215	220
His Gly Val Arg Ser Gly Lys Val Leu Ile Ser Arg Pro Gln Asp Ala		
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Ala Leu Leu Glu Pro Glu Gln Pro Thr Thr Leu Arg Ala Val Pro		
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(2395)
 <223> RXN00485

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 Val Ser Ser Val Asn
 1 5

gat ctt ttt gcc aag ccg tat gaa aac gct gat ctt gtg gtc acg gtg 163
 Asp Leu Phe Ala Lys Pro Tyr Glu Asn Ala Asp Leu Val Val Thr Val
 10 15 20

tct gcg aaa aac gaa gat tcc ttt gca gct ttt gag caa caa tta gct 211
 Ser Ala Lys Asn Glu Asp Ser Phe Ala Ala Phe Glu Gln Gln Leu Ala
 25 30 35

acg aca cct ggt gtt gaa gct ctg gct ttt gat caa aat ttt gca gcc 259
 Thr Thr Pro Gly Val Glu Ala Leu Ala Phe Asp Gln Asn Phe Ala Ala
 40 45 50

tct gta aag caa tca gac ggg att tac gcc agt act tca gtc cag tca 307
 Ser Val Lys Gln Ser Asp Gly Ile Tyr Ala Ser Thr Ser Val Gln Ser
 55 60 65

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 Ile Ser Glu Gly Pro Leu Gln Trp Arg Pro Ile Leu Glu Gly Arg Leu
 70 75 80 85

ccc caa gga cct ggt gag att gca gta aca acg gcc ccg ggt gcg cct 403
 Pro Gln Gly Pro Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala Pro
 90 95 100

gaa gtt ggt gag cac gta tcc att cgc ctg tcc caa aac act gag gac 451
 Glu Val Gly Glu His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu Asp
 105 110 115

act gag gtt ctt gtg gtt ggc gtg gtg gag cca gcg gcg cag gaa act 499
 Thr Glu Val Leu Val Val Gly Val Val Glu Pro Ala Ala Gln Glu Thr
 120 125 130

tta ggt ggc gca ccg ttc gtt gtg gcg tct cct gat gcg ctg atg gag 547
 Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met Glu
 135 140 145

tgg aat tct tcc ggt gtg cgg ggt gaa ttc cga gtg gca act tcc gat	595
Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser Asp	
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cct gcc tcg cta gag gct gca agc ttt agc gac gct acg gtg gtg gtt	643
Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val Val	
170 175 180	
gct tcg gcg gag ggg cac gtc gat aag ctt gct gat tct tat ttg ggc	691
Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu Gly	
185 190 195	
cag cga gat cgc tat ttc ttg ctg ctc gca gcg ttt gtg gca gtg gct	739
Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val Ala	
200 205 210	
gct gcc gtg gcg ttt ttg gtg gtc ttt tct gca tat tcg gtg ctc act	787
Ala Ala Val Ala Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu Thr	
215 220 225	
ggg gag cga gtt cgc gag ttc ggg ctg att cgt tca gtg ggc gca tcg	835
Gly Glu Arg Val Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala Ser	
230 235 240 245	
acg ccg cag att ttg ggg tca gtg att ttt gaa gcc ggc atc ctc ggt	883
Thr Pro Gln Ile Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu Gly	
250 255 260	
gtg gtg gct gct ggt ttt ggt gcg ccc gcc gga ttg atg gcg gcg cgt	931
Val Val Ala Ala Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala Arg	
265 270 275	
ttg ttg gcg gat aat gcc gca cgt ttt ggc att cgt gtg ccc att gat	979
Leu Leu Ala Asp Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile Asp	
280 285 290	
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Val Ile Asp Leu Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val Gly	
295 300 305	
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Val Val Met Ser Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val Cys	
310 315 320 325	
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Arg Lys Ser Ala Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg Thr	
330 335 340	
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Ser Pro Trp Phe Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val Gly	
345 350 355	
gcc ggc gga atg tgg gcg tat gag gca acc tcg gac tac cgc ggc atg	1219
Ala Gly Gly Met Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly Met	
360 365 370	
cgt tca gtg gct tta tcc atc gcc ggt tca ggc gct ttg gtg tgt gcg	1267
Arg Ser Val Ala Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys Ala	
375 380 385	

ttg ttg att gcc acg gcg gtg ctc gtg ccc tgg tta ttg cac gta ttc	1315
Leu Leu Ile Ala Thr Ala Val Leu Val Pro Trp Leu Leu His Val Phe	
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Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu Ala	
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Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val Ile	
425 430 435	
ctt gct ggt tct gca tta agc tcc gct gtt ctg cat ggc cag gca cat	1459
Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala His	
440 445 450	
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Ile Gly Thr His Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr Asp	
455 460 465	
atg atg gtt aca gcg ctt gat ggg gaa atc ccc gcc gga atg ctg gag	1555
Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu Glu	
470 475 480 485	
gaa atc tct agc atc gac ggc gtg aaa act gcc atc gcg cca gcc acc	1603
Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala Thr	
490 495 500	
acc gct gtg gaa ttg gaa gat tcc ggc aat ttc tct gtg ctc atg ctc	1651
Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met Leu	
505 510 515	
gct gaa gaa gac gga gcc tcc gtg atg cgc gca ggc gat act ggt gca	1699
Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly Ala	
520 525 530	
cca gct ggt ggc ctt gtt ttg ggc aga aac tct cct gac cag gat gct	1747
Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp Ala	
535 540 545	
tac ccg gcc ggc cag gct gca aac atc att gtc gcg gat acc cca acg	1795
Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro Thr	
550 555 560 565	
cag gcg gaa atc ttc cac agc gac aac tac ttc tcc atg atc gac cca	1843
Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp Pro	
570 575 580	
gca ctc gcc acc ggc ccc agc acc aca cgc aac gta ctg atc ctg ctc	1891
Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu Leu	
585 590 595	
gac ggc gac tcc aac cag gcc ccc gac aac gcc acg gcg cag gcg gta	1939
Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala Val	
600 605 610	
cgc aag acc att tgc ctt ttc gac gga cga tac tcc atc acc gag ggt	1987
Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu Gly	
615 620 625	
ttc tcc gcc cgc caa aac act ttt gaa ctg gtt tcc cgc atc acc acc	2035

Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr Thr
 630 635 640 645
 atg tcc aca ctg ctt gcc atc gtg gcc tta gcg atc gct gcc gtt ggc 2083
 Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val Gly
 650 655 660
 ctg atc aac aca gtg gca ctc acc att tct gag cgt gcc cgc gat cgt 2131
 Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp Arg
 665 670 675
 tat ttg ctg cgc acc att gga ctg acc tca act ggt cag att ctg gtg 2179
 Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu Val
 680 685 690
 atg gct att gaa atg atc gcg ctc tca ttg ccg gct gcc att gtt ggt 2227
 Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val Gly
 695 700 705
 gca gtt tcg gga gga ttc tta ggc aga ttc gtt gcc agt tct gcc acc 2275
 Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala Thr
 710 715 720 725
 aac acc gct gcg acg gca cca ctt caa gta gac att ctc ggc gga acg 2323
 Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly Thr
 730 735 740
 gtt ctc gcg atg gtc gca gga tct gta ctg tgc gcg ctc atc gtg ctg 2371
 Val Leu Ala Met Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val Leu
 745 750 755
 gcg aac aaa cga cgt cgg gtg gtt tgattataaa atccaaaaat cga 2418
 Ala Asn Lys Arg Arg Arg Val Val
 760 765

<210> 246

<211> 765

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

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Leu Val Val Thr Val Ser Ala Lys Asn Glu Asp Ser Phe Ala Ala Phe
 20 25 30

Glu Gln Gln Leu Ala Thr Thr Pro Gly Val Glu Ala Leu Ala Phe Asp
 35 40 45

Gln Asn Phe Ala Ala Ser Val Lys Gln Ser Asp Gly Ile Tyr Ala Ser
 50 55 60

Thr Ser Val Gln Ser Ile Ser Glu Gly Pro Leu Gln Trp Arg Pro Ile
 65 70 75 80

Leu Glu Gly Arg Leu Pro Gln Gly Pro Gly Glu Ile Ala Val Thr Thr
 85 90 95

Ala Pro Gly Ala Pro Glu Val Gly Glu His Val Ser Ile Arg Leu Ser

100					105					110					
Gln	Asn	Thr	Glu	Asp	Thr	Glu	Val	Leu	Val	Val	Gly	Val	Val	Glu	Pro
	115						120					125			
Ala	Ala	Gln	Glu	Thr	Leu	Gly	Gly	Ala	Pro	Phe	Val	Val	Ala	Ser	Pro
	130					135					140				
Asp	Ala	Leu	Met	Glu	Trp	Asn	Ser	Ser	Gly	Val	Arg	Gly	Glu	Phe	Arg
145					150					155					160
Val	Ala	Thr	Ser	Asp	Pro	Ala	Ser	Leu	Glu	Ala	Ala	Ser	Phe	Ser	Asp
				165					170					175	
Ala	Thr	Val	Val	Val	Ala	Ser	Ala	Glu	Gly	His	Val	Asp	Lys	Leu	Ala
		180						185					190		
Asp	Ser	Tyr	Leu	Gly	Gln	Arg	Asp	Arg	Tyr	Phe	Leu	Leu	Leu	Ala	Ala
	195						200					205			
Phe	Val	Ala	Val	Ala	Ala	Ala	Val	Ala	Phe	Leu	Val	Val	Phe	Ser	Ala
	210						215					220			
Tyr	Ser	Val	Leu	Thr	Gly	Glu	Arg	Val	Arg	Glu	Phe	Gly	Leu	Ile	Arg
225						230					235				240
Ser	Val	Gly	Ala	Ser	Thr	Pro	Gln	Ile	Leu	Gly	Ser	Val	Ile	Phe	Glu
				245					250					255	
Ala	Gly	Ile	Leu	Gly	Val	Val	Ala	Ala	Gly	Phe	Gly	Ala	Pro	Ala	Gly
			260					265					270		
Leu	Met	Ala	Ala	Arg	Leu	Leu	Ala	Asp	Asn	Ala	Ala	Arg	Phe	Gly	Ile
	275						280					285			
Arg	Val	Pro	Ile	Asp	Val	Ile	Asp	Leu	Pro	Ser	Ser	Thr	Met	Trp	Leu
	290					295					300				
Ile	Ala	Gly	Val	Gly	Val	Val	Met	Ser	Val	Ile	Ala	Ala	Leu	Pro	Ala
305						310					315			320	
Val	Phe	Ser	Val	Cys	Arg	Lys	Ser	Ala	Val	Glu	Ser	Leu	Ser	Thr	Pro
				325					330					335	
Ala	Ile	Ser	Arg	Thr	Ser	Pro	Trp	Phe	Gly	Ala	Leu	Trp	Leu	Leu	Leu
			340					345					350		
Ala	Gly	Ile	Val	Gly	Ala	Gly	Gly	Met	Trp	Ala	Tyr	Glu	Ala	Thr	Ser
		355					360					365			
Asp	Tyr	Arg	Gly	Met	Arg	Ser	Val	Ala	Leu	Ser	Ile	Ala	Gly	Ser	Gly
	370					375					380				
Ala	Leu	Val	Cys	Ala	Leu	Leu	Ile	Ala	Thr	Ala	Val	Leu	Val	Pro	Trp
385						390					395			400	
Leu	Leu	His	Val	Phe	Ser	Arg	Ile	Val	Gly	Gly	Thr	Val	Pro	Thr	Leu
			405						410					415	
Gln	Leu	Gly	Leu	Ala	Phe	Ala	Ala	Lys	Gln	Lys	Ser	Arg	Ser	Ala	Ala
			420					425					430		

Leu Ile Ala Val Ile Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu
 435 440 445
 His Gly Gln Ala His Ile Gly Thr His Leu Val Ala Val Ala Lys Gly
 450 455 460
 Met Gly Gly Thr Asp Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro
 465 470 475 480
 Ala Gly Met Leu Glu Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala
 485 490 495
 Ile Ala Pro Ala Thr Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe
 500 505 510
 Ser Val Leu Met Leu Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala
 515 520 525
 Gly Asp Thr Gly Ala Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser
 530 535 540
 Pro Asp Gln Asp Ala Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val
 545 550 555 560
 Ala Asp Thr Pro Thr Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe
 565 570 575
 Ser Met Ile Asp Pro Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn
 580 585 590
 Val Leu Ile Leu Leu Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala
 595 600 605
 Thr Ala Gln Ala Val Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr
 610 615 620
 Ser Ile Thr Glu Gly Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val
 625 630 635 640
 Ser Arg Ile Thr Thr Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala
 645 650 655
 Ile Ala Ala Val Gly Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu
 660 665 670
 Arg Ala Arg Asp Arg Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr
 675 680 685
 Gly Gln Ile Leu Val Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro
 690 695 700
 Ala Ala Ile Val Gly Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val
 705 710 715 720
 Ala Ser Ser Ala Thr Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp
 725 730 735
 Ile Leu Gly Gly Thr Val Leu Ala Met Val Ala Gly Ser Val Leu Cys
 740 745 750

Ala Leu Ile Val Leu Ala Asn Lys Arg Arg Arg Val Val
 755 760 765

<210> 247
 <211> 2166
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2143)
 <223> FRXA00485

<400> 247
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 Leu Pro Gln Gly Pro
 1 5
 ggt gag att gca gta aca acg gcc ccg ggt gcg cct gaa gtt ggt gag 163
 Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala Pro Glu Val Gly Glu
 10 15 20
 cac gta tcc att cgc ctg tcc caa aac act gag gac act gag gtt ctt 211
 His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu Asp Thr Glu Val Leu
 25 30 35
 gtg gtt ggc gtg gtg gag cca gcg gcg cag gaa act tta ggt ggc gca 259
 Val Val Gly Val Val Glu Pro Ala Ala Gln Glu Thr Leu Gly Gly Ala
 40 45 50
 ccg ttc gtt gtg gcg tct cct gat gcg ctg atg gag tgg aat tct tcc 307
 Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met Glu Trp Asn Ser Ser
 55 60 65
 ggt gtg cgg ggt gaa ttc cga gtg gca act tcc gat cct gcc tcg cta 355
 Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser Asp Pro Ala Ser Leu
 70 75 80 85
 gag gct gca agc ttt agc gac gct acg gtg gtg gtt gct tcg gcg gag 403
 Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val Val Ala Ser Ala Glu
 90 95 100
 ggg cac gtc gat aag ctt gct gat tct tat ttg ggc cag cga gat cgc 451
 Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu Gly Gln Arg Asp Arg
 105 110 115
 tat ttc ttg ctg ctc gca gcg ttt gtg gca gtg gct gct gcc gtg gcg 499
 Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val Ala Ala Val Ala
 120 125 130
 ttt ttg gtg gtc ttt tct gca tat tcg gtg ctc act ggt gag cga gtt 547
 Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu Thr Gly Glu Arg Val
 135 140 145
 cgc gag ttc ggg ctg att cgt tca gtg ggc gca tcg acg ccg cag att 595
 Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala Ser Thr Pro Gln Ile
 150 155 160 165

ttg ggg tca gtg att ttt gaa gcc ggc atc ctc ggt gtg gtg gct gct	643
Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu Gly Val Val Ala Ala	
170 175 180	
ggg ttt ggt gcg ccc gcc gga ttg atg gcg gcg cgt ttg ttg gcg gat	691
Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala Arg Leu Leu Ala Asp	
185 190 195	
aat gcc gca cgt ttt ggc att cgt gtg ccc att gat gtg att gat ctg	739
Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile Asp Val Ile Asp Leu	
200 205 210	
cca agt agc acg atg tgg ctc atc gct ggc gtc ggc gtg gtg atg tcc	787
Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val Gly Val Val Met Ser	
215 220 225	
gtg att gcg gca tta ccg gca gtg ttc agt gtg tgc aga aaa tcc gca	835
Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val Cys Arg Lys Ser Ala	
230 235 240 245	
gtg gaa tca ctg agt acg cct gct att tcg agg act tcc ccc tgg ttc	883
Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg Thr Ser Pro Trp Phe	
250 255 260	
ggg gca tta tgg ttg ctg ctc gcg ggc att gtg ggc gcc ggc gga atg	931
Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val Gly Ala Gly Gly Met	
265 270 275	
tgg gcg tat gag gca acc tcg gac tac cgc ggc atg cgt tca gtg gct	979
Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly Met Arg Ser Val Ala	
280 285 290	
tta tcc atc gcc ggt tca ggc gct ttg gtg tgt gcg ttg ttg att gcc	1027
Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys Ala Leu Leu Ile Ala	
295 300 305	
acg gcg gtg ctc gtg ccc tgg tta ttg cac gta ttc tcc agg att gtg	1075
Thr Ala Val Leu Val Pro Trp Leu Leu His Val Phe Ser Arg Ile Val	
310 315 320 325	
ggc ggc acc gtc cca aca ctt cag ttg gga ttg gcg ttt gca gca aag	1123
Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu Ala Phe Ala Ala Lys	
330 335 340	
cag aaa tct cgt tcg gcg gcg ctg atc gct gtg att ctt gct ggt tct	1171
Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val Ile Leu Ala Gly Ser	
345 350 355	
gca tta agc tcc gct gtt ctg cat ggc cag gca cat atc ggc acg cat	1219
Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala His Ile Gly Thr His	
360 365 370	
ttg gtg gcc gtg gct aaa ggc atg ggc ggc aca gac atg atg gtt aca	1267
Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr Asp Met Met Val Thr	
375 380 385	
gcg ctt gat ggg gaa atc ccc gcc gga atg ctg gag gaa atc tct agc	1315
Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu Glu Glu Ile Ser Ser	
390 395 400 405	
atc gac ggc gtg aaa act gcc atc gcg cca gcc acc acc gct gtg gaa	1363

Ile Asp Gly Val	Lys Thr Ala Ile	Ala Pro Ala Thr	Thr Thr Ala Val	Glu	
	410	415		420	
ttg gaa gat tcc ggc aat ttc tct gtg ctc atg ctc gct gaa gaa gac	1411				
Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met Leu Ala Glu Glu Asp					
	425	430		435	
gga gcc tcc gtg atg cgc gca ggc gat act ggt gca cca gct ggt ggc	1459				
Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly Ala Pro Ala Gly Gly					
	440	445		450	
ctt gtt ttg ggc aga aac tct cct gac cag gat gct tac ccg gcc ggc	1507				
Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp Ala Tyr Pro Ala Gly					
	455	460		465	
cag gct gca aac atc att gtc gcg gat acc cca acg cag gcg gaa atc	1555				
Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro Thr Gln Ala Glu Ile					
	470	475		480	485
ttc cac agc gac aac tac ttc tcc atg atc gac cca gca ctc gcc acc	1603				
Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp Pro Ala Leu Ala Thr					
	490	495		500	
ggc ccc agc acc aca cgc aac gta ctg atc ctg ctc gac ggc gac tcc	1651				
Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu Leu Asp Gly Asp Ser					
	505	510		515	
aac cag gcc ccc gac aac gcc acg gcg cag gcg gta cgc aag acc att	1699				
Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala Val Arg Lys Thr Ile					
	520	525		530	
tcg ctt ttc gac gga cga tac tcc atc acc gag ggt ttc tcc gcc cgc	1747				
Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu Gly Phe Ser Ala Arg					
	535	540		545	
caa aac act ttt gaa ctg gtt tcc cgc atc acc acc atg tcc aca ctg	1795				
Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr Thr Met Ser Thr Leu					
	550	555		560	565
ctt gcc atc gtg gcc tta gcg atc gct gcc gtt ggc ctg atc aac aca	1843				
Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val Gly Leu Ile Asn Thr					
	570	575		580	
gtg gca ctc acc att tct gag cgt gcc cgc gat cgt tat ttg ctg cgc	1891				
Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp Arg Tyr Leu Leu Arg					
	585	590		595	
acc att gga ctg acc tca act ggt cag att ctg gtg atg gct att gaa	1939				
Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu Val Met Ala Ile Glu					
	600	605		610	
atg atc gcg ctc tca ttg ccg gct gcc att gtt ggt gca gtt tcg gga	1987				
Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val Gly Ala Val Ser Gly					
	615	620		625	
gga ttc tta ggc aga ttc gtt gcc agt tct gcc acc aac acc gct gcg	2035				
Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala Thr Asn Thr Ala Ala					
	630	635		640	645
acg gca cca ctt caa gta gac att ctc ggc gga acg gtt ctc gcg atg	2083				
Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly Thr Val Leu Ala Met					

650 655 660
 gtc gca gga tct gta ctg tgc gcg ctc atc gtg ctg gcg aac aaa cga 2131
 Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val Leu Ala Asn Lys Arg
 665 670 675

cgt cgg gtg gtt tgattataaaa atccaaaaat cga 2166
 Arg Arg Val Val
 680

<210> 248
 <211> 681
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 248
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 20 25 30
 Asp Thr Glu Val Leu Val Val Gly Val Val Glu Pro Ala Ala Gln Glu
 35 40 45
 Thr Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met
 50 55 60
 Glu Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser
 65 70 75 80
 Asp Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val
 85 90 95
 Val Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu
 100 105 110
 Gly Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val
 115 120 125
 Ala Ala Ala Val Ala Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu
 130 135 140
 Thr Gly Glu Arg Val Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala
 145 150 155 160
 Ser Thr Pro Gln Ile Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu
 165 170 175
 Gly Val Val Ala Ala Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala
 180 185 190
 Arg Leu Leu Ala Asp Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile
 195 200 205
 Asp Val Ile Asp Leu Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val
 210 215 220
 Gly Val Val Met Ser Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val
 225 230 235 240

Cys Arg Lys Ser Ala Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg
 245 250 255
 Thr Ser Pro Trp Phe Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val
 260 265 270
 Gly Ala Gly Gly Met Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly
 275 280 285
 Met Arg Ser Val Ala Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys
 290 295 300
 Ala Leu Leu Ile Ala Thr Ala Val Leu Val Pro Trp Leu Leu His Val
 305 310 315 320
 Phe Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu
 325 330 335
 Ala Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val
 340 345 350
 Ile Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala
 355 360 365
 His Ile Gly Thr His Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr
 370 375 380
 Asp Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu
 385 390 395 400
 Glu Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala
 405 410 415
 Thr Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met
 420 425 430
 Leu Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly
 435 440 445
 Ala Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp
 450 455 460
 Ala Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro
 465 470 475 480
 Thr Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp
 485 490 495
 Pro Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu
 500 505 510
 Leu Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala
 515 520 525
 Val Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu
 530 535 540
 Gly Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr
 545 550 555 560

Thr Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val
565 570 575

Gly Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp
580 585 590

Arg Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu
595 600 605

Val Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val
610 615 620

Gly Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala
625 630 635 640

Thr Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly
645 650 655

Thr Val Leu Ala Met Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val
660 665 670

Leu Ala Asn Lys Arg Arg Arg Val Val
675 680

<210> 249

<211> 1149

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1126)

<223> RXN00496

<400> 249

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Met Thr Arg Arg Leu
1 5

cat ggt ggt gag cag gat ggc cag gaa cac gtt aaa gga cag cta aag 163
His Gly Gly Glu Gln Asp Gly Gln Glu His Val Lys Gly Gln Leu Lys
10 15 20

cag ctg ttc gac gac gac gcg ttc ttg act gac ctg tcc cgc ggc gtt 211
Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp Leu Ser Arg Gly Val
25 30 35

gat ccc tca gag ggc gat gac gcc ctc gct ggc ctc ctc ctc gat tta 259
Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly Leu Leu Leu Asp Leu
40 45 50

aca aag gaa gct cag gag ccg ccg gca aca atg ccg gat tgg tct act 307
Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met Pro Asp Trp Ser Thr
55 60 65

ttg ctc cct gga att ttg gat cag gat cag gat ttg cca gtg gaa tcc 355
Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp Leu Pro Val Glu Ser
70 75 80 85

act tcg gac acc acg gtt atg cag gca tca aac cct gca acc caa gaa	403
Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn Pro Ala Thr Gln Glu	
90 95 100	
ttc gca cct gtt tct att tct gat acc ccc aac act gca act aat tca	451
Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn Thr Ala Thr Asn Ser	
105 110 115	
gct gat gca gat gag tcc gca act gtt gtt cca ctt gca gca cgc cgt	499
Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro Leu Ala Ala Arg Arg	
120 125 130	
gag aag cgt gcc aag agc gga tca agc ggg gtt cat tca ctg gat gct	547
Glu Lys Arg Ala Lys Ser Gly Ser Ser Gly Val His Ser Leu Asp Ala	
135 140 145	
tcg gca acc cag cgc aaa tct cac cca ttc ctt agc ggt ttg gtg ggt	595
Ser Ala Thr Gln Arg Lys Ser His Pro Phe Leu Ser Gly Leu Val Gly	
150 155 160 165	
gct gca gct gca act cta gtc atc gca ggc ggt gga gca gca gtg tac	643
Ala Ala Ala Ala Thr Leu Val Ile Ala Gly Gly Gly Ala Ala Val Tyr	
170 175 180	
aac gct gat gaa aac tcc ccg ttg tat ggc atg aat cag cag ctg ttt	691
Asn Ala Asp Glu Asn Ser Pro Leu Tyr Gly Met Asn Gln Gln Leu Phe	
185 190 195	
ggc aat caa gat tct cca agc gtg gtg gag ctt gcc tcc acg ctg gaa	739
Gly Asn Gln Asp Ser Pro Ser Val Val Glu Leu Ala Ser Thr Leu Glu	
200 205 210	
gaa gtt gat agt cgt aca gct agt ggc gat gtg gaa ggg gca cgt gct	787
Glu Val Asp Ser Arg Thr Ala Ser Gly Asp Val Glu Gly Ala Arg Ala	
215 220 225	
cta ctc gag cag gct cga gca atg ctg gat ggc atg gca cct cct cga	835
Leu Leu Glu Gln Ala Arg Ala Met Leu Asp Gly Met Ala Pro Pro Arg	
230 235 240 245	
aag gcg ccg tcg gag gca acc cga acg gtt gaa tct gaa cca ggt act	883
Lys Ala Pro Ser Glu Ala Thr Arg Thr Val Glu Ser Glu Pro Gly Thr	
250 255 260	
cag acg ttg act gca acg gtt act gaa tcc gca agt ccg gaa cca ccg	931
Gln Thr Leu Thr Ala Thr Val Thr Glu Ser Ala Ser Pro Glu Pro Pro	
265 270 275	
gtc acg gaa act caa act gtt acc tcc acc gag gta cag aca gtg aca	979
Val Thr Glu Thr Gln Thr Val Thr Ser Thr Glu Val Gln Thr Val Thr	
280 285 290	
acc act gcg gtt gct cca ccg gtc tgg act cct aat cca gag cca aca	1027
Thr Thr Ala Val Ala Pro Pro Val Trp Thr Pro Asn Pro Glu Pro Thr	
295 300 305	
acc aca gct gcc ccg act tct acg cct tca act ggt ggc ggt gag gga	1075
Thr Thr Ala Ala Pro Thr Ser Thr Pro Ser Thr Gly Gly Gly Glu Gly	
310 315 320 325	

acc ggc aat gat ggt gac tct gga ctt gtg cca cct cag act cct gga 1123
 Thr Gly Asn Asp Gly Asp Ser Gly Leu Val Pro Pro Gln Thr Pro Gly
 330 335 340

aac taggtaaaaa tataaaaaact gct 1149
 Asn

<210> 250
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 250
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Lys Gly Gln Leu Lys Gln Leu Phe Asp Asp Ala Phe Leu Thr Asp
 20 25 30

Leu Ser Arg Gly Val Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly
 35 40 45

Leu Leu Leu Asp Leu Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met
 50 55 60

Pro Asp Trp Ser Thr Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp
 65 70 75 80

Leu Pro Val Glu Ser Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn
 85 90 95

Pro Ala Thr Gln Glu Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn
 100 105 110

Thr Ala Thr Asn Ser Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro
 115 120 125

Leu Ala Ala Arg Arg Glu Lys Arg Ala Lys Ser Gly Ser Ser Gly Val
 130 135 140

His Ser Leu Asp Ala Ser Ala Thr Gln Arg Lys Ser His Pro Phe Leu
 145 150 155 160

Ser Gly Leu Val Gly Ala Ala Ala Ala Thr Leu Val Ile Ala Gly Gly
 165 170 175

Gly Ala Ala Val Tyr Asn Ala Asp Glu Asn Ser Pro Leu Tyr Gly Met
 180 185 190

Asn Gln Gln Leu Phe Gly Asn Gln Asp Ser Pro Ser Val Val Glu Leu
 195 200 205

Ala Ser Thr Leu Glu Glu Val Asp Ser Arg Thr Ala Ser Gly Asp Val
 210 215 220

Glu Gly Ala Arg Ala Leu Leu Glu Gln Ala Arg Ala Met Leu Asp Gly
 225 230 235 240

Met Ala Pro Pro Arg Lys Ala Pro Ser Glu Ala Thr Arg Thr Val Glu

ttc gca cct gtt tct att tct gat acc ccc aac act gca act aat tca 451
Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn Thr Ala Thr Asn Ser
105 110 115

gct gat gca gat gag tcc gca act gtt gtt cca ctt gca gca cgc cgt 499
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120 125 130

gag 502
Glu

<210> 252
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 252
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Lys Gly Gln Leu Lys Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp
20 25 30

Leu Ser Arg Gly Val Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly
35 40 45

Leu Leu Leu Asp Leu Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met
50 55 60

Pro Asp Trp Ser Thr Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp
65 70 75 80

Leu Pro Val Glu Ser Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn
85 90 95

Pro Ala Thr Gln Glu Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn
100 105 110

Thr Ala Thr Asn Ser Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro
115 120 125

Leu Ala Ala Arg Arg Glu
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<210> 253
<211> 1845
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1822)
<223> RXN00503

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	Met Lys Pro Val Phe	
	1 5	
tcc gtt gac caa atc cga cgc gca gaa aac acc ctt ttt gag ctt cag	163	
Ser Val Asp Gln Ile Arg Arg Ala Glu Asn Thr Leu Phe Glu Leu Gln		
10 15 20		
gca gat ccg gat gag ctg atg atc tcc gcg gca tcg gcg gtg gcc gat	211	
Ala Asp Pro Asp Glu Leu Met Ile Ser Ala Ala Ser Ala Val Ala Asp		
25 30 35		
gtc gcg ttg gca atg gtg gac ggc ccc gct cca gcg gtc tcc agt gag	259	
Val Ala Leu Ala Met Val Asp Gly Pro Ala Pro Ala Val Ser Ser Glu		
40 45 50		
gag tca atc ctg ctg ctg gtc ggc ccc ggt ggc aac ggt ggc gac gcc	307	
Glu Ser Ile Leu Leu Leu Val Gly Pro Gly Gly Asn Gly Gly Asp Ala		
55 60 65		
ttg tat gca ggc gcg ttc ctt gca gaa gaa ggc cac cac gtt gat gct	355	
Leu Tyr Ala Gly Ala Phe Leu Ala Glu Glu Gly His His Val Asp Ala		
70 75 80 85		
ttg ctg ttg gga aac ggc aaa gtc cat caa tca gca ttg gca tat tat	403	
Leu Leu Leu Gly Asn Gly Lys Val His Gln Ser Ala Leu Ala Tyr Tyr		
90 95 100		
gag tct ttg ggc ggg cag atc att tcc gat ttt ccc cct cac tac ctc	451	
Glu Ser Leu Gly Gly Gln Ile Ile Ser Asp Phe Pro Pro His Tyr Leu		
105 110 115		
tac cgc ctg gtg att gat ggt ttg ttt ggc atc ggt ggt cgg gga ggg	499	
Tyr Arg Leu Val Ile Asp Gly Leu Phe Gly Ile Gly Gly Arg Gly Gly		
120 125 130		
ctc acc cca gag ctg gcc agt ttg gtg gag tct ttt tcc gct tca ggt	547	
Leu Thr Pro Glu Leu Ala Ser Leu Val Glu Ser Phe Ser Ala Ser Gly		
135 140 145		
atc ccc att ttg gcg att gat gtg ccg tct ggc gtg cat gcc gat agt	595	
Ile Pro Ile Leu Ala Ile Asp Val Pro Ser Gly Val His Ala Asp Ser		
150 155 160 165		
ggt gaa ctg ccg ccc ggc gtg atg gtg acg gtg gaa gga ttt gat aat	643	
Gly Glu Leu Pro Pro Gly Val Met Val Thr Val Glu Gly Phe Asp Asn		
170 175 180		
gat gca ccg atg gcg cgt cag aaa att ccg gca cac att gac gct gat	691	
Asp Ala Pro Met Ala Arg Gln Lys Ile Pro Ala His Ile Asp Ala Asp		
185 190 195		
gtc acg atc acg ttt ggc ggt ttg aga cgc gcc cac gcg gtc agt cct	739	
Val Thr Ile Thr Phe Gly Gly Leu Arg Arg Ala His Ala Val Ser Pro		
200 205 210		
gcg tgt ggt gaa gtg ctc tgt gct gat atc aac atc gct ggt ggc ggc	787	
Ala Cys Gly Glu Val Leu Cys Ala Asp Ile Asn Ile Ala Gly Gly Gly		
215 220 225		
gga aaa tcg ctg tcc gct gag ttg agt cag gtg cag gca gaa gac gcg	835	

Gly 230	Lys	Ser	Leu	Ser	Ala 235	Glu	Leu	Ser	Gln	Val 240	Gln	Ala	Glu	Asp	Ala 245	
acc	ccg	cag	atg	ttt	gcc	tcc	aag	gcg	tat	caa	cgg	aaa	gat	tcg	ctt	883
Thr	Pro	Gln	Met	Phe 250	Ala	Ser	Lys	Ala	Tyr 255	Gln	Arg	Lys	Asp	Ser 260	Leu	
ttt	gag	cgc	gcg	aat	ctc	aaa	gct	acg	gcg	cca	cat	atc	cat	agg	atc	931
Phe	Glu	Arg	Ala	Asn 265	Leu	Lys	Ala	Thr 270	Ala	Pro	His	Ile	His	Arg 275	Ile	
ggc	cag	cac	ttt	acc	gtg	ttg	aac	atg	gag	cct	ggc	ccg	gat	cat	gat	979
Gly	Gln	His	Phe	Thr 280	Val	Leu	Asn 285	Met	Glu	Pro	Gly	Pro	Asp	His	Asp	
aaa	tac	agt	ggc	gga	att	gtc	ggc	att	gtt	gca	ggt	agt	ggc	acc	tat	1027
Lys	Tyr 295	Ser	Gly	Gly	Ile	Val 300	Gly	Ile	Val	Ala	Gly 305	Ser	Gly	Thr	Tyr	
cca	ggt	gct	gct	gtg	ctg	tcg	gtg	aag	gcg	gct	gtc	agg	gcc	aca	agc	1075
Pro	Gly	Ala	Ala	Val	Leu	Ser 315	Val	Lys	Ala	Ala	Val	Arg	Ala	Thr	Ser 325	
gcc	atg	gtt	cga	tac	gtt	ggc	cct	gcg	tta	aat	ttt	gtc	atc	cag	tcg	1123
Ala	Met	Val	Arg	Tyr 330	Val	Gly	Pro	Ala	Leu 335	Asn	Phe	Val	Ile	Gln 340	Ser	
ctg	ccg	gag	gtc	gtc	gca	acg	caa	tca	ctt	gcc	acc	gcc	ggc	cgc	gtg	1171
Leu	Pro	Glu	Val	Val	Ala	Thr 345	Gln	Ser	Leu 350	Ala	Thr	Ala	Gly	Arg 355	Val	
caa	gcg	tgg	gtg	cac	ggc	ccc	gga	cgc	ggg	ctg	gag	gct	gag	caa	tca	1219
Gln	Ala	Trp 360	Val	His	Gly	Pro	Gly 365	Arg	Gly	Leu	Glu	Ala	Glu	Gln	Ser	
gcc	gag	ctt	gcg	gag	ctt	ttg	agc	cgg	cct	gag	cct	gtg	ctt	atc	gac	1267
Ala	Glu	Leu	Ala	Glu	Leu	Leu 380	Ser	Arg	Pro	Glu	Pro	Val	Leu	Ile	Asp	
gcc	gac	agc	ctc	tca	tta	ctc	cag	ctc	tca	gcg	gag	ctt	cgg	cag	gcg	1315
Ala	Asp	Ser	Leu	Ser	Leu	Leu 395	Gln	Leu	Ser	Ala	Glu	Leu	Arg	Gln	Ala 405	
ttg	cgc	gag	cga	aaa	gca	cca	acg	gtg	ctc	act	ccg	cac	aag	ggc	gaa	1363
Leu	Arg	Glu	Arg	Lys 410	Ala	Pro	Thr	Val	Leu 415	Thr	Pro	His	Lys	Gly 420	Glu	
ttt	gaa	cgc	atc	gca	gca	gaa	tta	cgc	tct	gaa	ggc	gtc	gag	att	ccc	1411
Phe	Glu	Arg	Ile	Ala	Ala	Glu	Leu	Arg	Ser 430	Glu	Gly	Val	Glu	Ile 435	Pro	
caa	gcg	gac	aaa	gat	ccc	att	ggt	gct	gcg	caa	gcg	tta	gct	aaa	gaa	1459
Gln	Ala	Asp	Lys	Asp	Pro	Ile	Gly 445	Ala	Ala	Gln	Ala	Leu	Ala	Lys	Glu	
ttt	gat	tgt	tgc	gta	ctg	ctc	aag	ggg	aaa	tac	acc	gtc	att	gca	gct	1507
Phe	Asp	Cys	Cys	Val	Leu	Leu 460	Lys	Gly	Lys	Tyr	Thr	Val	Ile	Ala	Ala	
cac	gac	ttt	gtg	cat	gcg	atc	aac	gct	ggg	cat	tcc	tgg	ttg	gct	aca	1555
His	Asp	Phe	Val	His	Ala	Ile	Asn	Ala	Gly	His	Ser	Trp	Leu	Ala	Thr	

470	475	480	485	
cct ggc tct ggc gat	gtg ttg tca ggt	ctt gtc ggt gca cac	ttg gct	1603
Pro Gly Ser Gly Asp	Val Leu Ser Gly	Leu Val Gly Ala His	Leu Ala	
	490	495	500	
caa agc tac gca gaa	tta aac cgc ttg	cgc gag ttt ttc	ccc gat gtg	1651
Gln Ser Tyr Ala Glu	Leu Asn Arg Leu	Pro Glu Phe Phe	Pro Asp Val	
	505	510	515	
acc ttg tct gat tcg	gcg att tac acc	cag att gca cct	gct gcg acc	1699
Thr Leu Ser Asp Ser	Ala Ile Tyr Thr	Gln Ile Ala Pro	Ala Ala Thr	
	520	525	530	
atc cac gcg gtt gct	gct ggg ttg gcc	gca cga acc gaa	ttt ggg ttt	1747
Ile His Ala Val Ala	Ala Gly Leu Ala	Ala Arg Thr Glu	Phe Gly Phe	
	535	540	545	
gcg ccg acc tcc gca	agt ttg atc gct	gat gcc atc cct	gca gcg acc	1795
Ala Pro Thr Ser Ala	Ser Leu Ile Ala	Asp Ala Ile Pro	Ala Ala Thr	
	550	555	560	565
gcc aag gtg gat ttg	aag cga att gtc	tagctctgca tgaattccgt		1842
Ala Lys Val Asp Leu	Lys Arg Ile Val			
	570			
atg				1845

<210> 254

<211> 574

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met Lys Pro Val Phe Ser Val Asp Gln Ile Arg Arg Ala Glu Asn Thr
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Leu Phe Glu Leu Gln Ala Asp Pro Asp Glu Leu Met Ile Ser Ala Ala
20 25 30

Ser Ala Val Ala Asp Val Ala Leu Ala Met Val Asp Gly Pro Ala Pro
35 40 45

Ala Val Ser Ser Glu Glu Ser Ile Leu Leu Leu Val Gly Pro Gly Gly
50 55 60

Asn Gly Gly Asp Ala Leu Tyr Ala Gly Ala Phe Leu Ala Glu Glu Gly
65 70 75 80

His His Val Asp Ala Leu Leu Leu Gly Asn Gly Lys Val His Gln Ser
85 90 95

Ala Leu Ala Tyr Tyr Glu Ser Leu Gly Gly Gln Ile Ile Ser Asp Phe
100 105 110

Pro Pro His Tyr Leu Tyr Arg Leu Val Ile Asp Gly Leu Phe Gly Ile
115 120 125

Gly Gly Arg Gly Gly Leu Thr Pro Glu Leu Ala Ser Leu Val Glu Ser
130 135 140

Phe Ser Ala Ser Gly Ile Pro Ile Leu Ala Ile Asp Val Pro Ser Gly
 145 150 155 160
 Val His Ala Asp Ser Gly Glu Leu Pro Pro Gly Val Met Val Thr Val
 165 170 175
 Glu Gly Phe Asp Asn Asp Ala Pro Met Ala Arg Gln Lys Ile Pro Ala
 180 185 190
 His Ile Asp Ala Asp Val Thr Ile Thr Phe Gly Gly Leu Arg Arg Ala
 195 200 205
 His Ala Val Ser Pro Ala Cys Gly Glu Val Leu Cys Ala Asp Ile Asn
 210 215 220
 Ile Ala Gly Gly Gly Gly Lys Ser Leu Ser Ala Glu Leu Ser Gln Val
 225 230 235 240
 Gln Ala Glu Asp Ala Thr Pro Gln Met Phe Ala Ser Lys Ala Tyr Gln
 245 250 255
 Arg Lys Asp Ser Leu Phe Glu Arg Ala Asn Leu Lys Ala Thr Ala Pro
 260 265 270
 His Ile His Arg Ile Gly Gln His Phe Thr Val Leu Asn Met Glu Pro
 275 280 285
 Gly Pro Asp His Asp Lys Tyr Ser Gly Gly Ile Val Gly Ile Val Ala
 290 295 300
 Gly Ser Gly Thr Tyr Pro Gly Ala Ala Val Leu Ser Val Lys Ala Ala
 305 310 315 320
 Val Arg Ala Thr Ser Ala Met Val Arg Tyr Val Gly Pro Ala Leu Asn
 325 330 335
 Phe Val Ile Gln Ser Leu Pro Glu Val Val Ala Thr Gln Ser Leu Ala
 340 345 350
 Thr Ala Gly Arg Val Gln Ala Trp Val His Gly Pro Gly Arg Gly Leu
 355 360 365
 Glu Ala Glu Gln Ser Ala Glu Leu Ala Glu Leu Leu Ser Arg Pro Glu
 370 375 380
 Pro Val Leu Ile Asp Ala Asp Ser Leu Ser Leu Leu Gln Leu Ser Ala
 385 390 395 400
 Glu Leu Arg Gln Ala Leu Arg Glu Arg Lys Ala Pro Thr Val Leu Thr
 405 410 415
 Pro His Lys Gly Glu Phe Glu Arg Ile Ala Ala Glu Leu Arg Ser Glu
 420 425 430
 Gly Val Glu Ile Pro Gln Ala Asp Lys Asp Pro Ile Gly Ala Ala Gln
 435 440 445
 Ala Leu Ala Lys Glu Phe Asp Cys Cys Val Leu Leu Lys Gly Lys Tyr
 450 455 460

Thr Val Ile Ala Ala His Asp Phe Val His Ala Ile Asn Ala Gly His
465 470 475 480

Ser Trp Leu Ala Thr Pro Gly Ser Gly Asp Val Leu Ser Gly Leu Val
485 490 495

Gly Ala His Leu Ala Gln Ser Tyr Ala Glu Leu Asn Arg Leu Pro Glu
500 505 510

Phe Phe Pro Asp Val Thr Leu Ser Asp Ser Ala Ile Tyr Thr Gln Ile
515 520 525

Ala Pro Ala Ala Thr Ile His Ala Val Ala Ala Gly Leu Ala Ala Arg
530 535 540

Thr Glu Phe Gly Phe Ala Pro Thr Ser Ala Ser Leu Ile Ala Asp Ala
545 550 555 560

Ile Pro Ala Ala Thr Ala Lys Val Asp Leu Lys Arg Ile Val
565 570

<210> 255

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXN00504

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caagtggccg agatgtgaag cgcacgggta attgagagggc atg acc tac gga ttt 115
Met Thr Tyr Gly Phe
1 5

ctt gtc aac aca gat ctc acc cac cgc gcg att gac ttt gat tta gaa 163
Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile Asp Phe Asp Leu Glu
10 15 20

aac gct gcg aag ttc ctc ggc ggt gcc gat gat ggc cgc gtc gct gtc 211
Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp Gly Arg Val Ala Val
25 30 35

gct ttc caa gag gat ggc acc ttg tac gcc gct ctc tac agc gcc agc 259
Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala Leu Tyr Ser Ala Ser
40 45 50

gca aaa gat gag ggt gcc gca gca aac cca gta gca tcc ctt ggc cgc 307
Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val Ala Ser Leu Gly Arg
55 60 65

aac gcc gct gct acc ggt gat ggc tcc ttc ttc tct gat ccg acc act 355
Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe Ser Asp Pro Thr Thr
70 75 80 85

gca atc tgt ggc cct gtg atc ttc gtg ggg gcc gaa ggc gaa gac atc 403
Ala Ile Cys Gly Pro Val Ile Phe Val Gly Ala Glu Gly Glu Asp Ile

	90	95	100	
acg ttg gat gaa att gag cga att aag gac ggc att cgc gcc gct cgt				451
Thr Leu Asp Glu Ile Glu Arg Ile Lys Asp Gly Ile Arg Ala Ala Arg				
	105	110	115	
aac tac cgc gat gat tat cca gag gaa ttc aac ctg tgg cgc aac gct				499
Asn Tyr Arg Asp Asp Tyr Pro Glu Glu Phe Asn Leu Trp Arg Asn Ala				
	120	125	130	
gta tat aac ctg cgt acg gct taaagtttgg ctgccatgtg aat				543
Val Tyr Asn Leu Arg Thr Ala				
	135	140		

<210> 256
 <211> 140
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 256
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 20 25 30
 Gly Arg Val Ala Val Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala
 35 40 45
 Leu Tyr Ser Ala Ser Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val
 50 55 60
 Ala Ser Leu Gly Arg Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe
 65 70 75 80
 Ser Asp Pro Thr Thr Ala Ile Cys Gly Pro Val Ile Phe Val Gly Ala
 85 90 95
 Glu Gly Glu Asp Ile Thr Leu Asp Glu Ile Glu Arg Ile Lys Asp Gly
 100 105 110
 Ile Arg Ala Ala Arg Asn Tyr Arg Asp Asp Tyr Pro Glu Glu Phe Asn
 115 120 125
 Leu Trp Arg Asn Ala Val Tyr Asn Leu Arg Thr Ala
 130 135 140

<210> 257
 <211> 346
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(346)
 <223> FRXA00504

<400> 257
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caagtggccg agatgtgaag cgcacgggta attgagaggc atg acc tac gga ttt 115
Met Thr Tyr Gly Phe
1 5

ctt gtc aac aca gat ctc acc cac cgc gcg att gac ttt gat tta gaa 163
Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile Asp Phe Asp Leu Glu
10 15 20

aac gct gcg aag ttc ctc ggc ggt gcc gat gat ggc cgc gtc gct gtc 211
Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp Gly Arg Val Ala Val
25 30 35

gct ttc caa gag gat ggc acc ttg tac gcc gct ctc tac agc gcc agc 259
Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala Leu Tyr Ser Ala Ser
40 45 50

gca aaa gat gag ggt gcc gca gca aac cca gta gca tcc ctt ggc cgc 307
Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val Ala Ser Leu Gly Arg
55 60 65

aac gcc gct gct acc ggt gat ggc tcc ttc ttc tct gat 346
Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe Ser Asp
70 75 80

<210> 258

<211> 82

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Thr Tyr Gly Phe Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile
1 5 10 15

Asp Phe Asp Leu Glu Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp
20 25 30

Gly Arg Val Ala Val Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala
35 40 45

Leu Tyr Ser Ala Ser Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val
50 55 60

Ala Ser Leu Gly Arg Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe
65 70 75 80

Ser Asp

<210> 259

<211> 618

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(595)

<223> RXN00505

<400> 259

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tccgcgcata tgtttaagtg aatacgttta aggagcagca atg aaa tct gag ttt 115
Met Lys Ser Glu Phe
1 5

ccg gta tcc ggc acg agg cgt ttt gag cat gcc gca gat acc caa aat 163
Pro Val Ser Gly Thr Arg Arg Phe Glu His Ala Ala Asp Thr Gln Asn
10 15 20

ttt ggg gaa gaa tta ggc agg cat cta gaa gct ggc gat gtg gtg att 211
Phe Gly Glu Glu Leu Gly Arg His Leu Glu Ala Gly Asp Val Val Ile
25 30 35

ttg gac ggc ccg ctg ggt gct gga aaa acc aca ttt act caa ggt atc 259
Leu Asp Gly Pro Leu Gly Ala Gly Lys Thr Thr Phe Thr Gln Gly Ile
40 45 50

gct cgt gga ttg cag gtg aag ggg cgg gtg aca tcg ccg acg ttt gtg 307
Ala Arg Gly Leu Gln Val Lys Gly Arg Val Thr Ser Pro Thr Phe Val
55 60 65

atc gcg agg gaa cac cgc tcg gaa atc ggt ggg cca gat ctg atc cac 355
Ile Ala Arg Glu His Arg Ser Glu Ile Gly Gly Pro Asp Leu Ile His
70 75 80 85

atg gat gcc tac cga ttg ctg ggc gaa gac agc gag gat gct gat ccg 403
Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu Asp Ala Asp Pro
90 95 100

atc ggt gcg ctg gac tct ttg gat ttg gat acc gat ttg gac ttg gct 451
Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp Leu Asp Leu Ala
105 110 115

gtg gtt gtt gcg gaa tgg ggc ggt ggc ttg gtg gag cag atc gct gac 499
Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu Gln Ile Ala Asp
120 125 130

tcg tat ctt ttg att acc att gat cga gag acc gct gtg cag gaa gac 547
Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala Val Gln Glu Asp
135 140 145

ccg gaa tct gag gct cga att ttc cat tgg gaa tgg cgc gaa ggc cgc 595
Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp Arg Glu Gly Arg
150 155 160 165

tgagaaagtt ttccacgcta aaa 618

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<210> 260

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

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Ala Asp Thr Gln Asn Phe Gly Glu Glu Leu Gly Arg His Leu Glu Ala
20 25 30

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Gly Asp Val Val Ile Leu Asp Gly Pro Leu Gly Ala Gly Lys Thr Thr
 35 40 45
 Phe Thr Gln Gly Ile Ala Arg Gly Leu Gln Val Lys Gly Arg Val Thr
 50 55 60
 Ser Pro Thr Phe Val Ile Ala Arg Glu His Arg Ser Glu Ile Gly Gly
 65 70 75 80
 Pro Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser
 85 90 95
 Glu Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr
 100 105 110
 Asp Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val
 115 120 125
 Glu Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr
 130 135 140
 Ala Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu
 145 150 155 160
 Trp Arg Glu Gly Arg
 165

<210> 261
 <211> 275
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(252)
 <223> FRXA00505

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 Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu
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 gat gct gat ccg atc ggt gcg ctg gac tct ttg gat ttg gat acc gat 96
 Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp
 20 25 30
 ttg gac ttg gct gtg gtt gtt gcg gaa tgg ggc ggt ggc ttg gtg gag 144
 Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu
 35 40 45
 cag atc gct gac tcg tat ctt ttg att acc att gat cga gag acc gct 192
 Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala
 50 55 60
 gtg cag gaa gac ccg gaa tct gag gct cga att ttc cat tgg gaa tgg 240
 Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp
 65 70 75 80
 cgc gaa ggc cgc tgagaaagtt ttccacgcta aaa 275

Arg Glu Gly Arg

<210> 262

<211> 84

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu
 1 5 10 15

Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp
 20 25 30

Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu
 35 40 45

Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala
 50 55 60

Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp
 65 70 75 80

Arg Glu Gly Arg

<210> 263

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(955)

<223> RXN00507

<400> 263

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 Val Ala Glu Asn Leu
 1 5

aac aaa cac ctg tcc aaa ctg tcc aag cgc gga ccg cac cgc gtg ctg 163
 Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly Pro His Arg Val Leu
 10 15 20

gta ggc gat atg aac tac gcc ggc atc ccg ggc aaa atc tac acc cca 211
 Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly Lys Ile Tyr Thr Pro
 25 30 35

gca gaa ggc gac ggc atc cca ggt gta gct ttc ggc cac gac tgg atg 259
 Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe Gly His Asp Trp Met
 40 45 50

aaa tcc atc aag tac tac cac caa act ttg cga cac ctc gcg tcc tgg 307
 Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg His Leu Ala Ser Trp
 55 60 65

ggc atc gct gtt gcc gcc cca gac acc gaa aat ggc ttc atg cca gac 355
 Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn Gly Phe Met Pro Asp
 70 75 80 85

cac aaa ggt ttc gcc tct gac ctc gaa tcc tcc att cag att ctc ggc 403
 His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser Ile Gln Ile Leu Gly
 90 95 100

ggc gta aaa ctc gcc tcc gga aac gtc acc gtc aac cca gcc tgc ctc 451
 Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val Asn Pro Ala Cys Leu
 105 110 115

ggt gta gta ggc cac ggc atg ggt gct ggg gct gca gta cta tcc gca 499
 Gly Val Val Gly His Gly Met Gly Ala Gly Ala Ala Val Leu Ser Ala
 120 125 130

gca aac cgc gac ctc gtg cgc gca gtc gga gca atc tac cca gcg aaa 547
 Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala Ile Tyr Pro Ala Lys
 135 140 145

acc tcc ccc tca gca atc gac gcc gcc ttc gct gtc aaa gcc cca ggc 595
 Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala Val Lys Ala Pro Gly
 150 155 160 165

cta gtc atc gga tcc tcc agc ctc ggc ctc ttt gaa tcc ggc gag cca 643
 Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe Glu Ser Gly Glu Pro
 170 175 180

gca aaa ctc gca gcc aac tgg gcc ggc gat gtc tgc tac cgc gaa tca 691
 Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val Cys Tyr Arg Glu Ser
 185 190 195

gaa aaa ggc aac caa cag ggc ttc tct gaa gac acc atg ttc aaa ctt 739
 Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp Thr Met Phe Lys Leu
 200 205 210

gtc gca gga atc ggc agc cca caa acc gga gct caa gaa acc gtc cgc 787
 Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala Gln Glu Thr Val Arg
 215 220 225

ggc ctc ctc acc gga ttc ctt ctc cac caa ctt gcc gga gaa aag aaa 835
 Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu Ala Gly Glu Lys Lys
 230 235 240 245

tac aaa gca ttc tcc gaa cca gac gct gaa gct aag aaa gtt gtc tcc 883
 Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala Lys Lys Val Val Ser
 250 255 260

tac ttc ggc cag gag ctg cag gaa cat gcc ttc cct aag gac acg tcc 931
 Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe Pro Lys Asp Thr Ser
 265 270 275

cca ttc gcg ttc ctt aac gag aag tagttcgctt ttcttagtggtg gtg 978
 Pro Phe Ala Phe Leu Asn Glu Lys
 280 285

<210> 264

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

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 Pro His Arg Val Leu Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly
 20 25 30
 Lys Ile Tyr Thr Pro Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe
 35 40 45
 Gly His Asp Trp Met Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg
 50 55 60
 His Leu Ala Ser Trp Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn
 65 70 75 80
 Gly Phe Met Pro Asp His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser
 85 90 95
 Ile Gln Ile Leu Gly Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val
 100 105 110
 Asn Pro Ala Cys Leu Gly Val Val Gly His Gly Met Gly Ala Gly Ala
 115 120 125
 Ala Val Leu Ser Ala Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala
 130 135 140
 Ile Tyr Pro Ala Lys Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala
 145 150 155 160
 Val Lys Ala Pro Gly Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe
 165 170 175
 Glu Ser Gly Glu Pro Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val
 180 185 190
 Cys Tyr Arg Glu Ser Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp
 195 200 205
 Thr Met Phe Lys Leu Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala
 210 215 220
 Gln Glu Thr Val Arg Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu
 225 230 235 240
 Ala Gly Glu Lys Lys Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala
 245 250 255
 Lys Lys Val Val Ser Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe
 260 265 270
 Pro Lys Asp Thr Ser Pro Phe Ala Phe Leu Asn Glu Lys
 275 280 285

<210> 265

<211> 978

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(955)

<223> FRXA00507

<400> 265

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                               Val Ala Glu Asn Leu
                               1 5

aac aaa cac ctg tcc aaa ctg tcc aag cgc gga ccg cac cgc gtg ctg 163
Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly Pro His Arg Val Leu
                               10 15 20

gta ggc gat atg aac tac gcc ggc atc ccg ggc aaa atc tac acc cca 211
Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly Lys Ile Tyr Thr Pro
                               25 30 35

gca gaa ggc gac ggc atc cca ggt gta gct ttc ggc cac gac tgg atg 259
Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe Gly His Asp Trp Met
                               40 45 50

aaa tcc atc aag tac tac cac caa act ttg cga cac ctc gcg tcc tgg 307
Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg His Leu Ala Ser Trp
                               55 60 65

ggc atc gct gtt gcc gcc cca gac acc gaa aat ggc ttc atg cca gac 355
Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn Gly Phe Met Pro Asp
                               70 75 80 85

cac aaa ggt ttc gcc tct gac ctc gaa tcc tcc att cag att ctc ggc 403
His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser Ile Gln Ile Leu Gly
                               90 95 100

ggc gta aaa ctc ggc tcc gga aac gtc acc gtc aac cca gcc tgc ctc 451
Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val Asn Pro Ala Cys Leu
                               105 110 115

ggt gta gta ggc cac ggc atg ggt gct ggg gct gca gta cta tcc gca 499
Gly Val Val Gly His Gly Met Gly Ala Gly Ala Ala Val Leu Ser Ala
                               120 125 130

gca aac cgc gac ctc gtg cgc gca gtc gga gca atc tac cca gcg aaa 547
Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala Ile Tyr Pro Ala Lys
                               135 140 145

acc tcc ccc tca gca atc gac gcc gcc ttc gct gtc aaa gcc cca ggc 595
Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala Val Lys Ala Pro Gly
                               150 155 160 165

cta gtc atc gga tcc tcc agc ctc ggc ctc ttt gaa tcc ggc gag cca 643
Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe Glu Ser Gly Glu Pro
                               170 175 180

gca aaa ctc gca gcc aac tgg gcc ggc gat gtc tgc tac cgc gaa tca 691
Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val Cys Tyr Arg Glu Ser
                               185 190 195

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gaa aaa ggc aac caa cag ggc ttc tct gaa gac acc atg ttc aaa ctt 739
 Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp Thr Met Phe Lys Leu
 200 205 210

gtc gca gga atc ggc agc cca caa acc gga gct caa gaa acc gtc cgc 787
 Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala Gln Glu Thr Val Arg
 215 220 225

ggc ctc ctc acc gga ttc ctt ctc cac caa ctt gcc gga gaa aag aaa 835
 Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu Ala Gly Glu Lys Lys
 230 235 240 245

tac aaa gca ttc tcc gaa cca gac gct gaa gct aag aaa gtt gtc tcc 883
 Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala Lys Lys Val Val Ser
 250 255 260

tac ttc ggc cag gag ctg cag gaa cat gcc ttc cct aag gac acg tcc 931
 Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe Pro Lys Asp Thr Ser
 265 270 275

cca ttc gcg ttc ctt aac gag aag tagttcgctt ttcttagtggtg 978
 Pro Phe Ala Phe Leu Asn Glu Lys
 280 285

<210> 266

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Val Ala Glu Asn Leu Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly
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Pro His Arg Val Leu Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly
 20 25 30

Lys Ile Tyr Thr Pro Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe
 35 40 45

Gly His Asp Trp Met Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg
 50 55 60

His Leu Ala Ser Trp Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn
 65 70 75 80

Gly Phe Met Pro Asp His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser
 85 90 95

Ile Gln Ile Leu Gly Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val
 100 105 110

Asn Pro Ala Cys Leu Gly Val Val Gly His Gly Met Gly Ala Gly Ala
 115 120 125

Ala Val Leu Ser Ala Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala
 130 135 140

Ile Tyr Pro Ala Lys Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala
 145 150 155 160

Pro Lys Asp Thr Ser Pro Phe Ala Phe Leu Asn Glu Lys
275 280 285

<213> Corynebacterium glutamicum

<223> RXN00510

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gcc ggc tac gga gca gtg atc tcc gca cta caa ggc gcc agt ggt ggg 163
Ala Gly Tyr Gly Ala Val Ile Ser Ala Leu Gln Gly Ala Ser Gly Gly
10 15 20

atg tat cgc gga ccg gcg aaa tcc gaa ggc cag ttg cgc gag atg tac 211
Met Tyr Arg Gly Pro Ala Lys Ser Glu Gly Gln Leu Arg Glu Met Tyr
25 30 35

caa acc atc gaa ggg cta gac acc agc tcg ttg cgc gaa gct gcc gaa 259
Gln Thr Ile Glu Gly Leu Asp Thr Ser Ser Leu Arg Glu Ala Ala Glu
40 45 50

gca gca gtg ggc gga acg aac gaa gcc aga ata caa ggg tgg gtc ggc 307
Ala Ala Val Gly Gly Thr Asn Glu Ala Arg Ile Gln Gly Trp Val Gly
55 60 65

cgc ctc ttg aaa ttc ttc ggg acg gtt ggc ggg gga atg atc gcc acg 355
Pro Leu Leu Lys Phe Phe Gly Thr Val Gly Gly Gly Met Ile Ala Thr

70	75	80	85	
gag ata gct gaa cgg gca gtc gat tgg ttc aaa aac cgt aat gat gtg				403
Glu Ile Ala Glu Arg Ala Val Asp Trp Phe Lys Asn Arg Asn Asp Val				
	90	95	100	
gaa gaa gtc agc gaa gcc gct gat aaa gcc gcc gat gcg atc gac tcc				451
Glu Glu Val Ser Glu Ala Ala Asp Lys Ala Ala Asp Ala Ile Asp Ser				
	105	110	115	
act gtc aca gag tcc gac cag ggc atg atg cac att atc cag cag ctc				499
Thr Val Thr Glu Ser Asp Gln Gly Met Met His Ile Ile Gln Gln Leu				
	120	125	130	
ttg gac att gtg tct acg ttg acg cag att ctt ggc agc atg gat cgg				547
Leu Asp Ile Val Ser Thr Leu Thr Gln Ile Leu Gly Ser Met Asp Arg				
	135	140	145	
ggg aaa ttt cct caa gaa ttc cgg gac tgt gtc caa act gga gct gat				595
Gly Lys Phe Pro Gln Glu Phe Arg Asp Cys Val Gln Thr Gly Ala Asp				
	150	155	160	165
ctt att gac cag gca ggg gac atg ctt gaa gga ttg tgc gct gat cga				643
Leu Ile Asp Gln Ala Gly Asp Met Leu Glu Gly Leu Cys Ala Asp Arg				
	170	175	180	
gat gat gcg att tca cag tgt ttc tcc gcg ttg acc gat cat gga aaa				691
Asp Asp Ala Ile Ser Gln Cys Phe Ser Ala Leu Thr Asp His Gly Lys				
	185	190	195	
caa gtt tgt gaa act gag cca aag ccg ttg tgt agt gca gct tct ggg				739
Gln Val Cys Glu Thr Glu Pro Lys Pro Leu Cys Ser Ala Ala Ser Gly				
	200	205	210	
ggt tca tct ggt gga gcg act tct tcg gct gcg gcc tct tca ggt ggt				787
Gly Ser Ser Gly Gly Ala Thr Ser Ser Ala Ala Ala Ser Ser Gly Gly				
	215	220	225	
tca agc tcg agc act gct agc tct ggg agt tct ggc gga tcg agc agt				835
Ser Ser Ser Ser Thr Ala Ser Ser Gly Ser Ser Gly Gly Ser Ser Ser				
	230	235	240	245
gct gcg gat agt tcg acg tcg acc aat gct gaa tcc agt gtt gaa aag				883
Ala Ala Asp Ser Ser Thr Ser Thr Asn Ala Glu Ser Ser Val Glu Lys				
	250	255	260	
gaa aag acc aca cct gct gcc gtt gag aaa cct gac gag aaa cca gtg				931
Glu Lys Thr Thr Pro Ala Ala Val Glu Lys Pro Asp Glu Lys Pro Val				
	265	270	275	
gag aag ccg gtt gaa aag acg cca gaa aag ccg gta gaa aaa cct gtc				979
Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro Val				
	280	285	290	
gag aag caa gag tgt gaa gaa aag cct gac cct gac ccg gaa aaa tgc				1027
Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Lys Cys				
	295	300	305	
aaa aca gag ccg gtc gag tgt gag cca aca ccg aaa cct gaa aca gag				1075
Lys Thr Glu Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu Thr Glu				
	310	315	320	325

cct gaa cca aaa ccg aca ccc acg ccc aca ccc gga aca cca aca cca 1123
 Pro Glu Pro Lys Pro Thr Pro Thr Pro Thr Pro Gly Thr Pro Thr Pro
 330 335 340

ata cct gag cta gag act gag gat tgt gaa cct ggc aag gag acg ggc 1171
 Ile Pro Glu Leu Glu Thr Glu Asp Cys Glu Pro Gly Lys Glu Thr Gly
 345 350 355

aca gac tca gaa tct gaa tcg gaa gag tgc gcc ccc gag ctc aat gac 1219
 Thr Asp Ser Glu Ser Glu Ser Glu Glu Cys Ala Pro Glu Leu Asn Asp
 360 365 370

gtt cca gaa gag tcg gat ctg att ggg caa ctc atc aag gga gca atc 1267
 Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu Ile Lys Gly Ala Ile
 375 380 385

ggt att ggg att gtt gtt gta ggc gtt ggg ctg ttg gtg aat ttc ctg 1315
 Gly Ile Gly Ile Val Val Val Gly Val Gly Leu Leu Val Asn Phe Leu
 390 395 400 405

gag cag tgc gtc cct gtg att gaa gaa gta cct gtg ccg gag ccc gag 1363
 Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro Val Pro Glu Pro Glu
 410 415 420

cct ata cct gaa ccc gct ccg cag cct gag cca act tca gtg aaa cca 1411
 Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro Thr Ser Val Lys Pro
 425 430 435

cca gag tct gaa cta gat aag gtg gct gag cct gcg ccg aag cca att 1459
 Pro Glu Ser Glu Leu Asp Lys Val Ala Glu Pro Ala Pro Lys Pro Ile
 440 445 450

cca caa gct aat tac act gct gct gca gca act aac tat tcc gct ccc 1507
 Pro Gln Ala Asn Tyr Thr Thr Ala Ala Ala Thr Asn Tyr Ser Ala Pro
 455 460 465

gcg cac gct ccc gtt gtc cca att acg ccg gca gca cct gaa gtt ccg 1555
 Ala His Ala Pro Val Val Pro Ile Thr Pro Ala Ala Pro Glu Val Pro
 470 475 480 485

gca gca cca gaa gtg cct gca ccg gcg gtt aat ctt cac aag gcc ggc 1603
 Ala Ala Pro Glu Val Pro Ala Pro Ala Val Asn Leu His Lys Ala Gly
 490 495 500

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<210> 268

<211> 503

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

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 20 25 30

Gly Lys Glu Thr Gly Thr Asp Ser Glu Ser Glu Ser Glu Glu Cys Ala
 355 360 365
 Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu
 370 375 380
 Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val Val Gly Val Gly Leu
 385 390 395 400
 Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro
 405 410 415
 Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro
 420 425 430
 Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp Lys Val Ala Glu Pro
 435 440 445
 Ala Pro Lys Pro Ile Pro Gln Ala Asn Tyr Thr Ala Ala Ala Ala Thr
 450 455 460
 Asn Tyr Ser Ala Pro Ala His Ala Pro Val Val Pro Ile Thr Pro Ala
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 485 490 495
 Leu His Lys Ala Gly Gly Trp
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<210> 269
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 <223> FRXA00509

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 Leu Val Asp Val Glu
 1 5
 cta tcc gca gca ctg ctc gat ccg cca gaa ctc cca gag cta gca gtg 163
 Leu Ser Ala Ala Leu Leu Asp Pro Pro Glu Leu Pro Glu Leu Ala Val
 10 15 20
 ctc gag ctt gaa cca cct gaa gag gcc gca gcc gaa gaa gtc gct cca 211
 Leu Glu Leu Glu Pro Pro Glu Glu Ala Ala Glu Glu Val Ala Pro
 25 30 35
 cca gat gaa ccc cca gaa gct gca cta cac aac ggc ttt ggc tca gtt 259
 Pro Asp Glu Pro Pro Glu Ala Ala Leu His Asn Gly Phe Gly Ser Val
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Ser Gln Thr Cys Phe Pro
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<210> 270
<211> 59
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<213> Corynebacterium glutamicum

<400> 270
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Pro Glu Leu Ala Val Leu Glu Leu Glu Pro Pro Glu Glu Ala Ala Ala
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Glu Glu Val Ala Pro Pro Asp Glu Pro Pro Glu Ala Ala Leu His Asn
35 40 45

Gly Phe Gly Ser Val Ser Gln Thr Cys Phe Pro
50 55

<210> 271
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355,369,370,372,375,378-385
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<222> 32,91
<223> Xaa = Ile, Thr, Lys, or Arg

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<222> (35)
<223> Xaa = Lys or Asn

<220>
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<222> 36,60
<223> Xaa = His or Gln

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<223> Xaa = Leu, Phe, Gly, or Arg

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<222> 70,73,78,81

<223> Xaa = Val, Ala, Glu, or Gly

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<223> Xaa = Val, Ala, Asp, or Gly

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<223> Xaa = Asp, His, Asn, or Tyr

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<222> (80)

<223> Xaa = Ala, Phe, Ser, or Thr

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<222> (84)

<223> Xaa = Asp or Glu

<220>

<221> VARIANT

<222> (90)

<223> Xaa = Ala, Asp, Glu, Gly, or Val

<220>

<221> VARIANT

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<223> Xaa = Phe, Ser, Tyr, or Cys

<220>

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<223> Xaa = Cys, Phe, Leu, Trp, or Tyr

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<223> Xaa = any amino acid

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				Val	Glu	Lys	Pro	Val	
				1				5	

gaa	aag	acg	cca	gaa	aag	ccg	gta	gaa	aaa	cct	gtc	gag	aag	caa	gag	163
Glu	Lys	Thr	Pro	Glu	Lys	Pro	Val	Glu	Lys	Pro	Val	Glu	Lys	Gln	Glu	
			10				15							20		

tgt	gaa	gaa	aag	cct	gac	cct	gac	ccg	gaa	ana	atg	caa	aan	can	gag	211
Cys	Glu	Glu	Lys	Pro	Asp	Pro	Asp	Pro	Glu	Xaa	Met	Gln	Xaa	Xaa	Glu	
			25					30					35			

ccg	gtc	gag	tgt	gag	cca	aca	ccg	aaa	cct	gaa	aca	gag	cct	gaa	cca	259
Pro	Val	Glu	Cys	Glu	Pro	Thr	Pro	Lys	Pro	Glu	Thr	Glu	Pro	Glu	Pro	
			40				45					50				

aaa ccn gac acc cac gcc can cna ccc gga aca cca aca cca ata cct 307
 Lys Pro Asp Thr His Ala Xaa Xaa Pro Gly Thr Pro Thr Pro Ile Pro
 55 60 65

 gna gct aga gna ctg agg att gnt gna nac nct gng caa gga gan cgn 355
 Xaa Ala Arg Xaa Leu Arg Ile Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Arg
 70 75 80 85

 ggc aca gac tca gnn ana tnc tnn nnn nnn gaa tcg gaa gag tgc gcc 403
 Gly Thr Asp Ser Xaa Xaa Xaa Xaa Xaa Xaa Glu Ser Glu Glu Cys Ala
 90 95 100

 ccc gag ctc aat gac gtt cca gaa gag tcg gat ctg att ggg caa ctc 451
 Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu
 105 110 115

 atc aag gga gca atc ggt att ggg att gtt gtt gta ggc gtt ggg ctg 499
 Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val Val Gly Val Gly Leu
 120 125 130

 ttg gtg aat ttc ctg gag cag tgc gtc cct gtg att gaa gaa gta cct 547
 Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro
 135 140 145

 gtg ccg gag ccc gag cct ata cct gaa ccc gct ccg cag cct gag cca 595
 Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro
 150 155 160 165

 act tca gtg aaa cca cca gag tct gaa cta gat aag 631
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 170 175

<210> 272

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

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<222> 36,60

<223> Xaa = His or Gln

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<222> (61)

<223> Xaa = Leu, Phe, Gly, or Arg

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<221> VARIANT

<222> 70,73,78,81

<223> Xaa = Val, Ala, Glu, or Gly

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<221> VARIANT

<222> (77)

<223> Xaa = Val, Ala, Asp, or Gly

<220>

<221> VARIANT

<222> (79)

<223> Xaa = Asp, His, Asn, or Tyr

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<222> (80)

<223> Xaa = Ala, Phe, Ser, or Thr

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<222> (84)

<223> Xaa = Asp or Glu

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<223> Xaa = Ala, Asp, Glu, Gly, or Val

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<223> Xaa = Phe, Ser, Tyr, or Cys

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<222> (93)

<223> Xaa = Cys, Phe, Leu, Trp, or Tyr

<220>

<221> VARIANT

<222> (94)..(95)

<223> Xaa = any amino acid

<400> 272

Val Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro
1 5 10 15

Val Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Xaa
20 25 30

Met Gln Xaa Xaa Glu Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu
35 40 45

Thr Glu Pro Glu Pro Lys Pro Asp Thr His Ala Xaa Xaa Pro Gly Thr
50 55 60

Pro Thr Pro Ile Pro Xaa Ala Arg Xaa Leu Arg Ile Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Gln Gly Xaa Arg Gly Thr Asp Ser Xaa Xaa Xaa Xaa Xaa Glu
85 90 95

Ser Glu Glu Cys Ala Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp
 100 105 110

Leu Ile Gly Gln Leu Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val
 115 120 125

Val Gly Val Gly Leu Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val
 130 135 140

Ile Glu Glu Val Pro Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala
 145 150 155 160

Pro Gln Pro Glu Pro Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp
 165 170 175

Lys

<210> 273
 <211> 825
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(802)
 <223> RXN00515

<400> 273
 gttgacgcac tgaagaagta aagtctcttc acaaaaagcg ctgtgcttcc tcacatggaa 60

gcacagcgct ttttcatatt tttattgcc aatggggcac atg cgt ttt tct cga 115
 Met Arg Phe Ser Arg
 1 5

gtt ctt ccc gca ctt ctt atc acc acc gcc gtg agc atc cca aca gca 163
 Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val Ser Ile Pro Thr Ala
 10 15 20

tct gct gcc aca ctc acc gcc gac acc gac aag gaa ttg tgc atc gcc 211
 Ser Ala Ala Thr Leu Thr Ala Asp Thr Asp Lys Glu Leu Cys Ile Ala
 25 30 35

agc aac acc gac gat tcc gcg gtg gtt acc ttc tgg aac tcc att gaa 259
 Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe Trp Asn Ser Ile Glu
 40 45 50

gac tcc gtg cgc gaa caa cgc ctc gac gaa cta gac gcc caa gat cca 307
 Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu Asp Ala Gln Asp Pro
 55 60 65

gga atc aaa gcg gcg att gaa agc tac atc gcc caa gat gac aac gcc 355
 Gly Ile Lys Ala Ala Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala
 70 75 80 85

cca act gct gct gaa ctg caa gta cgc ctc gat gcc atc gaa tcc ggc 403
 Pro Thr Ala Ala Glu Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly
 90 95 100

gaa ggc cta gcc atg ctc ctc cca gac gat ccc acg ctg gca gac ccc 451

Glu Gly Leu Ala Met Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro
 105 110 115
 aac gcc gag gaa agt ttc aaa acg gag tac aca tac gac gaa gcc aaa 499
 Asn Ala Glu Glu Ser Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys
 120 125 130
 gac atc atc agc gga ttc tcc agc gat cca gcc agc gat gta ctc agc 547
 Asp Ile Ile Ser Gly Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser
 135 140 145
 caa ctt caa caa gcc gcc acc acc ggc acc cgc acc gca gaa atc cgc 595
 Gln Leu Gln Gln Ala Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg
 150 155 160 165
 gcc gaa gta ttc gcc gac cgc acc gat gat tac aac gaa tcc caa acc 643
 Ala Glu Val Phe Ala Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr
 170 175 180
 gct ctt aaa gag gat ttc caa aac tgc atc gat gcc atc gat gac gcc 691
 Ala Leu Lys Glu Asp Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala
 185 190 195
 cgc cca atc cca ctg cag tac atc ctg att gga ggc gcc atc gct ttg 739
 Arg Pro Ile Pro Leu Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu
 200 205 210
 gcg gtc atc gtc ctc ggg atc agg gcg tgg act aac tca agg aag cag 787
 Ala Val Ile Val Leu Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln
 215 220 225
 tcc aag cac agc cag taatacgcca agcaaaaaat tgc 825
 Ser Lys His Ser Gln
 230

<210> 274

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Arg Phe Ser Arg Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val
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 Ser Ile Pro Thr Ala Ser Ala Ala Thr Leu Thr Ala Asp Thr Asp Lys
 20 25 30
 Glu Leu Cys Ile Ala Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe
 35 40 45
 Trp Asn Ser Ile Glu Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu
 50 55 60
 Asp Ala Gln Asp Pro Gly Ile Lys Ala Ala Ile Glu Ser Tyr Ile Ala
 65 70 75 80
 Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu Leu Gln Val Arg Leu Asp
 85 90 95
 Ala Ile Glu Ser Gly Glu Gly Leu Ala Met Leu Leu Pro Asp Asp Pro

100	105	110
Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser Phe Lys Thr Glu Tyr Thr		
115	120	125
Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly Phe Ser Ser Asp Pro Ala		
130	135	140
Ser Asp Val Leu Ser Gln Leu Gln Gln Ala Ala Thr Thr Gly Thr Arg		
145	150	155
Thr Ala Glu Ile Arg Ala Glu Val Phe Ala Asp Arg Thr Asp Asp Tyr		
165	170	175
Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp Phe Gln Asn Cys Ile Asp		
180	185	190
Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu Gln Tyr Ile Leu Ile Gly		
195	200	205
Gly Ala Ile Ala Leu Ala Val Ile Val Leu Gly Ile Arg Ala Trp Thr		
210	215	220
Asn Ser Arg Lys Gln Ser Lys His Ser Gln		
225	230	

<210> 275

<211> 503

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(480)

<223> FRXA00515

<400> 275

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Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu	
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ctg caa gta cgc ctc gat gcc atc gaa tcc ggc gaa ggc cta gcc atg	96
Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly Glu Gly Leu Ala Met	
20 25 30	
ctc ctc cca gac gat ccc acg ctg gca gac ccc aac gcc gag gaa agt	144
Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser	
35 40 45	
ttc aaa acg gag tac aca tac gac gaa gcc aaa gac atc atc agc gga	192
Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly	
50 55 60	
ttc tcc agc gat cca gcc agc gat gta ctc agc caa ctt caa caa gcc	240
Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser Gln Leu Gln Gln Ala	
65 70 75 80	
gcc acc acc ggc acc cgc acc gca gaa atc cgc gcc gaa gta ttc gcc	288
Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg Ala Glu Val Phe Ala	
85 90 95	

gac cgc acc gat gat tac aac gaa tcc caa acc gct ctt aaa gag gat 336
 Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp
 100 105 110

 ttc caa aac tgc atc gat gcc atc gat gac gcc cgc cca atc cca ctg 384
 Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu
 115 120 125

 cag tac atc ctg att gga ggc gcc atc gct ttg gcg gtc atc gtc ctc 432
 Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu Ala Val Ile Val Leu
 130 135 140

 ggg atc agg gcg tgg act aac tca agg aag cag tcc aag cac agc cag 480
 Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln Ser Lys His Ser Gln
 145 150 155 160

 taatacgcca agcaaaaaat tgc 503

<210> 276
 <211> 160
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 276
 Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu
 1 5 10 15

 Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly Glu Gly Leu Ala Met
 20 25 30

 Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser
 35 40 45

 Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly
 50 55 60

 Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser Gln Leu Gln Gln Ala
 65 70 75 80

 Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg Ala Glu Val Phe Ala
 85 90 95

 Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp
 100 105 110

 Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu
 115 120 125

 Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu Ala Val Ile Val Leu
 130 135 140

 Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln Ser Lys His Ser Gln
 145 150 155 160

<210> 277
 <211> 298
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(298)

<223> FRXA00520

<400> 277

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gcacagcgct ttttcatatt tttattgccca taatgggcac atg cgt ttt tct cga 115
 Met Arg Phe Ser Arg
 1 5

gtt ctt ccc gca ctt ctt atc acc acc gcc gtg agc atc cca aca gca 163
 Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val Ser Ile Pro Thr Ala
 10 15 20

tct gct gcc aca ctc acc ggc gac acc gac aag gaa ttg tgc atc gcc 211
 Ser Ala Ala Thr Leu Thr Gly Asp Thr Asp Lys Glu Leu Cys Ile Ala
 25 30 35

agc aac acc gac gat tcc gcg gtg gtt acc ttc tgg aac tcc att gaa 259
 Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe Trp Asn Ser Ile Glu
 40 45 50

gac tcc gtg cgc gaa caa cgc ctc gac gaa cta gac gcc 298
 Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu Asp Ala
 55 60 65

<210> 278

<211> 66

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Met Arg Phe Ser Arg Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val
 1 5 10 15

Ser Ile Pro Thr Ala Ser Ala Ala Thr Leu Thr Gly Asp Thr Asp Lys
 20 25 30

Glu Leu Cys Ile Ala Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe
 35 40 45

Trp Asn Ser Ile Glu Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu
 50 55 60

Asp Ala
 65

<210> 279

<211> 1887

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1864)

<223> RXN00527

<400> 279

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tgccctcgttt tattttctgc gttcatcatc gaatgaccag gtg att gcc act tct 115
Val Ile Ala Thr Ser
1 5

gat gtt cgg gag att tcc tcc gag gga atc gtg gcg cgt gtg tct gtc 163
Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val Ala Arg Val Ser Val
10 15 20

aac gga aat att gaa gct gcg cga acc acc acc att tac acc agt ctg 211
Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr Ile Tyr Thr Ser Leu
25 30 35

act gtg ccg gtc gcg aac ttg ccg gtt gcg gtt ggt gac cgt gtg gca 259
Thr Val Pro Val Ala Asn Leu Pro Val Ala Val Gly Asp Arg Val Ala
40 45 50

gct gat cag gtg ttg gct gag ttg gat gcc tct gcc ctg caa cga cag 307
Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser Ala Leu Gln Arg Gln
55 60 65

ttg gat gaa act gat gcc aac aat gcg cgt gca gcc atg gcg aac cgc 355
Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala Ala Met Ala Asn Arg
70 75 80 85

aat tcc atc gcg cag tcg cag caa gca tat gag cag tcc agg gaa ctt 403
Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu Gln Ser Arg Glu Leu
90 95 100

ctt gat agt ggt ttg agc ccg gag atc aac tcg gcg cgg tcc tcg ttg 451
Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser Ala Arg Ser Ser Leu
105 110 115

cgg gcg tcc tca cag gca tat cag gat gcg atc cgc agt ttt gaa gcg 499
Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile Arg Ser Phe Glu Ala
120 125 130

aag cag cga gat gtg gat ggc gga ttg gat tcc acc atg gtc gct caa 547
Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser Thr Met Val Ala Gln
135 140 145

tcg gat gct ctc aag gca gct cgt gag caa gca gat gct gct gaa att 595
Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala Asp Ala Ala Glu Ile
150 155 160 165

gaa cga ctg cgc gcg gac ttc gga ctg ctc aac aac gat cgc agc aac 643
Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn Asn Asp Arg Ser Asn
170 175 180

ctc aac gat gtc att ggt ctg ctc gat gag aga gaa tct ttg gct tct 691
Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg Glu Ser Leu Ala Ser
185 190 195

gcg gaa tcc gaa cta gct caa gcc cgc gct gca ggt gac cta gag gca 739
Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala Gly Asp Leu Glu Ala
200 205 210

gtc gct gca gct gaa gca aag gtt gca ggc ctg gaa caa tca att gct 787

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Val	Ala	Ala	Ala	Glu	Ala	Lys	Val	Ala	Gly	Leu	Glu	Gln	Ser	Ile	Ala		
215						220					225						
tcc	aaa	acc	tcc	acg	tgg	cct	agc	caa	gat	cag	act	tac	ttg	cag	tcc		835
Ser	Lys	Thr	Ser	Thr	Trp	Pro	Ser	Gln	Asp	Gln	Thr	Tyr	Leu	Gln	Ser		
230					235					240					245		
tac	acc	gct	ttg	gag	gaa	gct	gag	cga	cgc	gtc	gca	tcc	acc	act	gaa		883
Tyr	Thr	Ala	Leu	Glu	Glu	Ala	Glu	Arg	Arg	Val	Ala	Ser	Thr	Thr	Glu		
				250					255						260		
gct	cta	gaa	ata	gcc	gag	cgg	atc	tac	att	gat	tca	ctc	gga	aaa	gtt		931
Ala	Leu	Glu	Ile	Ala	Glu	Arg	Ile	Tyr	Ile	Asp	Ser	Leu	Gly	Lys	Val		
			265					270					275				
gac	tca	gaa	cta	gcc	gcc	gca	cag	cgc	gcc	gtt	gcc	gaa	gcc	cac	tca		979
Asp	Ser	Glu	Leu	Ala	Ala	Ala	Gln	Arg	Ala	Val	Ala	Glu	Ala	His	Ser		
		280					285					290					
gca	caa	caa	gac	gca	gca	ctt	ggc	ctc	gag	acc	gcg	cag	ctt	tcc	acc		1027
Ala	Gln	Gln	Asp	Ala	Ala	Leu	Gly	Leu	Glu	Thr	Ala	Gln	Leu	Ser	Thr		
	295					300					305						
caa	cac	caa	ttg	gaa	gcc	caa	tca	agc	gcc	atc	gat	gca	gct	tta	ggt		1075
Gln	His	Gln	Leu	Glu	Ala	Gln	Ser	Ser	Ala	Ile	Asp	Ala	Ala	Leu	Gly		
310					315				320						325		
ttg	gca	tca	gta	gat	aat	gaa	gcc	gcc	acc	aga	tcc	acg	tcc	cag	ctg		1123
Leu	Ala	Ser	Val	Asp	Asn	Glu	Ala	Ala	Thr	Arg	Ser	Thr	Ser	Gln	Leu		
				330					335					340			
cgg	atg	gat	atc	aac	aac	acc	acc	gtt	cgc	tcc	cca	tac	tca	ggc	att		1171
Arg	Met	Asp	Ile	Asn	Asn	Thr	Thr	Val	Arg	Ser	Pro	Tyr	Ser	Gly	Ile		
			345					350					355				
gtt	tca	tcc	gtg	cag	gca	gcc	caa	ggt	caa	cca	gca	gcc	ggc	gca	ctg		1219
Val	Ser	Ser	Val	Gln	Ala	Ala	Gln	Gly	Gln	Pro	Ala	Ala	Gly	Ala	Leu		
		360					365					370					
ttg	agt	gtt	gct	gat	gat	tcc	gaa	ctg	aag	atc	acc	gcg	aat	gta	aaa		1267
Leu	Ser	Val	Ala	Asp	Asp	Ser	Glu	Leu	Lys	Ile	Thr	Ala	Asn	Val	Lys		
	375					380					385						
gaa	gcg	gag	atc	agc	aac	gtc	acc	atc	gga	tcc	cgc	gtc	acc	ttc	act		1315
Glu	Ala	Glu	Ile	Ser	Asn	Val	Thr	Ile	Gly	Ser	Arg	Val	Thr	Phe	Thr		
390					395				400						405		
acc	cca	tcg	acc	gga	acc	aaa	gaa	ttc	gcc	ggc	cga	gta	tcc	aaa	gtc		1363
Thr	Pro	Ser	Thr	Gly	Thr	Lys	Glu	Phe	Ala	Gly	Arg	Val	Ser	Lys	Val		
				410					415					420			
tcc	ccc	att	gca	gct	gcc	gcc	agt	gcc	cca	gct	aca	ggt	gaa	gga	gct		1411
Ser	Pro	Ile	Ala	Ala	Ala	Ala	Ser	Ala	Pro	Ala	Thr	Gly	Glu	Gly	Ala		
			425					430					435				
gcc	gca	ggc	gcc	aca	acc	acc	aac	act	gac	gtc	acc	ttc	ccc	atc	gaa		1459
Ala	Ala	Gly	Ala	Thr	Thr	Thr	Asn	Thr	Asp	Val	Thr	Phe	Pro	Ile	Glu		
		440					445					450					
att	tcc	gtc	acc	ggc	gac	cgc	gaa	ggc	ctc	aac	ctc	ggc	gga	tcc	gct		1507
Ile	Ser	Val	Thr	Gly	Asp	Arg	Glu	Gly	Leu	Asn	Leu	Gly	Gly	Ser	Ala		

455	460	465	
cga gta cgc atc gtc cat gaa atc gca cca cac gta ctg acc gtt cct			1555
Arg Val Arg Ile Val His Glu Ile Ala Pro His Val Leu Thr Val Pro			
470	475	480	485
ttg gaa gct gtg tac aaa aat gat gac ggc aaa gac gct gtt ttg atc			1603
Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys Asp Ala Val Leu Ile			
	490	495	500
atc agc gac gac aac aaa gta gaa gaa gta gaa gta aaa aca gct gaa			1651
Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu Val Lys Thr Ala Glu			
	505	510	515
tcc gat gac ttt gat atc gca gtc agc ggt gct gga att tca gaa gac			1699
Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala Gly Ile Ser Glu Asp			
	520	525	530
gct cga gtg ctc acc cag cct gga aac tac cgg ggc ctc atc gga gaa			1747
Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg Gly Leu Ile Gly Glu			
	535	540	545
act gtg aaa ctt cac gca gat acg gtg gag cag gcg gcg gct cct ttt			1795
Thr Val Lys Leu His Ala Asp Thr Val Glu Gln Ala Ala Pro Phe			
	550	555	560
agt cct gcg gcc cct ttt gac cct gca gcc cct gcc gtt tct gcc aag			1843
Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro Ala Val Ser Ala Lys			
	570	575	580
caa acc gtg ggc cag gtg att tagcctatga gcctcatcga aat			1887
Gln Thr Val Gly Gln Val Ile			
	585		

<210> 280

<211> 588

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

Val Ile Ala Thr Ser Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val			
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Ile Tyr Thr Ser Leu Thr Val Pro Val Ala Asn Leu Pro Val Ala Val			
	35	40	45
Gly Asp Arg Val Ala Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser			
	50	55	60
Ala Leu Gln Arg Gln Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala			
	65	70	75
Ala Met Ala Asn Arg Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu			
	85	90	95
Gln Ser Arg Glu Leu Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser			
	100	105	110

Ala Arg Ser Ser Leu Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile
 115 120 125
 Arg Ser Phe Glu Ala Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser
 130 135 140
 Thr Met Val Ala Gln Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala
 145 150 155 160
 Asp Ala Ala Glu Ile Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn
 165 170 175
 Asn Asp Arg Ser Asn Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg
 180 185 190
 Glu Ser Leu Ala Ser Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala
 195 200 205
 Gly Asp Leu Glu Ala Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu
 210 215 220
 Glu Gln Ser Ile Ala Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln
 225 230 235 240
 Thr Tyr Leu Gln Ser Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val
 245 250 255
 Ala Ser Thr Thr Glu Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp
 260 265 270
 Ser Leu Gly Lys Val Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val
 275 280 285
 Ala Glu Ala His Ser Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr
 290 295 300
 Ala Gln Leu Ser Thr Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile
 305 310 315 320
 Asp Ala Ala Leu Gly Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg
 325 330 335
 Ser Thr Ser Gln Leu Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser
 340 345 350
 Pro Tyr Ser Gly Ile Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro
 355 360 365
 Ala Ala Gly Ala Leu Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile
 370 375 380
 Thr Ala Asn Val Lys Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser
 385 390 395 400
 Arg Val Thr Phe Thr Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly
 405 410 415
 Arg Val Ser Lys Val Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala
 420 425 430

Thr Gly Glu Gly Ala Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val
435 440 445

Thr Phe Pro Ile Glu Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn
450 455 460

Leu Gly Gly Ser Ala Arg Val Arg Ile Val His Glu Ile Ala Pro His
465 470 475 480

Val Leu Thr Val Pro Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys
485 490 495

Asp Ala Val Leu Ile Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu
500 505 510

Val Lys Thr Ala Glu Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala
515 520 525

Gly Ile Ser Glu Asp Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg
530 535 540

Gly Leu Ile Gly Glu Thr Val Lys Leu His Ala Asp Thr Val Glu Gln
545 550 555 560

Ala Ala Ala Pro Phe Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro
565 570 575

Ala Val Ser Ala Lys Gln Thr Val Gly Gln Val Ile
580 585

<210> 281

<211> 1887

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1864)

<223> FRXA00527

<400> 281

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tgccctggttt tattttctgc gttoatcatc gaatgaccag gtg att gcc act tct 115
Val Ile Ala Thr Ser
1 5

gat gtt cgg gag att tcc tcc gag gga atc gtg gcg cgt gtg tct gtc 163
Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val Ala Arg Val Ser Val
10 15 20

aac gga aat att gaa gct gcg cga acc acc acc att tac acc agt ctg 211
Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr Ile Tyr Thr Ser Leu
25 30 35

act gtg ccg gtc gcg aac ttg ccg gtt gcg gtt ggt gac cgt gtg gca 259
Thr Val Pro Val Ala Asn Leu Pro Val Ala Val Gly Asp Arg Val Ala
40 45 50

gct gat cag gtg ttg gct gag ttg gat gcc tct gcc ctg caa cga cag 307

Ala	Asp	Gln	Val	Leu	Ala	Glu	Leu	Asp	Ala	Ser	Ala	Leu	Gln	Arg	Gln		
55						60					65						
ttg	gat	gaa	act	gat	gcc	aac	aat	gcg	cgt	gca	gcc	atg	gcg	aac	cgc	355	
Leu	Asp	Glu	Thr	Asp	Ala	Asn	Asn	Ala	Arg	Ala	Ala	Met	Ala	Asn	Arg		
70					75				80						85		
aat	tcc	atc	gcg	cag	tcg	cag	caa	gca	tat	gag	cag	tcc	agg	gaa	ctt	403	
Asn	Ser	Ile	Ala	Gln	Ser	Gln	Gln	Ala	Tyr	Glu	Gln	Ser	Arg	Glu	Leu		
				90					95					100			
ctt	gat	agt	ggg	ttg	agc	ccg	gag	atc	aac	tcg	gcg	cgg	tcc	tcg	ttg	451	
Leu	Asp	Ser	Gly	Leu	Ser	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Ser	Ser	Leu		
			105					110					115				
cgg	gcg	tcc	tca	cag	gca	tat	cag	gat	gcg	atc	cgc	agt	ttt	gaa	gcg	499	
Arg	Ala	Ser	Ser	Gln	Ala	Tyr	Gln	Asp	Ala	Ile	Arg	Ser	Phe	Glu	Ala		
		120					125					130					
aag	cag	cga	gat	gtg	gat	ggc	gga	ttg	gat	tcc	acc	atg	gtc	gct	caa	547	
Lys	Gln	Arg	Asp	Val	Asp	Gly	Gly	Leu	Asp	Ser	Thr	Met	Val	Ala	Gln		
	135					140					145						
tcg	gat	gct	ctc	aag	gca	gct	cgt	gag	caa	gca	gat	gct	gct	gaa	att	595	
Ser	Asp	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Gln	Ala	Asp	Ala	Ala	Glu	Ile		
150					155					160				165			
gaa	cga	ctg	cgc	gcg	gac	ttc	gga	ctg	ctc	aac	aac	gat	cgc	agc	aac	643	
Glu	Arg	Leu	Arg	Ala	Asp	Phe	Gly	Leu	Leu	Asn	Asn	Asp	Arg	Ser	Asn		
				170					175					180			
ctc	aac	gat	gtc	att	ggg	ctg	ctc	gat	gag	aga	gaa	tct	ttg	gct	tct	691	
Leu	Asn	Asp	Val	Ile	Gly	Leu	Leu	Asp	Glu	Arg	Glu	Ser	Leu	Ala	Ser		
			185					190					195				
gcg	gaa	tcc	gaa	cta	gct	caa	gcc	cgc	gct	gca	ggg	gac	cta	gag	gca	739	
Ala	Glu	Ser	Glu	Leu	Ala	Gln	Ala	Arg	Ala	Ala	Gly	Asp	Leu	Glu	Ala		
		200					205					210					
gtc	gct	gca	gct	gaa	gca	aag	gtt	gca	ggc	ctg	gaa	caa	tca	att	gct	787	
Val	Ala	Ala	Ala	Glu	Ala	Lys	Val	Ala	Gly	Leu	Glu	Gln	Ser	Ile	Ala		
		215				220					225						
tcc	aaa	acc	tcc	acg	tgg	cct	agc	caa	gat	cag	act	tac	ttg	cag	tcc	835	
Ser	Lys	Thr	Ser	Thr	Trp	Pro	Ser	Gln	Asp	Gln	Thr	Tyr	Leu	Gln	Ser		
230					235					240				245			
tac	acc	gct	ttg	gag	gaa	gct	gag	cga	cgc	gtc	gca	tcc	acc	act	gaa	883	
Tyr	Thr	Ala	Leu	Glu	Glu	Ala	Glu	Arg	Arg	Val	Ala	Ser	Thr	Thr	Glu		
				250					255					260			
gct	cta	gaa	ata	gcc	gag	cgg	atc	tac	att	gat	tca	ctc	gga	aaa	gtt	931	
Ala	Leu	Glu	Ile	Ala	Glu	Arg	Ile	Tyr	Ile	Asp	Ser	Leu	Gly	Lys	Val		
			265					270					275				
gac	tca	gaa	cta	gcc	gcc	gca	cag	cgc	gcc	gtt	gcc	gaa	gcc	cac	tca	979	
Asp	Ser	Glu	Leu	Ala	Ala	Ala	Gln	Arg	Ala	Val	Ala	Glu	Ala	His	Ser		
		280					285					290					
gca	caa	caa	gac	gca	gca	ctt	ggc	ctc	gag	acc	gcg	cag	ctt	tcc	acc	1027	
Ala	Gln	Gln	Asp	Ala	Ala	Leu	Gly	Leu	Glu	Thr	Ala	Gln	Leu	Ser	Thr		

295	300	305	
caa cac caa ttg gaa gcc	caa tca agc gcc	atc gat gca gct tta ggt	1075
Gln His Gln Leu Glu Ala	Gln Ser Ser Ala Ile	Asp Ala Ala Leu Gly	
310	315	320	325
ttg gca tca gta gat aat gaa gcc gcc	acc aga tcc acg tcc cag ctg		1123
Leu Ala Ser Val Asp Asn Glu Ala Ala	Thr Arg Ser Thr Ser Gln Leu		
	330	335	340
cgg atg gat atc aac aac acc acc gtt	cgc tcc cca tac tca ggc att		1171
Arg Met Asp Ile Asn Asn Thr Thr	Val Arg Ser Pro Tyr Ser Gly Ile		
	345	350	355
gtt tca tcc gtg cag gca gcc caa ggt	caa cca gca gcc ggc gca ctg		1219
Val Ser Ser Val Gln Ala Ala Gln Gly	Gln Pro Ala Ala Gly Ala Leu		
	360	365	370
ttg agt gtt gct gat gat tcc gaa ctg	aag atc acc gcg aat gta aaa		1267
Leu Ser Val Ala Asp Asp Ser Glu Leu	Lys Ile Thr Ala Asn Val Lys		
	375	380	385
gaa gcg gag atc agc aac gtc acc atc	gga tcc cgc gtc acc ttc act		1315
Glu Ala Glu Ile Ser Asn Val Thr Ile	Gly Ser Arg Val Thr Phe Thr		
	390	395	400
acc cca tcg acc gga acc aaa gaa ttc	gcc ggc cga gta tcc aaa gtc		1363
Thr Pro Ser Thr Gly Thr Lys Glu Phe	Ala Gly Arg Val Ser Lys Val		
	410	415	420
tcc ccc att gca gct gcc gcc agt gcc	cca gct aca ggt gaa gga gct		1411
Ser Pro Ile Ala Ala Ala Ala Ser Ala	Pro Ala Thr Gly Glu Gly Ala		
	425	430	435
gcc gca ggc gcc aca acc acc aac act	gac gtc acc ttc ccc atc gaa		1459
Ala Ala Gly Ala Thr Thr Thr Asn Thr	Asp Val Thr Phe Pro Ile Glu		
	440	445	450
att tcc gtc acc ggc gac cgc gaa ggc	ctc aac ctc ggc gga tcc gct		1507
Ile Ser Val Thr Gly Asp Arg Glu Gly	Leu Asn Leu Gly Gly Ser Ala		
	455	460	465
cga gta cgc atc gtc cat gaa atc gca	cca cac gta ctg acc gtt cct		1555
Arg Val Arg Ile Val His Glu Ile Ala	Pro His Val Leu Thr Val Pro		
	470	475	480
ttg gaa gct gtg tac aaa aat gat gac	ggc aaa gac gct gtt ttg atc		1603
Leu Glu Ala Val Tyr Lys Asn Asp Asp	Gly Lys Asp Ala Val Leu Ile		
	490	495	500
atc agc gac gac aac aaa gta gaa gaa	gta gaa gta aaa aca gct gaa		1651
Ile Ser Asp Asp Asn Lys Val Glu Glu	Val Glu Val Lys Thr Ala Glu		
	505	510	515
tcc gat gac ttt gat atc gca gtc agc	ggt gct gga att tca gaa gac		1699
Ser Asp Asp Phe Asp Ile Ala Val Ser	Gly Ala Gly Ile Ser Glu Asp		
	520	525	530
gct cga gtg ctc acc cag cct gga aac	tac cgg ggc ctc atc gga gaa		1747
Ala Arg Val Leu Thr Gln Pro Gly Asn	Tyr Arg Gly Leu Ile Gly Glu		
	535	540	545

act gtg aaa ctt cac gca gat acg gtg gag cag gcg gcg gct cct ttt 1795
 Thr Val Lys Leu His Ala Asp Thr Val Glu Gln Ala Ala Ala Pro Phe
 550 555 560 565

agt cct gcg gcc cct ttt gac cct gca gcc cct gcc gtt tct gcc aag 1843
 Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro Ala Val Ser Ala Lys
 570 575 580

caa acc gtg ggc cag gtg att tagcctatga gcctcatcga aat 1887
 Gln Thr Val Gly Gln Val Ile
 585

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 282
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 20 25 30

Ile Tyr Thr Ser Leu Thr Val Pro Val Ala Asn Leu Pro Val Ala Val
 35 40 45

Gly Asp Arg Val Ala Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser
 50 55 60

Ala Leu Gln Arg Gln Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala
 65 70 75 80

Ala Met Ala Asn Arg Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu
 85 90 95

Gln Ser Arg Glu Leu Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser
 100 105 110

Ala Arg Ser Ser Leu Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile
 115 120 125

Arg Ser Phe Glu Ala Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser
 130 135 140

Thr Met Val Ala Gln Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala
 145 150 155 160

Asp Ala Ala Glu Ile Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn
 165 170 175

Asn Asp Arg Ser Asn Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg
 180 185 190

Glu Ser Leu Ala Ser Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala
 195 200 205

Gly Asp Leu Glu Ala Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu
 210 215 220

Glu Gln Ser Ile Ala Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln
 225 230 235 240
 Thr Tyr Leu Gln Ser Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val
 245 250 255
 Ala Ser Thr Thr Glu Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp
 260 265 270
 Ser Leu Gly Lys Val Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val
 275 280 285
 Ala Glu Ala His Ser Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr
 290 295 300
 Ala Gln Leu Ser Thr Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile
 305 310 315 320
 Asp Ala Ala Leu Gly Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg
 325 330 335
 Ser Thr Ser Gln Leu Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser
 340 345 350
 Pro Tyr Ser Gly Ile Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro
 355 360 365
 Ala Ala Gly Ala Leu Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile
 370 375 380
 Thr Ala Asn Val Lys Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser
 385 390 395 400
 Arg Val Thr Phe Thr Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly
 405 410 415
 Arg Val Ser Lys Val Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala
 420 425 430
 Thr Gly Glu Gly Ala Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val
 435 440 445
 Thr Phe Pro Ile Glu Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn
 450 455 460
 Leu Gly Gly Ser Ala Arg Val Arg Ile Val His Glu Ile Ala Pro His
 465 470 475 480
 Val Leu Thr Val Pro Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys
 485 490 495
 Asp Ala Val Leu Ile Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu
 500 505 510
 Val Lys Thr Ala Glu Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala
 515 520 525
 Gly Ile Ser Glu Asp Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg
 530 535 540

Gly Leu Ile Gly Glu Thr Val Lys Leu His Ala Asp Thr Val Glu Gln
545 550 555 560

Ala Ala Ala Pro Phe Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro
565 570 575

Ala Val Ser Ala Lys Gln Thr Val Gly Gln Val Ile
580 585

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<220>

<221> CDS

<222> (101)..(1498)

<223> RXN00547

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gcagaaggta gaccgcgtat cgcccgggtga tagtgaaccg gtg gca cgg gat ttt 115
Val Ala Arg Asp Phe
1 5

atc aat gca atc ggc ggt cgg ttt ggt cgt ttt gcg cag gtg ggc act 163
Ile Asn Ala Ile Gly Gly Arg Phe Gly Arg Phe Ala Gln Val Gly Thr
10 15 20

cag cgg ttc tgg act ccc ctg cgt gtt ttg atc acc act tcc ctg gtg 211
Gln Arg Phe Trp Thr Pro Leu Arg Val Leu Ile Thr Thr Ser Leu Val
25 30 35

ttt ttg gcc atg ggg ttt tta aca aaa gcc aat tgc atc cag ggt tct 259
Phe Leu Ala Met Gly Phe Leu Thr Lys Ala Asn Cys Ile Gln Gly Ser
40 45 50

aga ggt act gat ggt gtg gtt tct ttg aac tgg tcg gga agt cgc cag 307
Arg Gly Thr Asp Gly Val Val Ser Leu Asn Trp Ser Gly Ser Arg Gln
55 60 65

tac acc tca gcc tgt tac aac gac atc gtt ccg ctc tat ggg ggg cgc 355
Tyr Thr Ser Ala Cys Tyr Asn Asp Ile Val Pro Leu Tyr Gly Gly Arg
70 75 80 85

gga att gat gcg cca ggt ttc cct tat gcc ttt tcg tgg cag gaa ggt 403
Gly Ile Asp Ala Pro Gly Phe Pro Tyr Ala Phe Ser Trp Gln Glu Gly
90 95 100

gat ctc acc agg tac atg gag tac ccg gtg ttg ggc gga att ttc cag 451
Asp Leu Thr Arg Tyr Met Glu Tyr Pro Val Leu Gly Gly Ile Phe Gln
105 110 115

tgg att tgt ggc att atc acg cgg ttt ttg tac ccg gtt gtt gat gtc 499
Trp Ile Cys Gly Ile Ile Thr Arg Phe Leu Tyr Pro Val Val Asp Val
120 125 130

att ccg ttt cat acg ctg cct gaa tct ggt ctt tat ttc atc gtc acc 547
Ile Pro Phe His Thr Leu Pro Glu Ser Gly Leu Tyr Phe Ile Val Thr

135	140	145	
gcg ctt gcg ttg gcg ttc ttt tgg gtg ttg gtc atc cgc atg atg gtg Ala Leu Ala Leu Ala Phe Phe Trp Val Leu Val Ile Arg Met Met Val 150 155 160 165			595
gag ctc act ggc aat cga gtg tgg gat acc gtc ctt gtt gcg gcg tct Glu Leu Thr Gly Asn Arg Val Trp Asp Thr Val Leu Val Ala Ala Ser 170 175 180			643
ccc ctg gtt gct gtg cat gcg ttt acc aac tgg gat act cca gcc att Pro Leu Val Ala Val His Ala Phe Thr Asn Trp Asp Thr Pro Ala Ile 185 190 195			691
gcg gcg gtg att ggt gcg atg ctt gcg gtg aaa cgc gga aac ccc ttg Ala Ala Val Ile Gly Ala Met Leu Ala Val Lys Arg Gly Asn Pro Leu 200 205 210			739
gtt gcg ggt gtg ctg atc ggc gcg ggt acg gcg ttc aaa ttg tgg ccg Val Ala Gly Val Leu Ile Gly Ala Gly Thr Ala Phe Lys Leu Trp Pro 215 220 225			787
ctt tat ctt ctt ggt gcg tat ttg gtg ctg gcg gtc aag aat aag aat Leu Tyr Leu Leu Gly Ala Tyr Leu Val Leu Ala Val Lys Asn Lys Asn 230 235 240 245			835
ctc aag ccg ttt atc acc atg gct gca gcg gct gcg gtg aca tgg ctc Leu Lys Pro Phe Ile Thr Met Ala Ala Ala Ala Val Thr Trp Leu 250 255 260			883
gtg gtg aat gtg cca gtg atg atc gcg tac ccc aag gcg tgg aat gaa Val Val Asn Val Pro Val Met Ile Ala Tyr Pro Lys Ala Trp Asn Glu 265 270 275			931
ttc ttg cgc ctg aac cgg gag cgt ggt gcg gag tgg acc acg att tac Phe Leu Arg Leu Asn Arg Glu Arg Gly Ala Glu Trp Thr Thr Ile Tyr 280 285 290			979
cag gtc atc gac cgt aat ttg ccg atc aat ttg aat gat cca gtg ctg Gln Val Ile Asp Arg Asn Leu Pro Ile Asn Leu Asn Asp Pro Val Leu 295 300 305			1027
ctt aat gtg ctg agc ttc ggc ttg ttt ggt gca tgc tgt gtg gcc att Leu Asn Val Leu Ser Phe Gly Leu Phe Gly Ala Ser Cys Val Ala Ile 310 315 320 325			1075
ttg atc ctt ggg ctc aag gtg cag cgc act ccc cga gtc gct gag ctg Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val Ala Glu Leu 330 335 340			1123
gcc ttt ttg att gtc gcg gcg ttt ttg ctg ttt aac aag gtg tgg agt Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys Val Trp Ser 345 350 355			1171
cct cag tat tca ctg tgg ctg gtc ccg ttg gct gtt ctg gca ttt cct Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu Ala Phe Pro 360 365 370			1219
cag tgg aaa gtg ctg ttc ccg tgg atg gtt aca gac gcc atg gtg tgg Gln Trp Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala Met Val Trp 375 380 385			1267

cca att ttg atg tgg cac atg ctc ggc acg gac aac aag gga ctc ccc 1315
 Pro Ile Leu Met Trp His Met Leu Gly Thr Asp Asn Lys Gly Leu Pro
 390 395 400 405

cat gaa atg ttg gat ctc atc gtg att tcc cga gat gcc ttc att gtg 1363
 His Glu Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala Phe Ile Val
 410 415 420

gtc atg ata gta ggt gta atc cgg cag atg ctc gga cga cgt gca gat 1411
 Val Met Ile Val Gly Val Ile Arg Gln Met Leu Gly Arg Arg Ala Asp
 425 430 435

ccg gtg atg gat gcg cac gcc ggg cgc gat ttg ttg gcc ggg ccc ttc 1459
 Pro Val Met Asp Ala His Ala Gly Arg Asp Leu Leu Ala Gly Pro Phe
 440 445 450

ggc gca ggc gag cgt cga aaa gca ttg aag gaa gta agt tgagcacaac 1508
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<211> 466

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

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Thr Thr Ser Leu Val Phe Leu Ala Met Gly Phe Leu Thr Lys Ala Asn
 35 40 45

Cys Ile Gln Gly Ser Arg Gly Thr Asp Gly Val Val Ser Leu Asn Trp
 50 55 60

Ser Gly Ser Arg Gln Tyr Thr Ser Ala Cys Tyr Asn Asp Ile Val Pro
 65 70 75 80

Leu Tyr Gly Gly Arg Gly Ile Asp Ala Pro Gly Phe Pro Tyr Ala Phe
 85 90 95

Ser Trp Gln Glu Gly Asp Leu Thr Arg Tyr Met Glu Tyr Pro Val Leu
 100 105 110

Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg Phe Leu Tyr
 115 120 125

Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu Ser Gly Leu
 130 135 140

Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Trp Val Leu Val
 145 150 155 160

Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp Asp Thr Val

<210> 285

<400> 286
Val Ala Ile Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val
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 Ala Val Lys Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala
 100 105 110

ggt acg gcg ttc aaa ttg tgg ccg ctt tat ctt ctt ggt gcg tat ttg 384
 Gly Thr Ala Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu
 115 120 125

gtg ctg gcg gtc aag aat aag aat ctc aag ccg ttt atc acc atg gct 432
 Val Leu Ala Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala
 130 135 140

gca gcg gct gcg gtg aca tgg ctc gtg gtg aat gtg cca gtg atg atc 480
 Ala Ala Ala Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile
 145 150 155 160

gcg tac ccc aag gcg tgg aat gaa ttc ttg cgc ctg aac cgg gag cgt 528
 Ala Tyr Pro Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg
 165 170 175

ggt gcg gag tgg acc acg att tac cag gtc atc gac cgt aat ttg ccg 576
 Gly Ala Glu Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro
 180 185 190

atc aat ttg aat gat cca gtg ctg ctt aat gtg ctg agc ttc ggc ttg 624
 Ile Asn Leu Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu
 195 200 205

ttt ggt gca tca gtg tgt ggc cat ttt gat cct tgg gct caa ggt gca 672
 Phe Gly Ala Ser Val Cys Gly His Phe Asp Pro Trp Ala Gln Gly Ala
 210 215 220

gcg cac tcc ccg agt cgc tgagctggcc tttttgattg tcg 713
 Ala His Ser Pro Ser Arg
 225 230

<210> 288
 <211> 230
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 288
 Pro Val Leu Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg
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Phe Leu Tyr Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu
 20 25 30

Ser Gly Leu Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Trp
 35 40 45

Val Leu Val Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp
 50 55 60

Asp Thr Val Leu Val Ala Ala Ser Pro Leu Val Ala Val His Ala Phe
 65 70 75 80

Thr Asn Trp Asp Thr Pro Ala Ile Ala Ala Val Ile Gly Ala Met Leu
 85 90 95

Ala Val Lys Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala
 100 105 110

Gly Thr Ala Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu
 115 120 125

Val Leu Ala Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala
 130 135 140

Ala Ala Ala Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile
 145 150 155 160

Ala Tyr Pro Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg
 165 170 175

Gly Ala Glu Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro
 180 185 190

Ile Asn Leu Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu
 195 200 205

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Ala His Ser Pro Ser Arg
 225 230

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1036)
 <223> RXN00552

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gtttttaagg tagccacaca tcgcactaga ctgaagaact gtg gct acc tca aaa 115
 Val Ala Thr Ser Lys
 1 5

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 Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val
 10 15 20

cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc 211
 Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg
 25 30 35

atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att 259
 Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile
 40 45 50

gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc 307
 Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe
 55 60 65

aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca	355
Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro	
70 75 80 85	
aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca	403
Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro	
90 95 100	
gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac	451
Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His	
105 110 115	
ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa	499
Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu	
120 125 130	
gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag	547
Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys	
135 140 145	
ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc	595
Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile	
150 155 160 165	
gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg	643
Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val	
170 175 180	
gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc	691
Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu	
185 190 195	
atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc	739
Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile	
200 205 210	
gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc	787
Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser	
215 220 225	
ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac	835
Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr	
230 235 240 245	
aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt	883
Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe	
250 255 260	
gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc	931
Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys	
265 270 275	
cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc	979
Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg	
280 285 290	
tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc	1027
Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu	
295 300 305	
gtt act tct taaaaagggt atggtggctg ggt	1059

Val Thr Ser
310

<210> 290

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
1 5 10 15

Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
20 25 30

Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
35 40 45

Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
50 55 60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
65 70 75 80

Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
85 90 95

Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
100 105 110

Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
115 120 125

Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
130 135 140

Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
145 150 155 160

Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
165 170 175

Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
180 185 190

Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln
195 200 205

Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly
210 215 220

Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu
225 230 235 240

Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr
245 250 255

Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu
260 265 270

Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His
 275 280 285

Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln
 290 295 300

Gly Ile Asp Pro Leu Val Thr Ser
 305 310

<210> 291

<211> 740

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(717)

<223> FRXA00552

<400> 291

ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca aag ctc agt gtc	48
Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro Lys Leu Ser Val	
1 5 10 15	
aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca gat gag ctc aaa	96
Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro Asp Glu Leu Lys	
20 25 30	
gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac ctg aaa cca cag	144
Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His Leu Lys Pro Gln	
35 40 45	
cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa gtt gtg ttc ttt	192
Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu Val Val Phe Phe	
50 55 60	
gac ggc cgc aac gca atg gaa gcc cag atc ggc aag ttc aag gac gct	240
Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys Phe Lys Asp Ala	
65 70 75 80	
gtt gtc cct gac gta gaa acc act cat gat ttc atc gca gaa att gag	288
Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile Ala Glu Ile Glu	
85 90 95	
tct gga aaa tac gac gat ctc aaa gac aag cct gtg gtc acc tac tgc	336
Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val Val Thr Tyr Cys	
100 105 110	
acc ggc gga att cgt tgt gag atc ctg agt tca ctc atg atc aac cgt	384
Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu Met Ile Asn Arg	
115 120 125	
ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc gtt cgc tac ggc	432
Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile Val Arg Tyr Gly	
130 135 140	
gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc ctc tac gtt ttc	480
Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser Leu Tyr Val Phe	
145 150 155 160	

gat aag cgc atg cat atg gaa ttc ggc gag gat tac aaa gag gtc gga 528
Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr Lys Glu Val Gly
165 170 175

cac tgc atc cat tgc gat act ccc acc aac aaa ttt gag cac tgc ctc 576
His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe Glu His Cys Leu
180 185 190

aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc cct gat tgc ttc 624
Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys Pro Asp Cys Phe
195 200 205

gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc tgt gca gca att 672
Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg Cys Ala Ala Ile
210 215 220

gct gcg gat ttc gct gag caa gga att gat ccg ctc gtt act tct 717
Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu Val Thr Ser
225 230 235

taaaaagggt atggtggctg ggt 740

<210> 292
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 292
Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro Lys Leu Ser Val
1 5 10 15

Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro Asp Glu Leu Lys
20 25 30

Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His Leu Lys Pro Gln
35 40 45

Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu Val Val Phe Phe
50 55 60

Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys Phe Lys Asp Ala
65 70 75 80

Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile Ala Glu Ile Glu
85 90 95

Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val Val Thr Tyr Cys
100 105 110

Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu Met Ile Asn Arg
115 120 125

Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile Val Arg Tyr Gly
130 135 140

Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser Leu Tyr Val Phe
145 150 155 160

Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr Lys Glu Val Gly
165 170 175

His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe Glu His Cys Leu
 180 185 190
 Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys Pro Asp Cys Phe
 195 200 205
 Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg Cys Ala Ala Ile
 210 215 220
 Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu Val Thr Ser
 225 230 235

<210> 293
 <211> 1062
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1039)
 <223> RXN00555

<400> 293
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 cggttcttaa cagttttctc catctcaact ccggaatttg atg aaa caa ccc ctt 115
 Met Lys Gln Pro Leu
 1 5
 cgc gta ctt att tct tgt cga ccc gaa gaa aat tcg ggt ggc aaa cgt 163
 Arg Val Leu Ile Ser Cys Arg Pro Glu Glu Asn Ser Gly Gly Lys Arg
 10 15 20
 agt gaa caa aat gat gct gtt ttt gag ttc gcc gca tgg cta gct cgt 211
 Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala Ala Trp Leu Ala Arg
 25 30 35
 act tca gac atc aat gtt cgt gga atc aca act ttc ata cgc cct tgg 259
 Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr Phe Ile Arg Pro Trp
 40 45 50
 ccg tct tcc tcc atc agt aag ctc gga gga aaa tat cat aag tgg tat 307
 Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys Tyr His Lys Trp Tyr
 55 60 65
 aag aat tta gat tct tac tac cgc agt cgc acg atc aag gga ctc aaa 355
 Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr Ile Lys Gly Leu Lys
 70 75 80 85
 gag gcc gga gtt gag aag tcc caa tgg gac gat gat gtt tca gtt ttt 403
 Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp Val Ser Val Phe
 90 95 100
 gta gat ggt cct tct gaa tcc acg ctg ctc acc cat gct gct gaa gaa 451
 Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr His Ala Ala Glu Glu
 105 110 115
 ttc gaa gcg gac ctc att ctg ctt ggc tct gat gcg acc gca cca aaa 499
 Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp Ala Thr Ala Pro Lys

120	125	130	
ggc cgc ttt ctg gcc agc tcc acc gca gat gcc ctc ctt cac tcc tcg			547
Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala Leu Leu His Ser Ser			
135	140	145	
ccc gtc cca cta gga ctt gtg ccg cga ggg gtg aag ctt tcc aaa aag			595
Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val Lys Leu Ser Lys Lys			
150	155	160	165
ggt gtc acc cgc gtc aac tac gct ttc acc aat gaa agc gat gac ttt			643
Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn Glu Ser Asp Asp Phe			
170	175	180	
gag caa ggt tta cgc tct tcc gcg gag ctc gcc acc aat tgg aac gtt			691
Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala Thr Asn Trp Asn Val			
185	190	195	
cct ctt cgg atc ctt gct ttt tca ccc aca ggc att act tcc gca cca			739
Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly Ile Thr Ser Ala Pro			
200	205	210	
acg tcg cgg agc ttg gat att tcc act gag ctt tcc tcc gag tgg cgt			787
Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu Ser Ser Glu Trp Arg			
215	220	225	
gaa cta acg ctc gcc atg ctt gat cga gcc cgt gat ggc gtc ctc aca			835
Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg Asp Gly Val Leu Thr			
230	235	240	245
gac cac cca aac ttg agc gtg agc agt gaa acc ggt tct ggc tgg ggt			883
Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr Gly Ser Gly Trp Gly			
250	255	260	
tgg agc ggt gca att gat gct ttg cga tgg aag aaa ggt gac ctg ctg			931
Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys Lys Gly Asp Leu Leu			
265	270	275	
tgc atg gga agc cat cgc aca gac acc ctt tca cgt gtc ttt gtc ggt			979
Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser Arg Val Phe Val Gly			
280	285	290	
tcg gaa aca atg gaa att atc cga aac tct cct gta ccg acc atc att			1027
Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro Val Pro Thr Ile Ile			
295	300	305	
tat ccc ggt ctt taggctctcc aacagcagag gac			1062
Tyr Pro Gly Leu			
310			

<210> 294

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Met	Lys	Gln	Pro	Leu	Arg	Val	Leu	Ile	Ser	Cys	Arg	Pro	Glu	Glu	Asn
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Ser	Gly	Gly	Lys	Arg	Ser	Glu	Gln	Asn	Asp	Ala	Val	Phe	Glu	Phe	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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<210> 295
<211> 914
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (1)..(891)

<223> FRXA00555

<400> 295

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Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala	
1 5 10 15	
gca tgg cta gct cgt act tca gac atc aat gtt cgt gga atc aca act	96
Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr	
20 25 30	
ttc ata cgc cct tgg ccg tct tcc tcc atc agt aag ctc gga gga aaa	144
Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys	
35 40 45	
tat cat aag tgg tat aag aat tta gat tct tac tac cgc agt cgc acg	192
Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr	
50 55 60	
atc aag gga ctc aaa gag gcc gga gtt gag aag tcc caa tgg gac gat	240
Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp	
65 70 75 80	
gat gtt tca gtt ttt gta gat ggt cct tct gaa tcc acg ctg ctc acc	288
Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr	
85 90 95	
cat gct gct gaa gaa ttc gaa gcg gac ctc att ctg ctt ggc tct gat	336
His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp	
100 105 110	
gcg acc gca cca aaa ggc cgc ttt ctg gcc agc tcc acc gca gat gcc	384
Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala	
115 120 125	
ctc ctt cac tcc tcg ccc gtc cca cta gga ctt gtg ccg cga ggg gtg	432
Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val	
130 135 140	
aag ctt tcc aaa aag ggt gtc acc cgc gtc aac tac gct ttc acc aat	480
Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn	
145 150 155 160	
gaa agc gat gac ttt gag caa ggt tta cgc tct tcc gcg gag ctc gcc	528
Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala	
165 170 175	
acc aat tgg aac gtt cct ctt cgg atc ctt gct ttt tca ccc aca ggc	576
Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly	
180 185 190	
att act tcc gca cca acg tcg cgg agc ttg gat att tcc act gag ctt	624
Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu	
195 200 205	
tcc tcc gag tgg cgt gaa cta acg ctc gcc atg ctt gat cga gcc cgt	672
Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg	

210	215	220	
gat ggc gtc ctc aca gac cac cca aac ttg agc gtg agc agt gaa acc			720
Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr			
225	230	235	240
ggt tct ggc tgg ggt tgg agc ggt gca att gat gct ttg cga tgg aag			768
Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys			
	245	250	255
aaa ggt gac ctg ctg tgc atg gga agc cat cgc aca gac acc ctt tca			816
Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser			
	260	265	270
cgt gtc ttt gtc ggt tcg gaa aca atg gaa att atc cga aac tct cct			864
Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro			
	275	280	285
gta ccg acc atc att tat ccc ggt ctt taggctctcc aacagcagag			911
Val Pro Thr Ile Ile Tyr Pro Gly Leu			
	290	295	
gac			914
<210> 296			
<211> 297			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 296			
Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala			
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Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr			
	20	25	30
Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys			
	35	40	45
Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr			
	50	55	60
Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp			
	65	70	75
Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr			
	85	90	95
His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp			
	100	105	110
Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala			
	115	120	125
Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val			
	130	135	140
Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn			
	145	150	155
			160

Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala
 165 170 175
 Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly
 180 185 190
 Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu
 195 200 205
 Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg
 210 215 220
 Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr
 225 230 235 240
 Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys
 245 250 255
 Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser
 260 265 270
 Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
 275 280 285
 Val Pro Thr Ile Ile Tyr Pro Gly Leu
 290 295

<210> 297
 <211> 498
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(475)
 <223> RXN00560

<400> 297
 aaggacgact tctgggggagc ggtgtggatt ctcacgggga ttctcatgcg gattatcaga 60
 catatggaca ctttaacggt tcgtactagg ctgatgcttc atg agg att gat ccg 115
 Met Arg Ile Asp Pro
 1 5
 ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
 Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
 10 15 20
 gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
 Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr
 25 30 35
 cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
 Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
 40 45 50
 gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
 Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
 55 60 65

aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag 355
 Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys
 70 75 80 85

acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt 403
 Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe
 90 95 100

gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg 451
 Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala
 105 110 115

gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt 498
 Asp Trp Leu Pro Val Val Lys Leu
 120 125

<210> 298

<211> 125

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
 1 5 10 15

Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
 20 25 30

Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
 35 40 45

Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
 50 55 60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
 65 70 75 80

Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
 85 90 95

Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
 100 105 110

Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
 115 120 125

<210> 299

<211> 337

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(337)

<223> FRXA00560

<400> 299

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	Met	Ser	Phe	Lys	Val	
	1				5	
att tcc act ggc ccc caa gcc atc ttc caa gac cga ggt cgc ttc ggt						163
Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp Arg Gly Arg Phe Gly						
	10			15	20	
ttt gcc agc gct ggt gtt gga acc tca gga tcc ttt gat cgt tta tcc						211
Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser Phe Asp Arg Leu Ser						
	25		30		35	
gct gct cgc gcg aat cac gct tta ggt aat gat ccc aat gca acc gtg						259
Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp Pro Asn Ala Thr Val						
	40		45		50	
gta gag att ctg ctc ggt ggc ttt gag gtg gag gcg ttg cac acc acc						307
Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu Ala Leu His Thr Thr						
	55		60		65	
tcg atc gtg ttc acg gga act gaa gct gaa gtg atg gtt cga acg gct						355
Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val Met Val Arg Thr Ala						
	70		75		80	85
ggt gga caa tcc aaa aat gcc acc acc aac acc atc atc gat gtt gca						403
Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr Ile Ile Asp Val Ala						
	90		95		100	
gct ggt gaa cgt atc cgc gtc gag ccc gca acc tat ggc atg cgt gcc						451
Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr Tyr Gly Met Arg Ala						
	105		110		115	
tac ttt gct gct cgc ggt gga ttt gca gta aaa aaa act ttg gga tct						499
Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys Lys Thr Leu Gly Ser						
	120		125		130	
gct tca acc gat ctg atc tcc cac atg ggc cct tgc ccg atc gag ccc						547
Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro Cys Pro Ile Glu Pro						
	135		140		145	
ggg gat gtc att gac gta gca aca gac att gca gat tct cag tgg tgg						595
Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala Asp Ser Gln Trp Trp						
	150		155		160	165
cca aaa ctt cgg caa ctg ccc acc tta tgg aaa cgc atg cca aca gaa						643
Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys Arg Met Pro Thr Glu						
	170		175		180	
acg ctt acc gtc atc cga ggt cca cgt gac aaa tgg ttc acg caa gaa						691
Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys Trp Phe Thr Gln Glu						
	185		190		195	
tcc ctc aac aac ttt ttt act cag gtg ttt acg gtg agc aat gac tcc						739
Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr Val Ser Asn Asp Ser						
	200		205		210	
aac cgg att ggt ttg cgc atg cac tca agc gag ccg atc caa cat cgt						787
Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu Pro Ile Gln His Arg						
	215		220		225	
gtg gaa ggc gag ctg aaa agt gaa gga atg gtc cgg ggg tcc atc cag						835
Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val Arg Gly Ser Ile Gln						

230	235	240	245	
att ccg cct ggt gga aac ccc gtg gtg ttt ggt ccc gat cat cct gtg				883
Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly Pro Asp His Pro Val				
250		255	260	
acc ggt ggc tat cca gta ata gca gta ctt aca tca agg tcg tgt gat				931
Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr Ser Arg Ser Cys Asp				
265	270	275		
cgt tcg gcc cag ctg ttg ccg ggc gat aaa gtc aga ttt aaa ttg ctt				979
Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val Arg Phe Lys Leu Leu				
280	285	290		
taggaacttt gagcttgctc tgg				1002

<210> 302

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Met Ser Phe Lys Val Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp				
1	5	10	15	
Arg Gly Arg Phe Gly Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser				
20	25	30		
Phe Asp Arg Leu Ser Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp				
35	40	45		
Pro Asn Ala Thr Val Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu				
50	55	60		
Ala Leu His Thr Thr Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val				
65	70	75	80	
Met Val Arg Thr Ala Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr				
85	90	95		
Ile Ile Asp Val Ala Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr				
100	105	110		
Tyr Gly Met Arg Ala Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys				
115	120	125		
Lys Thr Leu Gly Ser Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro				
130	135	140		
Cys Pro Ile Glu Pro Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala				
145	150	155	160	
Asp Ser Gln Trp Trp Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys				
165	170	175		
Arg Met Pro Thr Glu Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys				
180	185	190		
Trp Phe Thr Gln Glu Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr				
195	200	205		

Val Ser Asn Asp Ser Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu
 210 215 220

Pro Ile Gln His Arg Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val
 225 230 235 240

Arg Gly Ser Ile Gln Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly
 245 250 255

Pro Asp His Pro Val Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr
 260 265 270

Ser Arg Ser Cys Asp Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val
 275 280 285

Arg Phe Lys Leu Leu
 290

<210> 303
 <211> 1002
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(979)
 <223> FRXA00574

<400> 303
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tcaagcccgg tgattcagtt cgatttgtgc aggtgaagaa atg agc ttc aaa gta 115
 Met Ser Phe Lys Val
 1 5

att tcc act ggc ccc caa gcc atc ttc caa gac cga ggt cgc ttc ggt 163
 Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp Arg Gly Arg Phe Gly
 10 15 20

ttt gcc agc gct ggt gtt gga acc tca gga tcc ttt gat cgt tta tcc 211
 Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser Phe Asp Arg Leu Ser
 25 30 35

gct gct cgc gcg aat cac gct tta ggt aat gat ccc aat gca acc gtg 259
 Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp Pro Asn Ala Thr Val
 40 45 50

gta gag att ctg ctc ggt ggc ttt gag gtg gag gcg ttg cac acc acc 307
 Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu Ala Leu His Thr Thr
 55 60 65

tcg atc gtg ttc acg gga act gaa gct gaa gtg atg gtt cga acg gct 355
 Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val Met Val Arg Thr Ala
 70 75 80 85

ggt gga caa tcc aaa aat gcc acc acc aac acc atc atc gat gtt gca 403
 Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr Ile Ile Asp Val Ala
 90 95 100

gct ggt gaa cgt atc cgc gtc gag ccc gca acc tat ggc atg cgt gcc 451
 Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr Tyr Gly Met Arg Ala
 105 110 115

tac ttt gct gct cgc ggt gga ttt gca gta aaa aaa act ttg gga tct 499
 Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys Lys Thr Leu Gly Ser
 120 125 130

gct tca acc gat ctg atc tcc cac atg ggc cct tgc ccg atc gag ccc 547
 Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro Cys Pro Ile Glu Pro
 135 140 145

ggg gat gtc att gac gta gca aca gac att gca gat tct cag tgg tgg 595
 Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala Asp Ser Gln Trp Trp
 150 155 160 165

cca aaa ctt cgg caa ctg ccc acc tta tgg aaa cgc atg cca aca gaa 643
 Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys Arg Met Pro Thr Glu
 170 175 180

acg ctt acc gtc atc cga ggt cca cgt gac aaa tgg ttc acg caa gaa 691
 Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys Trp Phe Thr Gln Glu
 185 190 195

tcc ctc aac aac ttt ttt act cag gtg ttt acg gtg agc aat gac tcc 739
 Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr Val Ser Asn Asp Ser
 200 205 210

aac cgg att ggt ttg cgc atg cac tca agc gag ccg atc caa cat cgt 787
 Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu Pro Ile Gln His Arg
 215 220 225

gtg gaa ggc gag ctg aaa agt gaa gga atg gtc cgg ggg tcc atc cag 835
 Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val Arg Gly Ser Ile Gln
 230 235 240 245

att ccg cct ggt gga aac ccc gtg gtg ttt ggt ccc gat cat cct gtg 883
 Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly Pro Asp His Pro Val
 250 255 260

acc ggt ggc tat cca gta ata gca gta ctt aca tca agg tcg tgt gat 931
 Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr Ser Arg Ser Cys Asp
 265 270 275

cgt tcg gcc cag ctg ttg ccg ggc gat aaa gtc aga ttt aaa ttg ctt 979
 Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val Arg Phe Lys Leu Leu
 280 285 290

taggaacttt gagcttgctc tgg 1002

<210> 304

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met Ser Phe Lys Val Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp
 1 5 10 15

Arg Gly Arg Phe Gly Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser

20					25					30					
Phe	Asp	Arg	Leu	Ser	Ala	Ala	Arg	Ala	Asn	His	Ala	Leu	Gly	Asn	Asp
	35						40					45			
Pro	Asn	Ala	Thr	Val	Val	Glu	Ile	Leu	Leu	Gly	Gly	Phe	Glu	Val	Glu
	50					55					60				
Ala	Leu	His	Thr	Thr	Ser	Ile	Val	Phe	Thr	Gly	Thr	Glu	Ala	Glu	Val
	65					70					75				80
Met	Val	Arg	Thr	Ala	Gly	Gly	Gln	Ser	Lys	Asn	Ala	Thr	Thr	Asn	Thr
				85					90					95	
Ile	Ile	Asp	Val	Ala	Ala	Gly	Glu	Arg	Ile	Arg	Val	Glu	Pro	Ala	Thr
			100					105					110		
Tyr	Gly	Met	Arg	Ala	Tyr	Phe	Ala	Ala	Arg	Gly	Gly	Phe	Ala	Val	Lys
		115					120					125			
Lys	Thr	Leu	Gly	Ser	Ala	Ser	Thr	Asp	Leu	Ile	Ser	His	Met	Gly	Pro
	130					135					140				
Cys	Pro	Ile	Glu	Pro	Gly	Asp	Val	Ile	Asp	Val	Ala	Thr	Asp	Ile	Ala
	145					150			155						160
Asp	Ser	Gln	Trp	Trp	Pro	Lys	Leu	Arg	Gln	Leu	Pro	Thr	Leu	Trp	Lys
			165						170					175	
Arg	Met	Pro	Thr	Glu	Thr	Leu	Thr	Val	Ile	Arg	Gly	Pro	Arg	Asp	Lys
			180					185					190		
Trp	Phe	Thr	Gln	Glu	Ser	Leu	Asn	Asn	Phe	Phe	Thr	Gln	Val	Phe	Thr
		195					200					205			
Val	Ser	Asn	Asp	Ser	Asn	Arg	Ile	Gly	Leu	Arg	Met	His	Ser	Ser	Glu
	210					215					220				
Pro	Ile	Gln	His	Arg	Val	Glu	Gly	Glu	Leu	Lys	Ser	Glu	Gly	Met	Val
	225					230					235				240
Arg	Gly	Ser	Ile	Gln	Ile	Pro	Pro	Gly	Gly	Asn	Pro	Val	Val	Phe	Gly
			245						250					255	
Pro	Asp	His	Pro	Val	Thr	Gly	Gly	Tyr	Pro	Val	Ile	Ala	Val	Leu	Thr
			260					265					270		
Ser	Arg	Ser	Cys	Asp	Arg	Ser	Ala	Gln	Leu	Leu	Pro	Gly	Asp	Lys	Val
	275						280					285			
Arg	Phe	Lys	Leu	Leu											
	290														

<210> 305

<211> 573

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(550)

<223> RXN00589

<400> 305

ccgttatctc cgtaactggt gtttctgcag aaccatacaa ctcagcaaaa gccgcgacac 60

tccgcggcaa aaactaacca aggatttaaa agtcttcaaa atg aca act ctt tca 115
 Met Thr Thr Leu Ser
 1 5

cgt aag ttc ttc gtt tct gct acc aca gcc ctg gcg gca gtc gca ctg 163
 Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu Ala Ala Val Ala Leu
 10 15 20

gtt gcg tgt tcc cct aat gag att gat tct gaa ctg aag gtg cca acg 211
 Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu Leu Lys Val Pro Thr
 25 30 35

gca act ggc gtt tct tta cct tcg aag aac gtt tcc gcg acc tca act 259
 Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val Ser Ala Thr Ser Thr
 40 45 50

gct act aca gat gag gat gcg cct ggc tac att gat tgc gta gcc gca 307
 Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile Asp Cys Val Ala Ala
 55 60 65

cca act cag caa cct gct gaa atc tca cta aac tgt gca atg gat att 355
 Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn Cys Ala Met Asp Ile
 70 75 80 85

gat cgg ctg acg gat att tct tgg agc gaa tgg gat act gat tcc gca 403
 Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp Asp Thr Asp Ser Ala
 90 95 100

act gga acc ggt acc cgc atc gta acc gct gca aat ggt caa gag acc 451
 Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala Asn Gly Gln Glu Thr
 105 110 115

gaa acc gaa gat att gag gtg aag ctt tcc ttc ccc acc gag tct tcc 499
 Glu Thr Glu Asp Ile Glu Val Lys Leu Ser Phe Pro Thr Glu Ser Ser
 120 125 130

caa ggc cta gtg ttc act cag gtc acc gtc gat gga cag gtt ctg ttc 547
 Gln Gly Leu Val Phe Thr Gln Val Thr Val Asp Gly Gln Val Leu Phe
 135 140 145

ctc taatcctcca taattagaga gcg 573
 Leu
 150

<210> 306

<211> 150

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

Met Thr Thr Leu Ser Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu
 1 5 10 15

Ala Ala Val Ala Leu Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu

20	25	30
Leu Lys Val Pro Thr Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val		
35	40	45
Ser Ala Thr Ser Thr Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile		
50	55	60
Asp Cys Val Ala Ala Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn		
65	70	75
Cys Ala Met Asp Ile Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp		
85	90	95
Asp Thr Asp Ser Ala Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala		
100	105	110
Asn Gly Gln Glu Thr Glu Thr Glu Asp Ile Glu Val Lys Leu Ser Phe		
115	120	125
Pro Thr Glu Ser Ser Gln Gly Leu Val Phe Thr Gln Val Thr Val Asp		
130	135	140
Gly Gln Val Leu Phe Leu		
145	150	

<210> 307
 <211> 463
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(463)
 <223> FRXA00589

<400> 307
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 tccgcggcaa aaactaacca aggatttaaa agtcttcaaa atg aca act ctt tca 115
 Met Thr Thr Leu Ser
 1 5
 cgt aag ttc ttc gtt tct gct acc aca gcc ctg gcg gca gtc gca ctg 163
 Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu Ala Ala Val Ala Leu
 10 15 20
 gtt gcg tgt tcc cct aat gag att gat tct gaa ctg aag gtg cca acg 211
 Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu Leu Lys Val Pro Thr
 25 30 35
 gca act ggc gtt tct tta cct tcg aag aac gtt tcc gcg acc tca act 259
 Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val Ser Ala Thr Ser Thr
 40 45 50
 gct act aca gat gag gat gcg cct ggc tac att gat tgc gta gcc gca 307
 Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile Asp Cys Val Ala Ala
 55 60 65
 cca act cag caa cct gct gaa atc tca cta aac tgt gca atg gat att 355

Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn Cys Ala Met Asp Ile
 70 75 80 85
 gat cgg ctc acg gat att tct tgg agc gaa tgg gat act gat tcc gca 403
 Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp Asp Thr Asp Ser Ala
 90 95 100
 act gga acc ggt acc cgc atc gta acc gct gca aat ggt caa gag acc 451
 Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala Asn Gly Gln Glu Thr
 105 110 115
 gaa acc gaa gat 463
 Glu Thr Glu Asp
 120

<210> 308
 <211> 121
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 308
 Met Thr Thr Leu Ser Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu
 1 5 10 15
 Ala Ala Val Ala Leu Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu
 20 25 30
 Leu Lys Val Pro Thr Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val
 35 40 45
 Ser Ala Thr Ser Thr Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile
 50 55 60
 Asp Cys Val Ala Ala Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn
 65 70 75 80
 Cys Ala Met Asp Ile Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp
 85 90 95
 Asp Thr Asp Ser Ala Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala
 100 105 110
 Asn Gly Gln Glu Thr Glu Thr Glu Asp
 115 120

<210> 309
 <211> 468
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(445)
 <223> RXN00616

<400> 309
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 caatggaata cagattgagt tgatcaaagg agaaccacca atg aaa tca ctc ccc 115

	Met	Lys	Ser	Leu	Pro	
	1				5	
cgt ttc gcc cca ctg att acg att ctg gct ctg ctc gta ctc gtt gcc						163
Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu Leu Val Leu Val Ala						
				10	15	20
atc gga gga tct gca ctg gca aat aat cgt gct acc cct aat gtg gaa						211
Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala Thr Pro Asn Val Glu						
			25		30	35
agt gaa ccc gcc acg gtc aac cag cgt tcc act ccc aca act tcc gcg						259
Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr Pro Thr Thr Ser Ala						
		40		45		50
tat gag ccc cct gct aca gaa tct ccg gaa gaa cca acc aca caa att						307
Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu Pro Thr Thr Gln Ile						
	55			60		65
caa gaa tcc cca gta caa ccc cca gtt cct gcc ccc gct caa att cct						355
Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala Pro Ala Gln Ile Pro						
	70			75	80	85
caa gcc cca caa gtt cca ctc aat tat cag tac tat gac gat gac tgg						403
Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr Tyr Asp Asp Asp Trp						
		90		95		100
gac gac gac gat gat gac ttc gac gac gac tgg gac gac gac						445
Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp Asp Asp Asp						
		105		110		115
taactaaccctctgaggcact ttc						468

<210> 310

<211> 115

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Met	Lys	Ser	Leu	Pro	Arg	Phe	Ala	Pro	Leu	Ile	Thr	Ile	Leu	Ala	Leu
1				5					10					15	

Leu	Val	Leu	Val	Ala	Ile	Gly	Gly	Ser	Ala	Leu	Ala	Asn	Asn	Arg	Ala
			20					25					30		

Thr	Pro	Asn	Val	Glu	Ser	Glu	Pro	Ala	Thr	Val	Asn	Gln	Arg	Ser	Thr
		35					40					45			

Pro	Thr	Thr	Ser	Ala	Tyr	Glu	Pro	Pro	Ala	Thr	Glu	Ser	Pro	Glu	Glu
	50					55					60				

Pro	Thr	Thr	Gln	Ile	Gln	Glu	Ser	Pro	Val	Gln	Pro	Pro	Val	Pro	Ala
	65				70					75					80

Pro	Ala	Gln	Ile	Pro	Gln	Ala	Pro	Gln	Val	Pro	Leu	Asn	Tyr	Gln	Tyr
				85					90					95	

Tyr	Asp	Asp	Asp	Trp	Asp	Asp	Asp	Asp	Asp	Asp	Phe	Asp	Asp	Asp	Trp
			100				105						110		

Asp Asp Asp
115

<210> 311
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(445)
<223> FRXA00616

<400> 311
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caatggaata cagattgagt tgatcaaagg agaacccccca atg aaa tca ctc ccc 115
Met Lys Ser Leu Pro
1 5
cgt ttc gcc cca ctg att acg att ctg gct ctg ctc gta ctc gtt gcc 163
Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu Leu Val Leu Val Ala
10 15 20
atc gga gga tct gca ctg gca aat aat cgt gct acc cct aat gtg gaa 211
Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala Thr Pro Asn Val Glu
25 30 35
agt gaa ccc gcc acg gtc aac cag cgt tcc act ccc aca act tcc gcg 259
Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr Pro Thr Thr Ser Ala
40 45 50
tat gag ccc cct gct aca gaa tct ccg gaa gaa cca acc aca caa att 307
Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu Pro Thr Thr Gln Ile
55 60 65
caa gaa tcc cca gta caa ccc cca gtt cct gcc ccc gct caa att cct 355
Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala Pro Ala Gln Ile Pro
70 75 80 85
caa gcc cca caa gtt cca ctc aat tat cag tac tat gac gat gac tgg 403
Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr Tyr Asp Asp Asp Trp
90 95 100
gac gac gac gat gat gac ttc gac gac gac tgg gac gac gac 445
Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp Asp Asp Asp
105 110 115
taactaaccct ctgaggcact ttc 468

<210> 312
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 312
Met Lys Ser Leu Pro Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu
1 5 10 15

Leu Val Leu Val Ala Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala
 20 25 30
 Thr Pro Asn Val Glu Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr
 35 40 45
 Pro Thr Thr Ser Ala Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu
 50 55 60
 Pro Thr Thr Gln Ile Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala
 65 70 75 80
 Pro Ala Gln Ile Pro Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr
 85 90 95
 Tyr Asp Asp Asp Trp Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp
 100 105 110
 Asp Asp Asp
 115

<210> 313
 <211> 756
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(733)
 <223> RXN00647

<400> 313
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 agtcgagaaa taaccgaccg atgaaagagt tgagacgata atg ggc atc ttc gaa 115
 Met Gly Ile Phe Glu
 1 5
 gcc atc cga gcc gca cgc gcg aag acc aaa gct gag atc aaa gca gcc 163
 Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala Glu Ile Lys Ala Ala
 10 15 20
 gag gca aaa gta aaa act gag gcg aaa aac aaa gca aag cta gat ctc 211
 Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys Ala Lys Leu Asp Leu
 25 30 35
 aag cgc gag aag ctt ctt gtc cag cag gaa aag aat ctg ctc aag gtt 259
 Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys Asn Leu Leu Lys Val
 40 45 50
 gaa gaa aag ggc ctg aag aag cgc aac aag cat gag ctg aag atg gcc 307
 Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His Glu Leu Lys Met Ala
 55 60 65
 aaa aat atc ctt gag caa aag cgc caa gga cgc cta aac aaa gac aag 355
 Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg Leu Asn Lys Asp Lys
 70 75 80 85
 gtg aag cgc tgg gct ggc acc gca cgt gtg ctc act cca cta ctg ctg 403
 Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu Thr Pro Leu Leu Leu

90	95	100	
cct att att tat cga ctc tcc acc gaa gca cgc gat cag gtt gtt aag			451
Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg Asp Gln Val Val Lys			
105	110	115	
gga cgt gcc cgt cgt gca ggt gtc acc gcg gag cag ctt agc caa ttc			499
Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu Gln Leu Ser Gln Phe			
120	125	130	
gca ggt cac gca gca gcg ctg aag gct cgt att caa ggt gtt cgc gaa			547
Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile Gln Gly Val Arg Glu			
135	140	145	
acc gca aag aac tcc agc ctc cct gct ggc ttt gta cgc gat gtt gaa			595
Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe Val Arg Asp Val Glu			
150	155	160	165
gag cgt ctc aat gag ctc gag gct gct gcg aat aac tct gag ttc atg			643
Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn Asn Ser Glu Phe Met			
170	175	180	
tct cca cag cag agg aac cgt gcg cac cag tcg atc agt cgt gat ctg			691
Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser Ile Ser Arg Asp Leu			
185	190	195	
aac cag gtg tca gat cag att cag gat cga cta ctg gac aag			733
Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu Leu Asp Lys			
200	205	210	
tagctgctgg tcgagtcgct gcc			756

<210> 314

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

Met Gly Ile Phe Glu Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala
1 5 10 15

Glu Ile Lys Ala Ala Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys
20 25 30

Ala Lys Leu Asp Leu Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys
35 40 45

Asn Leu Leu Lys Val Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His
50 55 60

Glu Leu Lys Met Ala Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg
65 70 75 80

Leu Asn Lys Asp Lys Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu
85 90 95

Thr Pro Leu Leu Leu Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg
100 105 110

Asp Gln Val Val Lys Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu

115					120					125						
Gln	Leu	Ser	Gln	Phe	Ala	Gly	His	Ala	Ala	Ala	Leu	Lys	Ala	Arg	Ile	
130					135					140						
Gln	Gly	Val	Arg	Glu	Thr	Ala	Lys	Asn	Ser	Ser	Leu	Pro	Ala	Gly	Phe	
145					150					155					160	
Val	Arg	Asp	Val	Glu	Glu	Arg	Leu	Asn	Glu	Leu	Glu	Ala	Ala	Ala	Asn	
165					170					175						
Asn	Ser	Glu	Phe	Met	Ser	Pro	Gln	Gln	Arg	Asn	Arg	Ala	His	Gln	Ser	
180					185					190						
Ile	Ser	Arg	Asp	Leu	Asn	Gln	Val	Ser	Asp	Gln	Ile	Gln	Asp	Arg	Leu	
195					200					205						
Leu Asp Lys																
210																

<210> 315
 <211> 756
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(733)
 <223> FRXA00647

<400> 315
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 agtcgagaaa taaccgaccg atgaaagagt tgagacgata atg ggc atc ttc gaa 115
 Met Gly Ile Phe Glu 5
 gcc atc cga gcc gca cgc gcg aag acc aaa gct gag atc aaa gca gcc 163
 Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala Glu Ile Lys Ala Ala 20
 gag gca aaa gta aaa act gag gcg aaa aac aaa gca aag cta gat ctc 211
 Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys Ala Lys Leu Asp Leu 35
 aag cgc gag aag ctt ctt gtc cag cag gaa aag aat ctg ctc aag gtt 259
 Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys Asn Leu Leu Lys Val 50
 gaa gaa aag ggc ctg aag aag cgc aac aag cat gag ctg aag atg gcc 307
 Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His Glu Leu Lys Met Ala 65
 aaa aat atc ctt gag caa aag cgc caa gga cgc cta aac aaa gac aag 355
 Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg Leu Asn Lys Asp Lys 85
 gtg aag cgc tgg gct ggc acc gca cgt gtg ctc act cca cta ctg ctg 403
 Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu Thr Pro Leu Leu Leu 100

cct att att tat cga ctc tcc acc gaa gca cgc gat cag gtt gtt aag 451
 Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg Asp Gln Val Val Lys
 105 110 115

 gga cgt gcc cgt cgt gca ggt gtc acc gcg gag cag ctt agc caa ttc 499
 Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu Gln Leu Ser Gln Phe
 120 125 130

 gca ggt cac gca gca gcg ctg aag gct cgt att caa ggt gtt cgc gaa 547
 Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile Gln Gly Val Arg Glu
 135 140 145

 acc gca aag aac tcc agc ctc cct gct ggc ttt gta cgc gat gtt gaa 595
 Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe Val Arg Asp Val Glu
 150 155 160 165

 gag cgt ctc aat gag ctc gag gct gct gcg aat aac tct gag ttc atg 643
 Glu Arg Leu Asn Glu Leu Glu Ala Ala Asn Asn Ser Glu Phe Met
 170 175 180

 tct cca cag cag agg aac cgt gcg cac cag tcg atc agt cgt gat ctg 691
 Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser Ile Ser Arg Asp Leu
 185 190 195

 aac cag gtg tca gat cag att cag gat cga cta ctg gac aag 733
 Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu Leu Asp Lys
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 tagctgctgg tcgagtcgct gcc 756

<210> 316

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

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Glu Ile Lys Ala Ala Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys
 20 25 30

Ala Lys Leu Asp Leu Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys
 35 40 45

Asn Leu Leu Lys Val Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His
 50 55 60

Glu Leu Lys Met Ala Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg
 65 70 75 80

Leu Asn Lys Asp Lys Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu
 85 90 95

Thr Pro Leu Leu Leu Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg
 100 105 110

Asp Gln Val Val Lys Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu
 115 120 125

Gln Leu Ser Gln Phe Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile
 130 135 140

Gln Gly Val Arg Glu Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe
 145 150 155 160

Val Arg Asp Val Glu Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn
 165 170 175

Asn Ser Glu Phe Met Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser
 180 185 190

Ile Ser Arg Asp Leu Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu
 195 200 205

Leu Asp Lys
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<210> 317

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(865)

<223> RXN00653

<400> 317

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cgcggaatct tctcgcaatg gtaaaaagcc gcggcctcga gtg agt gtt tcc cag 115
 Val Ser Val Ser Gln
 1 5

gtt gtt ggt gaa atc ttg ctc acc gta ggc att ttg gcc ttg tta ttc 163
 Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile Leu Ala Leu Leu Phe
 10 15 20

gca tac tat gag gcc tat tgg acc aac gtg gaa tct ggg aaa tta caa 211
 Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu Ser Gly Lys Leu Gln
 25 30 35

gaa tcg gct ggt caa aag ctt gat gaa gac tgg aat gaa gct cgg gtg 259
 Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp Asn Glu Ala Arg Val
 40 45 50

aat cct cga caa aag ctc acc ccg gaa ctt ggt gag gca ttt gcc cgg 307
 Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly Glu Ala Phe Ala Arg
 55 60 65

atg tat gtt cca gct ttc ggc tct gac ttc aac ttc gca gtg att gaa 355
 Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn Phe Ala Val Ile Glu
 70 75 80 85

gga acc gat gag gaa gac ctt ctt gcc ggt cct ggc cgt tat gtg gat 403
 Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro Gly Arg Tyr Val Asp
 90 95 100

tcc caa atg cct ggt gaa gcc gga aac ttt gca gtg gca ggc cac cga 451
 Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala Val Ala Gly His Arg
 105 110 115

gtg ggc aag ggt gcg cca ttc aat gat cta gga aac ctg gaa gtc tgc 499
 Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly Asn Leu Glu Val Cys
 120 125 130

gat gcg atc gtg gtg gag act tac aat tcc tgg gat gtg tac cgc gtg 547
 Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp Asp Val Tyr Arg Val
 135 140 145

atg ccg atg tcc acc aac ggt gca gat cgt gca gca gaa gct gcg gat 595
 Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala Ala Glu Ala Ala Asp
 150 155 160 165

tgc ttc aac gaa aac cag gtc agc cgc atg gct gaa ggt gac tat gtg 643
 Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala Glu Gly Asp Tyr Val
 170 175 180

aat gtg tcc gga cga agc atc acc act ccg gat cgc atc gat gcc acc 691
 Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp Arg Ile Asp Ala Thr
 185 190 195

tac ccc aca ccg ggc gtc ttc gac act gca gtg cgt gaa gga tca gaa 739
 Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val Arg Glu Gly Ser Glu
 200 205 210

gct ctg ctt acc ttg acc acg tgt cac ccg cag ttc tcc aac gct gag 787
 Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln Phe Ser Asn Ala Glu
 215 220 225

cgc atg att gtg cac gca atg ttg gtg gaa gaa atc gat aaa tca agt 835
 Arg Met Ile Val His Ala Met Leu Val Glu Glu Ile Asp Lys Ser Ser
 230 235 240 245

ggc gaa cgc cct gca gct ttg gag gaa aac taaatgtatt cacttctgtg 885
 Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
 250 255

gca 888

<210> 318

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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Ser Gly Lys Leu Gln Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp
 35 40 45

Asn Glu Ala Arg Val Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly
 50 55 60

Glu Ala Phe Ala Arg Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn
 65 70 75 80
 Phe Ala Val Ile Glu Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro
 85 90 95
 Gly Arg Tyr Val Asp Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala
 100 105 110
 Val Ala Gly His Arg Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly
 115 120 125
 Asn Leu Glu Val Cys Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp
 130 135 140
 Asp Val Tyr Arg Val Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala
 145 150 155 160
 Ala Glu Ala Ala Asp Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala
 165 170 175
 Glu Gly Asp Tyr Val Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp
 180 185 190
 Arg Ile Asp Ala Thr Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val
 195 200 205
 Arg Glu Gly Ser Glu Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln
 210 215 220
 Phe Ser Asn Ala Glu Arg Met Ile Val His Ala Met Leu Val Glu Glu
 225 230 235 240
 Ile Asp Lys Ser Ser Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
 245 250 255

<210> 319
 <211> 888
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(865)
 <223> FRXA00653

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 Val Ser Val Ser Gln
 1 5

gtt gtt ggt gaa atc ttg ctc acc gta ggc att ttg gcc ttg tta ttc 163
 Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile Leu Ala Leu Leu Phe
 10 15 20

gca tac tat gag gcc tat tgg acc aac gtg gaa tct ggg aaa tta caa 211
 Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu Ser Gly Lys Leu Gln
 25 30 35

gaa tcg gct ggt. caa aag ctt gat gaa gac tgg aat gaa gct cgg gtg 259
 Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp Asn Glu Ala Arg Val
 40 45 50

aat cct cga caa aag ctc acc ccg gaa ctt ggt gag gca ttt gcc cgg 307
 Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly Glu Ala Phe Ala Arg
 55 60 65

atg tat gtt cca gct ttc ggc tct gac ttc aac ttc gca gtg att gaa 355
 Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn Phe Ala Val Ile Glu
 70 75 80 85

gga acc gat gag gaa gac ctt ctt gcc ggt cct ggc cgt tat gtg gat 403
 Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro Gly Arg Tyr Val Asp
 90 95 100

tcc caa atg cct ggt gaa gcc gga aac ttt gca gtg gca ggc cac cga 451
 Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala Val Ala Gly His Arg
 105 110 115

gtg ggc aag ggt gcg cca ttc aat gat cta gga aac ctg gaa gtc tgc 499
 Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly Asn Leu Glu Val Cys
 120 125 130

gat gcg atc gtg gtg gag act tac aat tcc tgg gat gtg tac cgc gtg 547
 Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp Asp Val Tyr Arg Val
 135 140 145

atg ccg atg tcc acc aac ggt gca gat cgt gca gca gaa gct gcg gat 595
 Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala Ala Glu Ala Ala Asp
 150 155 160 165

tgc ttc aac gaa aac cag gtc agc cgc atg gct gaa ggt gac tat gtg 643
 Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala Glu Gly Asp Tyr Val
 170 175 180

aat gtg tcc gga cga agc atc acc act ccg gat cgc atc gat gcc acc 691
 Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp Arg Ile Asp Ala Thr
 185 190 195

tac ccc aca ccg ggc gtc ttc gac act gca gtg cgt gaa gga tca gaa 739
 Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val Arg Glu Gly Ser Glu
 200 205 210

gct ctg ctt acc ttg acc acg tgt cac ccg cag ttc tcc aac gct gag 787
 Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln Phe Ser Asn Ala Glu
 215 220 225

cgc atg att gtg cac gca atg ttg gtg gaa gaa atc gat aaa tca agt 835
 Arg Met Ile Val His Ala Met Leu Val Glu Glu Ile Asp Lys Ser Ser
 230 235 240 245

ggc gaa cgc cct gca gct ttg gag gaa aac taaatgtatt cacttctgtg 885
 Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
 250 255

gca 888

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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Ser Gly Lys Leu Gln Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp
35 40 45

Asn Glu Ala Arg Val Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly
50 55 60

Glu Ala Phe Ala Arg Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn
65 70 75 80

Phe Ala Val Ile Glu Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro
85 90 95

Gly Arg Tyr Val Asp Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala
100 105 110

Val Ala Gly His Arg Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly
115 120 125

Asn Leu Glu Val Cys Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp
130 135 140

Asp Val Tyr Arg Val Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala
145 150 155 160

Ala Glu Ala Ala Asp Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala
165 170 175

Glu Gly Asp Tyr Val Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp
180 185 190

Arg Ile Asp Ala Thr Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val
195 200 205

Arg Glu Gly Ser Glu Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln
210 215 220

Phe Ser Asn Ala Glu Arg Met Ile Val His Ala Met Leu Val Glu Glu
225 230 235 240

Ile Asp Lys Ser Ser Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
245 250 255

<210> 321

<211> 1392

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1369)

<223> RXN00662

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                                   Val Ser Thr Ile Pro
                                   1 5

ctg aat cgt cta gcc gtt atc gct gcc atc att ggt gtc ggt acc ggg 163
Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile Gly Val Gly Thr Gly
              10              15              20

ctg ttt gtt gct gca ctg aac tgg tct gcc att ggc gtg gag cgt tta 211
Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile Gly Val Glu Arg Leu
              25              30              35

gtt tat ggc gct gac cat ttg cat aat tac aat ccg gtg gcc aat gtg 259
Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn Pro Val Ala Asn Val
              40              45              50

tcg cca ctt cgc ctg tcc atc acg gtg att gtg ctt agc gtg gtg gcc 307
Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val Leu Ser Val Val Ala
              55              60              65

tcc tgg gcg tgg ttt ttt gtg cac cgc acg ggg ccg aaa gag gtt tcg 355
Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly Pro Lys Glu Val Ser
              70              75              80              85

att gtg ggt gcg atc cgg ggc gag aag atg ccg att ttg gag acc ata 403
Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro Ile Leu Glu Thr Ile
              90              95              100

gcg tcc gca ttt ttg cag gtc acc acg gtt gct gcg ggt gcg ccg gtg 451
Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala Ala Gly Ala Pro Val
              105              110              115

ggt gca gag aac gct cca cgt att gct gga gcc ttg gtg gga gag ccg 499
Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala Leu Val Gly Glu Arg
              120              125              130

ttt agt cgg tgg ttg cag ctc gat att gat gca aag cgc atc ttg gtg 547
Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala Lys Arg Ile Leu Val
              135              140              145

gcc tct gcc gcg gga gct ggt ttg gga gca agc ttc cac ctt ccc cta 595
Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser Phe His Leu Pro Leu
              150              155              160              165

gca ggc gtg ctg ttt gcc ctt gag gtc cta ctg gtt gag gcc tcc act 643
Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu Val Glu Ala Ser Thr
              170              175              180

cgg acc gtg gtt atc gca att atc acc acg acc gcc gcc gtt gcc acc 691
Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr Ala Ala Val Ala Thr
              185              190              195

act gga ttt ttc gtg caa acc cca gat gtg ttc agc act gtc ccg ctg 739
Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe Ser Thr Val Pro Leu
              200              205              210

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acg gaa agc cca tgg atg ctg ctt gcc gcg atg gtc acc gga gta gtc 787
 Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met Val Thr Gly Val Val
 215 220 225

gcc ggc atg tgc ggg cac tgg ttt tca gcg gcg gcg cac aaa atg gcg 835
 Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala Ala His Lys Met Ala
 230 235 240 245

cag gcc tcg ccc aag ggt gtg aag att ttg tgg cag atg ccg ttg ggt 883
 Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp Gln Met Pro Leu Gly
 250 255 260

ttc gtg gtg atc gct gcg gtg att tat ttc ttc ccc gaa acc ctg gcg 931
 Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe Pro Glu Thr Leu Ala
 265 270 275

aat ccc cgt tgg ctt gcc gat tcc atg ctc ggc gat ggc ctg atc ctc 979
 Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly Asp Gly Leu Ile Leu
 280 285 290

agc acc att tta ttg gta ctt gtt ctg cgc acc gcc atg ttt ttg ctc 1027
 Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr Ala Met Phe Leu Leu
 295 300 305

gcc ttc cgc gtg ggc atg gtc ggc ggt aac ctg atc ccc gca ttc gca 1075
 Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu Ile Pro Ala Phe Ala
 310 315 320 325

ctc gga tcc atg gtc ggt ggg gta gtg ggt gct gta ttg gaa ccc atc 1123
 Leu Gly Ser Met Val Gly Gly Val Val Gly Ala Val Leu Glu Pro Ile
 330 335 340

act aac gtc ccg atc gcc gct ttt gcg ctg ctt ggc gcc gcc gca ttt 1171
 Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu Gly Ala Ala Ala Phe
 345 350 355

ttg tcc acc acc atg gca gcg cca ctg ttc ggg ctc atc gcc gca gtg 1219
 Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly Leu Ile Ala Ala Val
 360 365 370

gaa ttc acc gac atg gaa gcc caa ggc tac ctt ccg att ttc ctc gca 1267
 Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu Pro Ile Phe Leu Ala
 375 380 385

gta gcc tcc gcg gtc ctc gcc gtg cgc gtg tgg tct gtc atc gcc aag 1315
 Val Ala Ser Ala Val Leu Ala Val Arg Val Trp Ser Val Ile Ala Lys
 390 395 400 405

cac gag ctc cgc gcc atc ccg atc acg tac gcg agc tgg acg ggc gag 1363
 His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala Ser Trp Thr Gly Glu
 410 415 420

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 Leu Lys

<210> 322

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

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 Gly Val Glu Arg Leu Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn
 35 40 45
 Pro Val Ala Asn Val Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val
 50 55 60
 Leu Ser Val Val Ala Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly
 65 70 75 80
 Pro Lys Glu Val Ser Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro
 85 90 95
 Ile Leu Glu Thr Ile Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala
 100 105 110
 Ala Gly Ala Pro Val Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala
 115 120 125
 Leu Val Gly Glu Arg Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala
 130 135 140
 Lys Arg Ile Leu Val Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser
 145 150 155 160
 Phe His Leu Pro Leu Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu
 165 170 175
 Val Glu Ala Ser Thr Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr
 180 185 190
 Ala Ala Val Ala Thr Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe
 195 200 205
 Ser Thr Val Pro Leu Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met
 210 215 220
 Val Thr Gly Val Val Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala
 225 230 235 240
 Ala His Lys Met Ala Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp
 245 250 255
 Gln Met Pro Leu Gly Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe
 260 265 270
 Pro Glu Thr Leu Ala Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly
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 Asp Gly Leu Ile Leu Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr
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 Ala Met Phe Leu Leu Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu

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				Val	Ser	Thr	Ile	Pro								
				1				5								
ctg	aat	cgt	cta	gcc	gtt	atc	gct	gcc	atc	att	ggt	gtc	ggt	acc	ggg	163
Leu	Asn	Arg	Leu	Ala	Val	Ile	Ala	Ala	Ile	Ile	Gly	Val	Gly	Thr	Gly	
				10					15					20		
ctg	ttt	gtt	gct	gca	ctg	aac	tgg	tct	gcc	att	ggc	gtg	gag	cgt	tta	211
Leu	Phe	Val	Ala	Ala	Leu	Asn	Trp	Ser	Ala	Ile	Gly	Val	Glu	Arg	Leu	
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gtt	tat	ggc	gct	gac	cat	ttg	cat	aat	tac	aat	ccg	gtg	gcc	aat	gtg	259
Val	Tyr	Gly	Ala	Asp	His	Leu	His	Asn	Tyr	Asn	Pro	Val	Ala	Asn	Val	
		40					45					50				
tcg	cca	ctt	cgc	ctg	tcc	atc	acg	gtg	att	gtg	ctt	agc	gtg	gtg	gcc	307
Ser	Pro	Leu	Arg	Leu	Ser	Ile	Thr	Val	Ile	Val	Leu	Ser	Val	Val	Ala	
	55					60					65					
tcc	tgg	gcg	tgg	ttt	ttt	gtg	cac	cgc	acg	ggg	ccg	aaa	gag	gtt	tcg	355
Ser	Trp	Ala	Trp	Phe	Phe	Val	His	Arg	Thr	Gly	Pro	Lys	Glu	Val	Ser	
70					75					80					85	

att gtg ggt gcg atc cgg ggc gag aag atg ccg att ttg gag acc ata	403
Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro Ile Leu Glu Thr Ile	
90 95 100	
gcg tcc gca ttt ttg cag gtc acc acg gtt gct gcg ggt gcg ccg gtg	451
Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala Ala Gly Ala Pro Val	
105 110 115	
ggt gca gag aac gct cca cgt att gct gga gcc ttg gtg gga gag cgg	499
Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala Leu Val Gly Glu Arg	
120 125 130	
ttt agt cgg tgg ttg cag ctc gat att gat gca aag cgc atc ttg gtg	547
Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala Lys Arg Ile Leu Val	
135 140 145	
gcc tct gcc gcg gga gct ggt ttg gga gca agc ttc cac ctt ccc cta	595
Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser Phe His Leu Pro Leu	
150 155 160 165	
gca ggc gtg ctg ttt gcc ctt gag gtc cta ctg gtt gag gcc tcc act	643
Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu Val Glu Ala Ser Thr	
170 175 180	
cgg acc gtg gtt atc gca att atc acc acg acc gcc gcc gtt gcc acc	691
Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr Ala Ala Val Ala Thr	
185 190 195	
act gga ttt ttc gtg caa acc cca gat gtg ttc agc act gtc ccg ctg	739
Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe Ser Thr Val Pro Leu	
200 205 210	
acg gaa agc cca tgg atg ctg ctt gcc gcg atg gtc acc gga gta gtc	787
Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met Val Thr Gly Val Val	
215 220 225	
gcc ggc atg tgc ggg cac tgg ttt tca gcg gcg gcg cac aaa atg gcg	835
Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala Ala His Lys Met Ala	
230 235 240 245	
cag gcc tcg ccc aag ggt gtg aag att ttg tgg cag atg ccg ttg ggt	883
Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp Gln Met Pro Leu Gly	
250 255 260	
ttc gtg gtg atc gct gcg gtg att tat ttc ttc ccc gaa acc ctg gcg	931
Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe Pro Glu Thr Leu Ala	
265 270 275	
aat ccc cgt tgg ctt gcc gat tcc atg ctc ggc gat ggc ctg atc ctc	979
Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly Asp Gly Leu Ile Leu	
280 285 290	
agc acc att tta ttg gta ctt gtt ctg cgc acc gcc atg ttt ttg ctc	1027
Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr Ala Met Phe Leu Leu	
295 300 305	
gcc ttc cgc gtg ggc atg gtc ggc ggt aac ctg atc ccc gca ttc gca	1075
Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu Ile Pro Ala Phe Ala	
310 315 320 325	
ctc gga tcc atg gtc ggt ggg gta gtg ggt gct gta ttg gaa ccc atc	1123

Leu Gly Ser Met Val Gly Gly Val Val Gly Ala Val Leu Glu Pro Ile
 330 335 340
 act aac gtc ccg atc gcc gct ttt gcg ctg ctt ggc gcc gcc gca ttt 1171
 Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu Gly Ala Ala Ala Phe
 345 350 355
 ttg tcc acc acc atg gca gcg cca ctg ttc ggg ctc atc gcc gca gtg 1219
 Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly Leu Ile Ala Ala Val
 360 365 370
 gaa ttc acc gac atg gaa gcc caa ggc tac ctt ccg att ttc ctc gca 1267
 Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu Pro Ile Phe Leu Ala
 375 380 385
 gta gcc tcc gcg gtc ctc gcc gtg cgc gtg tgg tct gtc atc gcc aag 1315
 Val Ala Ser Ala Val Leu Ala Val Arg Val Trp Ser Val Ile Ala Lys
 390 395 400 405
 cac gag ctc cgc gcc atc ccg atc acg tac gcg agc tgg acg ggc gag 1363
 His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala Ser Trp Thr Gly Glu
 410 415 420
 ctt aaa taagcttgtc gacgcctccc tcc 1392
 Leu Lys

<210> 324
 <211> 423
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 324
 Val Ser Thr Ile Pro Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile
 1 5 10 15
 Gly Val Gly Thr Gly Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile
 20 25 30
 Gly Val Glu Arg Leu Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn
 35 40 45
 Pro Val Ala Asn Val Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val
 50 55 60
 Leu Ser Val Val Ala Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly
 65 70 75 80
 Pro Lys Glu Val Ser Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro
 85 90 95
 Ile Leu Glu Thr Ile Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala
 100 105 110
 Ala Gly Ala Pro Val Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala
 115 120 125
 Leu Val Gly Glu Arg Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala
 130 135 140

Lys Arg Ile Leu Val Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser
 145 150 155 160
 Phe His Leu Pro Leu Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu
 165 170 175
 Val Glu Ala Ser Thr Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr
 180 185 190
 Ala Ala Val Ala Thr Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe
 195 200 205
 Ser Thr Val Pro Leu Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met
 210 215 220
 Val Thr Gly Val Val Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala
 225 230 235 240
 Ala His Lys Met Ala Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp
 245 250 255
 Gln Met Pro Leu Gly Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe
 260 265 270
 Pro Glu Thr Leu Ala Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly
 275 280 285
 Asp Gly Leu Ile Leu Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr
 290 295 300
 Ala Met Phe Leu Leu Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu
 305 310 315 320
 Ile Pro Ala Phe Ala Leu Gly Ser Met Val Gly Gly Val Val Gly Ala
 325 330 335
 Val Leu Glu Pro Ile Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu
 340 345 350
 Gly Ala Ala Ala Phe Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly
 355 360 365
 Leu Ile Ala Ala Val Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu
 370 375 380
 Pro Ile Phe Leu Ala Val Ala Ser Ala Val Leu Ala Val Arg Val Trp
 385 390 395 400
 Ser Val Ile Ala Lys His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala
 405 410 415
 Ser Trp Thr Gly Glu Leu Lys
 420

<210> 325

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> RXN00666

<400> 325

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agtgggtgaat gctgggataag tttttaacat gtctagtgtgta gtcgggggaag gccccaaaacc 60

acgattgagc gtgcttgatc tcgtcgcgct gagtgaaggg atg acg gcc ggc gag 115
                Met Thr Ala Gly Glu
                1                    5

gcc att gca cac agt gtt cgc gct gcg cag atc gcc gaa gag cac aat 163
Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile Ala Glu Glu His Asn
                10                    15                    20

tat gcg cgt ttc tgg gtg gcg gag cac cac aac tcg gaa ggc ttg gca 211
Tyr Ala Arg Phe Trp Val Ala Glu His His Asn Ser Glu Gly Leu Ala
                25                    30                    35

tct tcc gcg acg acg ctg ctc atg ggt cat att gca ggc cac act tca 259
Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile Ala Gly His Thr Ser
                40                    45                    50

cgc att cgc gtt ggc tcc ggt ggc atc atg atg ccc aac cac tcc gcg 307
Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met Pro Asn His Ser Ala
                55                    60                    65

ctg cac gtc gcc gaa gaa ctc ggc acc ctt gag gcc att tac ccc ggc 355
Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu Ala Ile Tyr Pro Gly
                70                    75                    80                    85

cgc atc gag gcc ggc cta ggg cgc gca cca gga acc gac ccc atg acg 403
Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly Thr Asp Pro Met Thr
                90                    95                    100

gcg cgg gaa ttg ggt cgg gca agt tcg ctt gtc gac gac gtc ctc tcc 451
Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val Asp Asp Val Leu Ser
                105                    110                    115

aca atc gtc tcc ctc cag aat tat ttg gac acc ccc gaa gaa cgc ccg 499
Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr Pro Glu Glu Arg Pro
                120                    125                    130

aac atc atc gcg cat cca gga ata aat tcc cgt gtg ccg cta ttc atg 547
Asn Ile Ile Ala His Pro Gly Ile Asn Ser Arg Val Pro Leu Phe Met
                135                    140                    145

ctg gga tct tcc ctc aac ggc gct gcg atg gcc gct aaa tta gac ctt 595
Leu Gly Ser Ser Leu Asn Gly Ala Ala Met Ala Ala Lys Leu Asp Leu
                150                    155                    160                    165

cca ttc gcc ttc gcc agc cac ttc gca ccc ttc caa atg ggg ccc gcc 643
Pro Phe Ala Phe Ala Ser His Phe Ala Pro Phe Gln Met Gly Pro Ala
                170                    175                    180

atc gcc tcc tat cgc gaa cta gca gcc aat cct tat gtc atg gcc gca 691
Ile Ala Ser Tyr Arg Glu Leu Ala Ala Asn Pro Tyr Val Met Ala Ala
                185                    190                    195

gcg aat gtc ctg gtg tgc gac acc gag gaa gaa gcc gaa ttc cag atc 739
Ala Asn Val Leu Val Cys Asp Thr Glu Glu Glu Ala Glu Phe Gln Ile

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200	205	210	
tcc aca ctg cac caa atg ttc gcc gga atc gtg acg aac tcc cgc ggc			787
Ser Thr Leu His Gln Met Phe Ala Gly Ile Val Thr Asn Ser Arg Gly			
215	220	225	
aaa ctt gcc cca cca gtg cgg aat ctg aaa gac aaa ctc gac ccg atg			835
Lys Leu Ala Pro Pro Val Arg Asn Leu Lys Asp Lys Leu Asp Pro Met			
230	235	240	245
atc tgg aaa cac atc gaa gat tca ttg gaa atg act ttc atc gga aca			883
Ile Trp Lys His Ile Glu Asp Ser Leu Glu Met Thr Phe Ile Gly Thr			
250	255	260	
gcc gaa tca gtg gta tta caa ctg cag gaa ttc gct gat cgc tac aag			931
Ala Glu Ser Val Val Leu Gln Leu Gln Glu Phe Ala Asp Arg Tyr Lys			
265	270	275	
tta gat gag atc att aca gtc acc tac tcc tac gac ccc gaa gtc agg			979
Leu Asp Glu Ile Ile Thr Val Thr Tyr Ser Tyr Asp Pro Glu Val Arg			
280	285	290	
ttc cgc tcc ata gct gca ctt ggc acg gca tgg aat tagtgtcaaaa			1025
Phe Arg Ser Ile Ala Ala Leu Gly Thr Ala Trp Asn			
295	300	305	
agcctcaaaa ata			1038

<210> 326
 <211> 305
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 326
 Met Thr Ala Gly Glu Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile
 1 5 10 15
 Ala Glu Glu His Asn Tyr Ala Arg Phe Trp Val Ala Glu His His Asn
 20 25 30
 Ser Glu Gly Leu Ala Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile
 35 40 45
 Ala Gly His Thr Ser Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met
 50 55 60
 Pro Asn His Ser Ala Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu
 65 70 75 80
 Ala Ile Tyr Pro Gly Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly
 85 90 95
 Thr Asp Pro Met Thr Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val
 100 105 110
 Asp Asp Val Leu Ser Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr
 115 120 125
 Pro Glu Glu Arg Pro Asn Ile Ile Ala His Pro Gly Ile Asn Ser Arg
 130 135 140

Val Pro Leu Phe Met Leu Gly Ser Ser Leu Asn Gly Ala Ala Met Ala
 145 150 155 160
 Ala Lys Leu Asp Leu Pro Phe Ala Phe Ala Ser His Phe Ala Pro Phe
 165 170 175
 Gln Met Gly Pro Ala Ile Ala Ser Tyr Arg Glu Leu Ala Ala Asn Pro
 180 185 190
 Tyr Val Met Ala Ala Ala Asn Val Leu Val Cys Asp Thr Glu Glu Glu
 195 200 205
 Ala Glu Phe Gln Ile Ser Thr Leu His Gln Met Phe Ala Gly Ile Val
 210 215 220
 Thr Asn Ser Arg Gly Lys Leu Ala Pro Pro Val Arg Asn Leu Lys Asp
 225 230 235 240
 Lys Leu Asp Pro Met Ile Trp Lys His Ile Glu Asp Ser Leu Glu Met
 245 250 255
 Thr Phe Ile Gly Thr Ala Glu Ser Val Val Leu Gln Leu Gln Glu Phe
 260 265 270
 Ala Asp Arg Tyr Lys Leu Asp Glu Ile Ile Thr Val Thr Tyr Ser Tyr
 275 280 285
 Asp Pro Glu Val Arg Phe Arg Ser Ile Ala Ala Leu Gly Thr Ala Trp
 290 295 300

Asn
 305

<210> 327
 <211> 487
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(487)
 <223> FRXA00666

<400> 327
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acgattgagc gtgcttgatc tcgtcgcgct gagtgaaggg atg acg gcc ggc gag 115
 Met Thr Ala Gly Glu
 1 5

gcc att gca cac agt gtt cgc gct gcg cag atc gcc gaa gag cac aat 163
 Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile Ala Glu Glu His Asn
 10 15 20

tat gcg cgt ttc tgg gtg gcg gag cac cac aac tcg gaa ggc ttg gca 211
 Tyr Ala Arg Phe Trp Val Ala Glu His His Asn Ser Glu Gly Leu Ala
 25 30 35

tct tcc gcg acg acg ctg ctc atg ggt cat att gca ggc cac act tca 259

Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile Ala Gly His Thr Ser
 40 45 50

cgc att cgc gtt ggc tcc ggt ggc atc atg atg ccc aac cac tcc gcg 307
 Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met Pro Asn His Ser Ala
 55 60 65

ctg cac gtc gcc gaa gaa ctg ggc acc ctt gag gcc att tac ccc ggc 355
 Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu Ala Ile Tyr Pro Gly
 70 75 80 85

cgc atc gag gcc ggc cta ggg cgc gca cca gga acc gac ccc atg acg 403
 Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly Thr Asp Pro Met Thr
 90 95 100

gcg cgg gaa ttg ggt cgg gca agt tgc ctt gtc gac gac gtc ctc tcc 451
 Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val Asp Asp Val Leu Ser
 105 110 115

aca atc gtc tcc ctc cag aat tat ttg gac acc ccc 487
 Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr Pro
 120 125

<210> 328

<211> 129

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

Met Thr Ala Gly Glu Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile
 1 5 10 15

Ala Glu Glu His Asn Tyr Ala Arg Phe Trp Val Ala Glu His His Asn
 20 25 30

Ser Glu Gly Leu Ala Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile
 35 40 45

Ala Gly His Thr Ser Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met
 50 55 60

Pro Asn His Ser Ala Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu
 65 70 75 80

Ala Ile Tyr Pro Gly Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly
 85 90 95

Thr Asp Pro Met Thr Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val
 100 105 110

Asp Asp Val Leu Ser Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr
 115 120 125

Pro

<210> 329

<211> 750

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(727)

<223> RXN00704

<400> 329

tcaaattctg cgcacaaagt gttctaagac gacgtctgcc' catcggcgct ctaatgcaca 60
ttacagcggt tacagaattg aaaatgaaag gttcaaagcc ttg acc att act ttt 115
Leu Thr Ile Thr Phe
1 5

agc cgc gtt gct ctg acc acc ctg gca gtc acc gca acc act ttg tcc 163
Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr Ala Thr Thr Leu Ser
10 15 20

ctg agc act gct gcg aat gca cag tct tcc ttg ttg gat aag act ctt 211
Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu Leu Asp Lys Thr Leu
25 30 35

gat gcc cgt cag tgc atc gat gca gac aac gtc tgg gtc tca gtt gac 259
Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val Trp Val Ser Val Asp
40 45 50

tat ggt gca gat tcc gaa aaa gaa cca gag ggc gca tgt gcc acc gag 307
Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly Ala Cys Ala Thr Glu
55 60 65

ttc act gat ggt gtt gta gct ctt gaa tct gct ggg ttc aaa ctg acc 355
Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala Gly Phe Lys Leu Thr
70 75 80 85

ttt gac gaa tct gaa atg ggc aaa tac atg acc ggt atc aac gga gtt 403
Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr Gly Ile Asn Gly Val
90 95 100

gtt cct gat tgg gtt gaa act gga act tac tgg agt tac tac tct ggt 451
Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp Ser Tyr Tyr Ser Gly
105 110 115

gaa gtc gca gat gat tac agc gtg gac tac acc tac tac gag gtt ggt 499
Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr Tyr Tyr Glu Val Gly
120 125 130

gca tct aat tct gaa cct gaa ggt gga act gtt gag gct tgg gtt gtt 547
Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val Glu Ala Trp Val Val
135 140 145

ggc acc ggc gag gaa aca cca gca ctc gag act ctt cct gaa act cca 595
Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr Leu Pro Glu Thr Pro
150 155 160 165

gca gca acc gga tct tct gaa gac ggc ggc tgg att gca gtc atc gca 643
Ala Ala Thr Gly Ser Ser Glu Asp Gly Gly Trp Ile Ala Val Ile Ala
170 175 180

ggt ctt ctc gca ctg atc ggt ggt gga gtt gca gct ttg tac cag ggc 691
Gly Leu Leu Ala Leu Ile Gly Gly Gly Val Ala Ala Leu Tyr Gln Gly
185 190 195

ttg atc act atc cca ggt ctg gtt ctg cct aag ttt taagcaacct 737
 Leu Ile Thr Ile Pro Gly Leu Val Leu Pro Lys Phe
 200 205

aacctaaagc ttc 750

<210> 330
 <211> 209
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 330
 Leu Thr Ile Thr Phe Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr
 1 5 10 15
 Ala Thr Thr Leu Ser Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu
 20 25 30
 Leu Asp Lys Thr Leu Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val
 35 40 45
 Trp Val Ser Val Asp Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly
 50 55 60
 Ala Cys Ala Thr Glu Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala
 65 70 75 80
 Gly Phe Lys Leu Thr Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr
 85 90 95
 Gly Ile Asn Gly Val Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp
 100 105 110
 Ser Tyr Tyr Ser Gly Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr
 115 120 125
 Tyr Tyr Glu Val Gly Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val
 130 135 140
 Glu Ala Trp Val Val Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr
 145 150 155 160
 Leu Pro Glu Thr Pro Ala Ala Thr Gly Ser Ser Glu Asp Gly Gly Trp
 165 170 175
 Ile Ala Val Ile Ala Gly Leu Leu Ala Leu Ile Gly Gly Gly Val Ala
 180 185 190
 Ala Leu Tyr Gln Gly Leu Ile Thr Ile Pro Gly Leu Val Leu Pro Lys
 195 200 205

Phe

<210> 331
 <211> 636
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> FRXA00704

<400> 331

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tcaaattctg cgcacaaagt gttctaagac gacgtctgcc catcggcgct ctaatgcaca 60

ttacagcggtt tacagaattg aaaatgaaag gttcaaagcc ttg acc att act ttt 115
                                   Leu Thr Ile Thr Phe
                                   1                               5

agc cgc gtt gct ctg acc acc ctg gca gtc acc gca acc act ttg tcc 163
Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr Ala Thr Thr Leu Ser
                                   10                               15                               20

ctg agc act gct gcg aat gca cag tct tcc ttg ttg gat aag act ctt 211
Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu Leu Asp Lys Thr Leu
                                   25                               30                               35

gat gcc cgt cag tgc atc gat gca gac aac gtc tgg gtc tca gtt gac 259
Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val Trp Val Ser Val Asp
                                   40                               45                               50

tat ggt gca gat tcc gaa aaa gaa cca gag ggc gca tgt gcc acc gag 307
Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly Ala Cys Ala Thr Glu
                                   55                               60                               65

ttc act gat ggt gtt gta gct ctt gaa tct gct ggg ttc aaa ctg acc 355
Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala Gly Phe Lys Leu Thr
                                   70                               75                               80                               85

ttt gac gaa tct gaa atg ggc aaa tac atg acc ggt atc aac gga gtt 403
Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr Gly Ile Asn Gly Val
                                   90                               95                               100

gtt cct gat tgg gtt gaa act gga act tac tgg agt tac tac tct ggt 451
Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp Ser Tyr Tyr Ser Gly
                                   105                               110                               115

gaa gtc gca gat gat tac agc gtg gac tac acc tac tac gag gtt ggt 499
Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr Tyr Glu Val Gly
                                   120                               125                               130

gca tct aat tct gaa cct gaa ggt gga act gtt gag gct tgg gtt gtt 547
Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val Glu Ala Trp Val Val
                                   135                               140                               145

ggc acc ggc gag gaa aca cca gca ctc gag act ctt tct gaa act tca 595
Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr Leu Ser Glu Thr Ser
                                   150                               155                               160                               165

gca gca acc gga tct tct taagacggcg gctggattgc agt 636
Ala Ala Thr Gly Ser Ser
                                   170

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<210> 332

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Leu Thr Ile Thr Phe Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr
 1 5 10 15
 Ala Thr Thr Leu Ser Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu
 20 25 30
 Leu Asp Lys Thr Leu Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val
 35 40 45
 Trp Val Ser Val Asp Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly
 50 55 60
 Ala Cys Ala Thr Glu Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala
 65 70 75 80
 Gly Phe Lys Leu Thr Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr
 85 90 95
 Gly Ile Asn Gly Val Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp
 100 105 110
 Ser Tyr Tyr Ser Gly Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr
 115 120 125
 Tyr Tyr Glu Val Gly Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val
 130 135 140
 Glu Ala Trp Val Val Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr
 145 150 155 160
 Leu Ser Glu Thr Ser Ala Ala Thr Gly Ser Ser
 165 170

<210> 333

<211> 819

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(796)

<223> RXN00712

<400> 333

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 tcccagcata agtagtcgcc tagtttagga ggtacatggc atg tcc cta cgc aag 115
 Met Ser Leu Arg Lys
 1 5
 aat ctc gcc ctc gga agc agc aca gta cta ctc aca gcc gtg cta agc 163
 Asn Leu Ala Leu Gly Ser Ser Thr Val Leu Leu Thr Ala Val Leu Ser
 10 15 20
 ggg tgt gtt tcc ctt gat gag cgc tcc act gat aca tcc acg gag aat 211
 Gly Cys Val Ser Leu Asp Glu Arg Ser Thr Asp Thr Ser Thr Glu Asn
 25 30 35

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gtc acc acg gta act gcc aca ctc act tcc acc gcc gca gca gaa ccc 259
Val Thr Thr Val Thr Ala Thr Leu Thr Ser Thr Ala Ala Ala Glu Pro
      40                      45                      50

acc act aga acg act gtg caa agt gct aca gaa gcc tcc act act gca 307
Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala Ser Thr Thr Ala
      55                      60                      65

cca gtg caa tgc aat ttg gat ccc cgt acc tcg gat ttt ggg cca tat 355
Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp Phe Gly Pro Tyr
      70                      75                      80                      85

ctt gca caa tct cgc acc ccg gtt ggt gag cta gct gga tct gca gat 403
Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala Gly Ser Ala Asp
      90                      95                      100

tcc gtc gtg cag gtt cct gac tgg ttc tat cac ttc caa atg ggc gac 451
Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe Gln Met Gly Asp
      105                      110                      115

aac ggc tac gat tcc tgt tcc aag ctc agc tat gtg gtt ctc aac ggt 499
Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val Val Leu Asn Gly
      120                      125                      130

tcc aat gga gac gcc gaa cgt tct act gga acg ggt gct gcg atc gcc 547
Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly Ala Ala Ile Ala
      135                      140                      145

gac gtg gtg gtg ctg ttt atc gac ggc cat atg gtt gct cgt cct gct 595
Asp Val Val Val Leu Phe Ile Asp Gly His Met Val Ala Arg Pro Ala
      150                      155                      160                      165

cct ttt gaa atg aag acc gtg gaa tcc gtc acc aga gtg tca gat tca 643
Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg Val Ser Asp Ser
      170                      175                      180

gaa atc caa gtt gtt tac gga cat gcc ggc cga tct act gcc gaa ggt 691
Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser Thr Ala Glu Gly
      185                      190                      195

gtt acg gac tat ttc acc ttt aac ttc ttc gtt gac aac ggc gtt ctt 739
Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp Asn Gly Val Leu
      200                      205                      210

tca gga cgc ggc gat ctc cca gaa cac atc gat act cac atg cgt cta 787
Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr His Met Arg Leu
      215                      220                      225

tat ctg ctg tagcccccac taaaaactct tga 819
Tyr Leu Leu
230

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<210> 334

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

Met Ser Leu Arg Lys Asn Leu Ala Leu Gly Ser Ser Thr Val Leu Leu

1	5	10	15
Thr Ala Val Leu Ser Gly Cys Val Ser Leu Asp Glu Arg Ser Thr Asp	20	25	30
Thr Ser Thr Glu Asn Val Thr Thr Val Thr Ala Thr Leu Thr Ser Thr	35	40	45
Ala Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu	50	55	60
Ala Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser	65	70	75
Asp Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu	85	90	95
Ala Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His	100	105	110
Phe Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr	115	120	125
Val Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr	130	135	140
Gly Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met	145	150	155
Val Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr	165	170	175
Arg Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg	180	185	190
Ser Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val	195	200	205
Asp Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp	210	215	220
Thr His Met Arg Leu Tyr Leu Leu	225	230	

<210> 335
 <211> 572
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(549)
 <223> FRXA00712

<400> 335	
gca gca gaa ccc acc act aga acg act gtg caa agt gct aca gaa gcc	48
Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala	
1 5 10 15	
tcc act act gca cca gtg caa tgc aat ttg gat ccc cgt acc tcg gat	96

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Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp
      20                      25                      30

ttt ggg cca tat ctt gca caa tct cgc acc ccg gtt ggt gag cta gct 144
Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala
      35                      40                      45

gga tct gca gat tcc gtc gtg cag gtt cct gac tgg ttc tat cac ttc 192
Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe
      50                      55                      60

caa atg ggc gac aac ggc tac gat tcc tgt tcc aag ctc agc tat gtg 240
Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val
      65                      70                      75                      80

gtt ctc aac ggt tcc aat gga gac gcc gaa cgt tct act gga acg ggt 288
Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly
      85                      90                      95

gct gcg atc gcc gac gtg gtg gtg ctg ttt atc gac ggc cat atg gtt 336
Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met Val
      100                      105                      110

gct cgt cct gct cct ttt gaa atg aag acc gtg gaa tcc gtc acc aga 384
Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg
      115                      120                      125

gtg tca gat tca gaa atc caa gtt gtt tac gga cat gcc ggc cga tct 432
Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser
      130                      135                      140

act gcc gaa ggt gtt acg gac tat ttc acc ttt aac ttc ttc gtt gac 480
Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp
      145                      150                      155                      160

aac ggc gtt ctt tca gga cgc ggc gat ctc cca gaa cac atc gat act 528
Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr
      165                      170                      175

cac atg cgt cta tat ctg ctg tagcccccac taaaaactct tga 572
His Met Arg Leu Tyr Leu Leu
      180

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<210> 336

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala
  1                      5                      10                      15

Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp
      20                      25                      30

Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala
      35                      40                      45

Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe
      50                      55                      60

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Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val
 65 70 75 80
 Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly
 85 90 95
 Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met Val
 100 105 110
 Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg
 115 120 125
 Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser
 130 135 140
 Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp
 145 150 155 160
 Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr
 165 170 175
 His Met Arg Leu Tyr Leu Leu
 180

<210> 337
 <211> 789
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(766)
 <223> RXN00720

<400> 337
 ctgatctata cgctctgttg aagtagagaa gctttctggt caagttcctt gagtatgggtg 60
 gtccaagacc agcactccag attcaaggaa cttataaaac atg gca tca ccg cgc 115
 Met Ala Ser Pro Arg
 1 5
 cgc cca cag gtt gca gca cca cgc atc aaa gaa ctt cgc cta aca ggc 163
 Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu Leu Arg Leu Thr Gly
 10 15 20
 ctt gac aac gct gac cct caa gac atc gaa tcg aat gag cag ata gag 211
 Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser Asn Glu Gln Ile Glu
 25 30 35
 tca tgc cgt ttt aac gag gcc gag ctt tcc gaa cgc gat ctt tct ggt 259
 Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu Arg Asp Leu Ser Gly
 40 45 50
 gct ggt ttc att gaa tgt gaa ttc ctt ggg ctg gaa gca cac gaa acc 307
 Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu Glu Ala His Glu Thr
 55 60 65
 gag cta cgc cgg gct caa ttc gtg gaa aca cgc atc gaa aga gcc aat 355
 Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg Ile Glu Arg Ala Asn

70	75	80	85	
gct cca tct ttt aag gca gcc cgc tcc atc tgg cgc aac gca acg att				403
Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp Arg Asn Ala Thr Ile				
90		95	100	
tcc gac tcc cgc ttt ggt gcc gtc gaa atg tat gaa gca acc gtc caa				451
Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr Glu Ala Thr Val Gln				
105		110	115	
gct ttg aaa atc tct gat tct aag ctg tgc ttt gtc aat ctg cgg ggt				499
Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe Val Asn Leu Arg Gly				
120		125	130	
gca tcg tta cgg gat gtg ctc ttt gag aac tgt gtc atc gac gag ctt				547
Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys Val Ile Asp Glu Leu				
135		140	145	
gat ctt ggc caa gcc aga gca gaa cgc atc gct ttt aaa gac tgc acg				595
Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala Phe Lys Asp Cys Thr				
150		155	160	165
gtg cat tcg ctc acc ttt gat cat gcc gtg ctc agc aat gtg gat ctt				643
Val His Ser Leu Thr Phe Asp His Ala Val Leu Ser Asn Val Asp Leu				
170		175	180	
cgc ggt tta gat atc gag cgc atc agt ggc gtg gag tcc atg tcc gga				691
Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val Glu Ser Met Ser Gly				
185		190	195	
acc gtg atc tca tcc ctg cag gct gct gac ctg tgc gga gca ttt gca				739
Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu Ser Gly Ala Phe Ala				
200		205	210	
cgg cat tta gga att act gta aac gat tagaaatccg ctcttttgaa				786
Arg His Leu Gly Ile Thr Val Asn Asp				
215		220		
caa				789

<210> 338

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met	Ala	Ser	Pro	Arg	Arg	Pro	Gln	Val	Ala	Ala	Pro	Arg	Ile	Lys	Glu
1					5					10				15	

Leu	Arg	Leu	Thr	Gly	Leu	Asp	Asn	Ala	Asp	Pro	Gln	Asp	Ile	Glu	Ser
			20					25					30		

Asn	Glu	Gln	Ile	Glu	Ser	Cys	Arg	Phe	Asn	Glu	Ala	Glu	Leu	Ser	Glu
		35					40					45			

Arg	Asp	Leu	Ser	Gly	Ala	Gly	Phe	Ile	Glu	Cys	Glu	Phe	Leu	Gly	Leu
	50					55					60				

Glu	Ala	His	Glu	Thr	Glu	Leu	Arg	Arg	Ala	Gln	Phe	Val	Glu	Thr	Arg
65					70					75					80

gag cta cgc cgg gct caa ttc gtg gaa aca cgc atc gaa aga gcc aat 355
 Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg Ile Glu Arg Ala Asn
 70 75 80 85

 gct cca tct ttt aag gca gcc cgc tcc atc tgg cgc aac gca acg att 403
 Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp Arg Asn Ala Thr Ile
 90 95 100

 tcc gac tcc cgc ttt ggt gcc gtc gaa atg tat gaa gca acc gtc caa 451
 Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr Glu Ala Thr Val Gln
 105 110 115

 gct ttg aaa atc tct gat tct aag ctg tcg ttt gtc aat ctg cgg ggt 499
 Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe Val Asn Leu Arg Gly
 120 125 130

 gca tcg tta cgg gat gtg ctc ttt gag aac tgt gtc atc gac gag ctt 547
 Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys Val Ile Asp Glu Leu
 135 140 145

 gat ctt ggc caa gcc aga gca gaa cgc atc gct ttt aaa gac tgc acg 595
 Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala Phe Lys Asp Cys Thr
 150 155 160 165

 gtg cat tcg ctc acc ttt gat cat gcc gtg ctc agc aat gtg gat ctt 643
 Val His Ser Leu Thr Phe Asp His Ala Val Leu Ser Asn Val Asp Leu
 170 175 180

 cgc ggt tta gat atc gag cgc atc agt ggc gtg gag tcc atg tcc gga 691
 Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val Glu Ser Met Ser Gly
 185 190 195

 acc gtg atc tca tcc ctg cag gct gct gac ctg tcg gga gca ttt gca 739
 Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu Ser Gly Ala Phe Ala
 200 205 210

 cgg cat tta gga att act gta aac gat tagaaatccg ctcttttgaa 786
 Arg His Leu Gly Ile Thr Val Asn Asp
 215 220

 caa 789

<210> 340

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Ala Ser Pro Arg Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu
 1 5 10 15

 Leu Arg Leu Thr Gly Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser
 20 25 30

 Asn Glu Gln Ile Glu Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu
 35 40 45

 Arg Asp Leu Ser Gly Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu
 50 55 60

Glu Ala His Glu Thr Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg
 65 70 75 80
 Ile Glu Arg Ala Asn Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp
 85 90 95
 Arg Asn Ala Thr Ile Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr
 100 105 110
 Glu Ala Thr Val Gln Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe
 115 120 125
 Val Asn Leu Arg Gly Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys
 130 135 140
 Val Ile Asp Glu Leu Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala
 145 150 155 160
 Phe Lys Asp Cys Thr Val His Ser Leu Thr Phe Asp His Ala Val Leu
 165 170 175
 Ser Asn Val Asp Leu Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val
 180 185 190
 Glu Ser Met Ser Gly Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu
 195 200 205
 Ser Gly Ala Phe Ala Arg His Leu Gly Ile Thr Val Asn Asp
 210 215 220

<210> 341

<211> 1088

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1065)

<223> RXN00722

<400> 341

gct gtt ctc cga gaa gcc gga gtt gtt gat gcc ggg gga cag ggc cta 48
 Ala Val Leu Arg Glu Ala Gly Val Val Asp Ala Gly Gly Gln Gly Leu
 1 5 10 15
 gtt att ctc ctg gag tcc ctg gcc gaa caa atc aac gga aac cca cct 96
 Val Ile Leu Leu Glu Ser Leu Ala Glu Gln Ile Asn Gly Asn Pro Pro
 20 25 30
 cac cat cca tcg cac cac agt gaa cca gcc gaa gaa ccc tcc ttc cac 144
 His His Pro Ser His His Ser Glu Pro Ala Glu Glu Pro Ser Phe His
 35 40 45
 ggc aaa acc ggc gac cta gaa gtg atg ttt tac att gca tgc gac tcc 192
 Gly Lys Thr Gly Asp Leu Glu Val Met Phe Tyr Ile Ala Cys Asp Ser
 50 55 60
 gcg caa aca ctc gat gct ctc cac aac gaa ctt gaa aca cta ggc gac 240
 Ala Gln Thr Leu Asp Ala Leu His Asn Glu Leu Glu Thr Leu Gly Asp

65	70	75	80	
agc ctg ctc atc gcc cga gaa acc aat acc cgc ggc acc gtt cac atc				288
Ser Leu Leu Ile Ala Arg Glu Thr Asn Thr Arg Gly Thr Val His Ile				
85		90	95	
cat tcg cgc cgg gca ggc gag gtc atc caa aaa gca ttt gcc gca gga				336
His Ser Arg Arg Ala Gly Glu Val Ile Gln Lys Ala Phe Ala Ala Gly				
100		105	110	
gac gtc agc gaa ctc cgc ctt gaa atc ctc ccc gat act tcc ggc agc				384
Asp Val Ser Glu Leu Arg Leu Glu Ile Leu Pro Asp Thr Ser Gly Ser				
115		120	125	
ttc acg gaa gaa cca cgc cgg gtc ctc atg gct gtc gca cct gac ggc				432
Phe Thr Glu Glu Pro Arg Arg Val Leu Met Ala Val Ala Pro Asp Gly				
130		135	140	
ctg gtg gcg gag ctg tac cgc agc gct gga gtg aag gtg gtg gcc cgc				480
Leu Val Ala Glu Leu Tyr Arg Ser Ala Gly Val Lys Val Val Ala Arg				
145		150	155	160
aac atc gcg caa tcc aag tct gat gat gtg gtg gca aag atc gtt tcc				528
Asn Ile Ala Gln Ser Lys Ser Asp Asp Val Val Ala Lys Ile Val Ser				
165		170	175	
atc gcg cgc aag tct ggt gcc gat gag gtg atc ttg ctg ccc aac ggt				576
Ile Ala Arg Lys Ser Gly Ala Asp Glu Val Ile Leu Leu Pro Asn Gly				
180		185	190	
ctt ttg acc aag cgt gag ctg gtt tcc att gag cgt tcc agc cat gct				624
Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu Arg Ser Ser His Ala				
195		200	205	
ttt gag caa agt gtg gtt att ttg cct act gcc acg ttg gtt gca ggt				672
Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala Thr Leu Val Ala Gly				
210		215	220	
ctt gca gcg gtg tcc gtt cat gag cca gcg caa ccc ctg gcg gtg gat				720
Leu Ala Ala Val Ser Val His Glu Pro Ala Gln Pro Leu Ala Val Asp				
225		230	235	240
tcc tat gcc atg gca gag gcc gcc ggt tcc atg cgc acg gcc acg atc				768
Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met Arg Thr Ala Thr Ile				
245		250	255	
cgc gcc gcc acc agc gcc gcg ctc acc cag gcc ggc gca tgc tcc aag				816
Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala Gly Ala Cys Ser Lys				
260		265	270	
ggt gat cta tta agc ttc atc ggc ccg gag ata gct ctg gtc tcc gag				864
Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile Ala Leu Val Ser Glu				
275		280	285	
gag ctc aac gac gcg cta tcg cgc acc gct tta agg ctt ctc gac ggc				912
Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu Arg Leu Leu Asp Gly				
290		295	300	
tcc agc gag caa att acc ctt ctc ata gcg caa gac cgt cag tcc gcc				960
Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln Asp Arg Gln Ser Ala				
305		310	315	320

ttc gac gaa gat gtt ttc cgc cgt ggc ctg gga act cac acg gat gtg 1008
 Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly Thr His Thr Asp Val
 325 330 335

gag atc acg gtc tat cct gct act gga atg gag aat ctg gta gag atc 1056
 Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu Asn Leu Val Glu Ile
 340 345 350

gga gtg gag tagccacatg ttgggttggc atg 1088
 Gly Val Glu
 355

<210> 342

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Ala Val Leu Arg Glu Ala Gly Val Val Asp Ala Gly Gly Gln Gly Leu
 1 5 10 15

Val Ile Leu Leu Glu Ser Leu Ala Glu Gln Ile Asn Gly Asn Pro Pro
 20 25 30

His His Pro Ser His His Ser Glu Pro Ala Glu Glu Pro Ser Phe His
 35 40 45

Gly Lys Thr Gly Asp Leu Glu Val Met Phe Tyr Ile Ala Cys Asp Ser
 50 55 60

Ala Gln Thr Leu Asp Ala Leu His Asn Glu Leu Glu Thr Leu Gly Asp
 65 70 75 80

Ser Leu Leu Ile Ala Arg Glu Thr Asn Thr Arg Gly Thr Val His Ile
 85 90 95

His Ser Arg Arg Ala Gly Glu Val Ile Gln Lys Ala Phe Ala Ala Gly
 100 105 110

Asp Val Ser Glu Leu Arg Leu Glu Ile Leu Pro Asp Thr Ser Gly Ser
 115 120 125

Phe Thr Glu Glu Pro Arg Arg Val Leu Met Ala Val Ala Pro Asp Gly
 130 135 140

Leu Val Ala Glu Leu Tyr Arg Ser Ala Gly Val Lys Val Val Ala Arg
 145 150 155 160

Asn Ile Ala Gln Ser Lys Ser Asp Asp Val Val Ala Lys Ile Val Ser
 165 170 175

Ile Ala Arg Lys Ser Gly Ala Asp Glu Val Ile Leu Leu Pro Asn Gly
 180 185 190

Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu Arg Ser Ser His Ala
 195 200 205

Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala Thr Leu Val Ala Gly
 210 215 220

Leu Ala Ala Val Ser Val His Glu Pro Ala Gln Pro Leu Ala Val Asp
 225 230 235 240
 Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met Arg Thr Ala Thr Ile
 245 250 255
 Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala Gly Ala Cys Ser Lys
 260 265 270
 Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile Ala Leu Val Ser Glu
 275 280 285
 Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu Arg Leu Leu Asp Gly
 290 295 300
 Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln Asp Arg Gln Ser Ala
 305 310 315 320
 Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly Thr His Thr Asp Val
 325 330 335
 Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu Asn Leu Val Glu Ile
 340 345 350
 Gly Val Glu
 355

<210> 343
 <211> 542
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (16)..(519)
 <223> FRXA00722

<400> 343
 ccccccccggtgac tttg ctg ccc aac ggt ctt ttg acc aag cgt gag ctg 51
 Leu Leu Pro Asn Gly Leu Leu Thr Lys Arg Glu Leu
 1 5 10
 gtt tcc att gag cgt tcc agc cat gct ttt gag caa agt gtg gtt att 99
 Val Ser Ile Glu Arg Ser Ser His Ala Phe Glu Gln Ser Val Val Ile
 15 20 25
 ttg cct act gcc acg ttg gtt gca ggt ctt gca gcg gtg tcc gtt cat 147
 Leu Pro Thr Ala Thr Leu Val Ala Gly Leu Ala Ala Val Ser Val His
 30 35 40
 gag cca gcg caa ccc ctg gcg gtg gat tcc tat gcc atg gca gag gcc 195
 Glu Pro Ala Gln Pro Leu Ala Val Asp Ser Tyr Ala Met Ala Glu Ala
 45 50 55 60
 gcc ggt tcc atg cgc acg gcc acg atc cgc gcc gcc acc agc gcc gcg 243
 Ala Gly Ser Met Arg Thr Ala Thr Ile Arg Ala Ala Thr Ser Ala Ala
 65 70 75
 ctc acc cag gcc ggc gca tgc tcc aag ggt gat cta tta agc ttc atc 291

Leu Thr Gln Ala Gly Ala Cys Ser Lys Gly Asp Leu Leu Ser Phe Ile
 80 85 90
 ggc ccg gag ata gct ctg gtc tcc gag gag ctc aac gac gcg cta tcg 339
 Gly Pro Glu Ile Ala Leu Val Ser Glu Glu Leu Asn Asp Ala Leu Ser
 95 100 105
 cgc acc gct tta agg ctt ctc gac ggc tcc agc gag caa att acc ctt 387
 Arg Thr Ala Leu Arg Leu Leu Asp Gly Ser Ser Glu Gln Ile Thr Leu
 110 115 120
 ctc ata gcg caa gac cgt cag tcc gcc ttc gac gaa gat gtt ttc cgc 435
 Leu Ile Ala Gln Asp Arg Gln Ser Ala Phe Asp Glu Asp Val Phe Arg
 125 130 135 140
 cgt ggc ctg gga act cac acg gat gtg gag atc acg gtc tat cct gct 483
 Arg Gly Leu Gly Thr His Thr Asp Val Glu Ile Thr Val Tyr Pro Ala
 145 150 155
 act gga atg gag aat ctg gta gag atc gga gtg gag tagccacatg 529
 Thr Gly Met Glu Asn Leu Val Glu Ile Gly Val Glu
 160 165
 ttgggttggc atg 542

<210> 344

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Leu Leu Pro Asn Gly Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu
 1 5 10 15
 Arg Ser Ser His Ala Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala
 20 25 30
 Thr Leu Val Ala Gly Leu Ala Ala Val Ser Val His Glu Pro Ala Gln
 35 40 45
 Pro Leu Ala Val Asp Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met
 50 55 60
 Arg Thr Ala Thr Ile Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala
 65 70 75 80
 Gly Ala Cys Ser Lys Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile
 85 90 95
 Ala Leu Val Ser Glu Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu
 100 105 110
 Arg Leu Leu Asp Gly Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln
 115 120 125
 Asp Arg Gln Ser Ala Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly
 130 135 140
 Thr His Thr Asp Val Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu
 145 150 155 160

Asn Leu Val Glu Ile Gly Val Glu
165

<210> 345

<211> 1101

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1078)

<223> RXN00729

<400> 345

ttcagcacag atcacccttt gccagctacc gacttagttt cgtaacacgt atagtgggag 60

gcgttttgcc agacgccaaa gaaagataat tggattacct atg agc gcc acc aac 115
Met Ser Ala Thr Asn
1 5

cct gat gcc cta gac gtg cag cac gtc tat ccc atc aag acg aaa aag 163
Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro Ile Lys Thr Lys Lys
10 15 20

act cca ctt gcg gtg att ttc aac atc att agc ggt ggt ttg att gga 211
Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser Gly Gly Leu Ile Gly
25 30 35

atg gcg gag ttg gtg cca gga att tcc ggc gga act gtc gct ttg gtt 259
Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly Thr Val Ala Leu Val
40 45 50

ctt gga att tat gag cgc gca ctg cac aac ggt gat ctc ctc att gat 307
Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly Asp Leu Leu Ile Asp
55 60 65

ctg atc aag gtg ttg atc aag gac cgc tcg aag gtt aag gaa gct gcg 355
Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys Val Lys Glu Ala Ala
70 75 80 85

gcg aaa atc gac tgg tgg ttc ctc ggc gct atc ggc gtt ggc atg gtc 403
Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile Gly Val Gly Met Val
90 95 100

gtg atg gtc ttc tcg atg tca tcg att ttg cat aca gtt gtt gag gac 451
Val Met Val Phe Ser Met Ser Ser Ile Leu His Thr Val Val Glu Asp
105 110 115

tac cca gag atc act cgc ggt ctg ttc ctt gga atg gtt gcc gtg tct 499
Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly Met Val Ala Val Ser
120 125 130

atc ctt gtt ccg ttg gga atg atg gat atg cgg gat gcc aag aag cgc 547
Ile Leu Val Pro Leu Gly Met Met Asp Met Arg Asp Ala Lys Lys Arg
135 140 145

ctc gca atc gtc atc ccg cta ttt ata atc tgc gcc atg ctg gga ttc 595
Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys Ala Met Leu Gly Phe
150 155 160 165

ttt gga aca tcc ttc act agt gcg cct cgc acc gat cct tca ctg atc 643
 Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr Asp Pro Ser Leu Ile
 170 175 180

ttt gtc ttc atc tgt gct gcg atc gct gtg tgt gct ctt gtt ctt cct 691
 Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys Ala Leu Val Leu Pro
 185 190 195

ggt gtt tca gga tca ttc ttc ttg ctg gcg gtc ggt atg tac gcg cca 739
 Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val Gly Met Tyr Ala Pro
 200 205 210

atc atg gaa tct ctg tcc aac cgt gac ttg tcg gtc atc ggc gtg ttc 787
 Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser Val Ile Gly Val Phe
 215 220 225

ttg ctt ggc gcg ctc acc ggt gtg atc ttg ttt gtg aag gtt ttg tct 835
 Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe Val Lys Val Leu Ser
 230 235 240 245

tat gtt ctc gag cac cac cgc acc atc acg ctg acc atc atg gct ggt 883
 Tyr Val Leu Glu His His Arg Thr Ile Thr Leu Thr Ile Met Ala Gly
 250 255 260

ctc atg ctg ggt tca ctt cgt gcg ctg tgg cct tgg cag gac ggt gac 931
 Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro Trp Gln Asp Gly Asp
 265 270 275

gct aat cta ctt gct cct ggc gat aac gcc gtg atg att ttc agc atc 979
 Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val Met Ile Phe Ser Ile
 280 285 290

atc att ctt ggt ggc gcg att gtc gct gct ttg atg ttt gct gag cgt 1027
 Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu Met Phe Ala Glu Arg
 295 300 305

gtg tct tcc aag aac att gat tct gag acc gtg gca gaa gag cac ccg 1075
 Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val Ala Glu Glu His Pro
 310 315 320 325

cgc taaataagaa ctccacaaag aaa 1101
 Arg

<210> 346

<211> 326

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Met Ser Ala Thr Asn Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro
 1 5 10 15

Ile Lys Thr Lys Lys Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser
 20 25 30

Gly Gly Leu Ile Gly Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly
 35 40 45

Thr Val Ala Leu Val Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly
50 55 60

Asp Leu Leu Ile Asp Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys
65 70 75 80

Val Lys Glu Ala Ala Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile
85 90 95

Gly Val Gly Met Val Val Met Val Phe Ser Met Ser Ser Ile Leu His
100 105 110

Thr Val Val Glu Asp Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly
115 120 125

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
130 135 140

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
145 150 155 160

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
165 170 175

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
180 185 190

Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
195 200 205

Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
210 215 220

Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
225 230 235 240

Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
245 250 255

Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
260 265 270

Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
275 280 285

Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
290 295 300

Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
305 310 315 320

Ala Glu Glu His Pro Arg
325

<210> 347

<211> 665

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(642)

<223> FRXA00729

<400> 347

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atg gtt gcc gtg tct atc ctt gtt ccg ttg gga atg atg gat atg cgg	96
Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg	
20 25 30	
gat gcc aag aag cgc ctc gca atc gtc atc ccg cta ttt ata atc tgc	144
Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys	
35 40 45	
gcc atg ctg gga ttc ttt gga aca tcc ttc act agt gcg cct cgc acc	192
Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr	
50 55 60	
gat cct tca ctg atc ttt gtc ttc atc tgt gct gcg atc gct gtg tgt	240
Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys	
65 70 75 80	
gct ctt gtt ctt cct ggt gtt tca gga tca ttc ttc ttg ctg gcg gtc	288
Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val	
85 90 95	
ggt atg tac gcg cca atc atg gaa tct ctg tcc aac cgt gac ttg tcg	336
Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser	
100 105 110	
gtc atc ggc gtg ttc ttg ctt ggc gcg ctc acc ggt gtg atc ttg ttt	384
Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe	
115 120 125	
gtg aag gtt ttg tct tat gtt ctc gag cac cac cgc acc atc acg ctg	432
Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu	
130 135 140	
acc atc atg gct ggt ctc atg ctg ggt tca ctt cgt gcg ctg tgg cct	480
Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro	
145 150 155 160	
tgg cag gac ggt gac gct aat cta ctt gct cct ggc gat aac gcc gtg	528
Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val	
165 170 175	
atg att ttc agc atc atc att ctt ggt ggc gcg att gtc gct gct ttg	576
Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu	
180 185 190	
atg ttt gct gag cgt gtg tct tcc aag aac att gat tct gag acc gtg	624
Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val	
195 200 205	
gca gaa gag cac ccg cgc taaataagaa ctccacaaaag aaa	665
Ala Glu Glu His Pro Arg	
210	

<210> 348

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

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20 25 30

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
35 40 45

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
50 55 60

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
65 70 75 80

Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
85 90 95

Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
100 105 110

Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
115 120 125

Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
130 135 140

Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
145 150 155 160

Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
165 170 175

Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
180 185 190

Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
195 200 205

Ala Glu Glu His Pro Arg
210

<210> 349

<211> 706

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(706)

<223> FRXA02867

<400> 349

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                                         Met Ser Ala Thr Asn
                                         1 5
cct gat gcc cta gac gtg cag cac gtc tat ccc atc aag acg aaa aag 163
Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro Ile Lys Thr Lys Lys
      10 15 20
act cca ctt gcg gtg att ttc aac atc att agc ggt ggt ttg att gga 211
Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser Gly Gly Leu Ile Gly
      25 30 35
atg gcg gag ttg gtg cca gga att tcc ggc gga act gtc gct ttg gtt 259
Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly Thr Val Ala Leu Val
      40 45 50
ctt gga att tat gag cgc gca ctg cac aac ggt gat ctc ctc att gat 307
Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly Asp Leu Leu Ile Asp
      55 60 65
ctg atc aag gtg ttg atc aag gac cgc tcg aag gtt aag gaa gct gcg 355
Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys Val Lys Glu Ala Ala
      70 75 80 85
gcg aaa atc gac tgg tgg ttc ctc ggc gct atc ggc gtt ggc atg gtc 403
Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile Gly Val Gly Met Val
      90 95 100
gtg atg gtc ttc tcg atg tca tcg att ttg cat aca gtt gtt gag gac 451
Val Met Val Phe Ser Met Ser Ser Ile Leu His Thr Val Val Glu Asp
      105 110 115
tac cca gag atc act cgc ggt ctg ttc ctt gga atg gtt gcc gtg tct 499
Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly Met Val Ala Val Ser
      120 125 130
atc ctt gtt ccg ttg gga atg atg gat atg cgg gat gcc aag aag cgc 547
Ile Leu Val Pro Leu Gly Met Met Asp Met Arg Asp Ala Lys Lys Arg
      135 140 145
ctc gca atc gtc atc ccg cta ttt ata atc tgc gcc atg ctg gga ttc 595
Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys Ala Met Leu Gly Phe
      150 155 160 165
ttt gga aca tcc ttc act agt gcg cct cgc acc gat cct tca ctg atc 643
Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr Asp Pro Ser Leu Ile
      170 175 180
ttt gtc ttc atc tgt gct gcg atc gct gtg tgt gct ctt gtt ctt cct 691
Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys Ala Leu Val Leu Pro
      185 190 195
ggt gtt cag gat cac 706
Gly Val Gln Asp His
      200

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<210> 350

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Met Ser Ala Thr Asn Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro
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 20 25 30

Gly Gly Leu Ile Gly Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly
 35 40 45

Thr Val Ala Leu Val Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly
 50 55 60

Asp Leu Leu Ile Asp Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys
 65 70 75 80

Val Lys Glu Ala Ala Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile
 85 90 95

Gly Val Gly Met Val Val Met Val Phe Ser Met Ser Ser Ile Leu His
 100 105 110

Thr Val Val Glu Asp Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly
 115 120 125

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
 130 135 140

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
 145 150 155 160

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
 165 170 175

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
 180 185 190

Ala Leu Val Leu Pro Gly Val Gln Asp His
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<210> 351

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> RXN00730

<400> 351

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 Met Ser Ser Gln Gln
 1 5

acg atc ttc atc att ttg ctc ttt gcc gca gtg att ctc att tcc ata	163
Thr Ile Phe Ile Ile Leu Leu Phe Ala Ala Val Ile Leu Ile Ser Ile	
10 15 20	
gta atg att aca gct gcc ttc aaa acc cgg aaa aag cgc ttt gcc gcg	211
Val Met Ile Thr Ala Ala Phe Lys Thr Arg Lys Lys Arg Phe Ala Ala	
25 30 35	
cgg gct gaa gga atg gcc aac cct aca att cct gcg cca act gtg ccg	259
Arg Ala Glu Gly Met Ala Asn Pro Thr Ile Pro Ala Pro Thr Val Pro	
40 45 50	
tgg cag cgc ttc gcc gga gca ctt gca gcc ttg tac gct agg cct gaa	307
Trp Gln Arg Phe Ala Gly Ala Leu Ala Ala Leu Tyr Ala Arg Pro Glu	
55 60 65	
tgg cac aag acc cgc gga gcg aaa cga gtg tac tca gct gaa cag act	355
Trp His Lys Thr Arg Gly Ala Lys Arg Val Tyr Ser Ala Glu Gln Thr	
70 75 80 85	
tat ttt ggg ttt gtc tca gca atg cca ctg ggg atg gtg caa aac atg	403
Tyr Phe Gly Phe Val Ser Ala Met Pro Leu Gly Met Val Gln Asn Met	
90 95 100	
ctg caa aca gac tgg ggt gtg aaa aag tct gag cat gca gtt gat cag	451
Leu Gln Thr Asp Trp Gly Val Lys Lys Ser Glu His Ala Val Asp Gln	
105 110 115	
ctt tct aaa gga gtg gaa gtg atc gtt ggg gta gcc gca ggc aac tgg	499
Leu Ser Lys Gly Val Glu Val Ile Val Gly Val Ala Ala Gly Asn Trp	
120 125 130	
cgt aaa aac gga gta tca ccc gca caa gtg gaa gag gca ggc cag cgg	547
Arg Lys Asn Gly Val Ser Pro Ala Gln Val Glu Glu Ala Gly Gln Arg	
135 140 145	
tta gca gct gaa gga ttg gct cat cca cac ttt gtt gta ttc caa aag	595
Leu Ala Ala Glu Gly Leu Ala His Pro His Phe Val Val Phe Gln Lys	
150 155 160 165	
cag ctt caa cag gca gat cca aat gca gaa tat gat ctc gat gtg ctc	643
Gln Leu Gln Gln Ala Asp Pro Asn Ala Glu Tyr Asp Leu Asp Val Leu	
170 175 180	
gca ttt gat atc gca cgc gta gcc aac ctc ctt cgc tgg gct gct tat	691
Ala Phe Asp Ile Ala Arg Val Ala Asn Leu Leu Arg Trp Ala Ala Tyr	
185 190 195	
aca gat ctg ttg ctc cct gca gaa gcc cgt tgg ttc caa gac cag ctg	739
Thr Asp Leu Leu Leu Pro Ala Glu Ala Arg Trp Phe Gln Asp Gln Leu	
200 205 210	
gga att gcg gct gct gtg tcc ttt ggg agc tgg gaa gaa tac gga gag	787
Gly Ile Ala Ala Ala Val Ser Phe Gly Ser Trp Glu Glu Tyr Gly Glu	
215 220 225	
cga tac gtc cgt gga cta cag aag aac ttc aag ggc gga aac aag cca	835
Arg Tyr Val Arg Gly Leu Gln Lys Asn Phe Lys Gly Gly Asn Lys Pro	
230 235 240 245	
tat atc gaa gga gaa cgc tgg ctc aac act gag gct gaa agt cca tgg	883

Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn Thr Glu
245 250 255

Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
 260 265

<210> 353

<211> 356

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(333)

<223> FRXA00730

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His Phe Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala
  1      5      10      15

gaa tat gat ctc gat gtg ctc gca ttt gat atc gca cgc gta gcc aac 96
Glu Tyr Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn
      20      25      30

ctc ctt cgc tgg gct gct tat aca gat ctg ttg ctc cct gca gaa gcc 144
Leu Leu Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala
      35      40      45

cgt tgg ttc caa gac cag ctg gga att gcg gct gct gtg tcc ttt ggg 192
Arg Trp Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly
      50      55      60

agc tgg gaa gaa tac gga gag cga tac gtc cgt gga cta cag aag aac 240
Ser Trp Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn
  65      70      75      80

ttc aag ggc gga aac aag cca tat atc gaa gga gaa cgc tgg ctc aac 288
Phe Lys Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn
      85      90      95

act gag gct gaa agt cca tgg aag acc caa aag tgg att agc gcc 333
Thr Glu Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
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taactgctca tgagctaagc ggc 356

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<210> 354

<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

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His Phe Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala
  1      5      10      15

Glu Tyr Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn
      20      25      30

Leu Leu Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala
      35      40      45

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Arg Trp Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly
 50 55 60

Ser Trp Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn
 65 70 75 80

Phe Lys Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn
 85 90 95

Thr Glu Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
 100 105 110

<210> 355
 <211> 2619
 <212> DNA
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 <223> RXN00731

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 Met Lys Asp Ala Ser
 1 5

cag tcc tac tta tta ttc ggt ctg aga tgg ctg ggc agg tcc ctg cgt 163
 Gln Ser Tyr Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg
 10 15 20

ttc gca ccg tta agc ctg ctc atg atc gtt gtc atg cgg ggt ttg agg 211
 Phe Ala Pro Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg
 25 30 35

gaa gtg ttt ggc gcc gaa gat ccc gca aat agc tct ttg gta gac aac 259
 Glu Val Phe Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn
 40 45 50

ctt ggg ctc acc ctg ccg tgg tct ctt aat gat ccg cat ttt ctc acc 307
 Leu Gly Leu Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr
 55 60 65

gca ggg ttt agc gct tcc acc acc aca gca gcg ctc atg tcc acg ttg 355
 Ala Gly Phe Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu
 70 75 80 85

tgg atc atc gtg ttt gcg gtg ccc tct gaa cgg att ctg ggc agc ctc 403
 Trp Ile Ile Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu
 90 95 100

aaa ttc gcg atc aca gca gcg ctt atc cac atc act tcc att ccg ctg 451
 Lys Phe Ala Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu
 105 110 115

ggc atc ggc atc gcc cac ctc atc gaa gaa gcc gat ctc aac cgc tgg 499
 Gly Ile Gly Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp

120	125	130	
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ttc ggc gtc gcc gct ttc gca tcc gcc tcc atg cca ctg ctc tgg cga Phe Gly Val Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg 150 155 160 165			595
cgg cgc acc cga ttg ttc ctc ttt act atc acc ttg acg ctg ctg ctt Arg Arg Thr Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu 170 175 180			643
tat acg ggc acg ctt gcc gac gtc acc atg ctc acc gcg acc atc atc Tyr Thr Gly Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile 185 190 195			691
ggc acc gtt gcc ggc gag ttg aac agg cat cgg aaa acc cca ggt ggc Gly Thr Val Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly 200 205 210			739
cgc tgg ctt ccc ggt tcc ctc acc gtg cgt gaa gcg cgc att atg acg Arg Trp Leu Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr 215 220 225			787
gcc att ttg gtc act gcc gta gca gca ggt cca gtg ctt gct gcg ctt Ala Ile Leu Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu 230 235 240 245			835
aat cca ctc acc cac ggc cct ttt tcc agt gca acg aaa ttg atc tgg Asn Pro Leu Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp 250 255 260			883
cag ccc ctt gtc act gaa gaa cac atg cat cac ctc tgc cac aca gac Gln Pro Leu Val Thr Glu Glu His Met His His Leu Cys His Thr Asp 265 270 275			931
agc acc tct gat gca tgc caa ggt gcg ctt gat cag ctc caa cag cac Ser Thr Ser Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His 280 285 290			979
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gcg gtt ttg gcc cag ctc att tcc atc gca gtg ttg atg ttc cag ctg Ala Val Leu Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu 330 335 340			1123
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375 380 385	
tcc tta ggc gct ctc atg gtt aca tgg ttg gca acg gca gca ttg tgg	1315
Ser Leu Gly Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp	
390 395 400 405	
atc ctt gcc aca ttg ttc ctg cca cac gca ttc cac cca cat cca aca	1363
Ile Leu Ala Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr	
410 415 420	
ttg ggg ctg gct ttc aaa gaa ctc ccc ttc cgc tat ctc cca cca act	1411
Leu Gly Leu Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr	
425 430 435	
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Ile Glu Thr Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly	
440 445 450	
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Trp Ala Val Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala	
455 460 465	
gca act ctt tat cat ctg ctc atg ggt gtg ccc agc aac aaa gcg cac	1555
Ala Thr Leu Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His	
470 475 480 485	
gag gac caa gaa aac gca gcg act ctc ctg cgc tct ggc agc ggc gat	1603
Glu Asp Gln Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp	
490 495 500	
cac ttg tcc tgg atg acc att tgg ggt ggc aat acg tat tgg tgg gca	1651
His Leu Ser Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala	
505 510 515	
cca gaa aat gca gga tat gtg gcc tac cgc gtg aaa agg ggc atc gca	1699
Pro Glu Asn Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala	
520 525 530	
att aca ttg ggt gag cct att ctg ggt ccg gat tca tcc gtc tct aaa	1747
Ile Thr Leu Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys	
535 540 545	
gca gag ctg gcc gca cag ttt gaa gaa ttt gcc agc aac caa ggc tgg	1795
Ala Glu Leu Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp	
550 555 560 565	
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Ile Val Ala Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile	
570 575 580	
aac gct ggc cac cac aca ctt cgt gtg gct gag gaa gca gtc tta agc	1891
Asn Ala Gly His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser	
585 590 595	
tca gct aat gcg gat ttc aaa ggt aag cac ttc caa aat gtc cgc acc	1939
Ser Ala Asn Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr	
600 605 610	

gcc cga aac cgc gcg gcc aaa gag ggc gta agt tcc atc tgg aca acc 1987
 Ala Arg Asn Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr
 615 620 625

tgg gct gat ttg agt gcc gaa atg cag cac aag atc atc acg ctg tcg 2035
 Trp Ala Asp Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser
 630 635 640 645

gaa gaa tgg gtc tct gat aaa gct ctg ccg gag atg ggc ttc acg ctt 2083
 Glu Glu Trp Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu
 650 655 660

ggc act gtc aac gag ctc tca gat cca gat acc tat ctt ctt ctc gcg 2131
 Gly Thr Val Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala
 665 670 675

att gat gag gaa gag cat ctg cac ggt gtg acc agt tgg ttg ccg gtc 2179
 Ile Asp Glu Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val
 680 685 690

tat gaa aaa gga cgc atc gtc ggc tac aca ctt gat gtg atg cgc cgt 2227
 Tyr Glu Lys Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg
 695 700 705

gat ccg caa ggc ttt aaa tct gtc atc gag ttt ctc att tcc gag gcc 2275
 Asp Pro Gln Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala
 710 715 720 725

gtc gtt atc gca agg gat cac gat ctg gaa tgg atg tcg atg tcc ggc 2323
 Val Val Ile Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly
 730 735 740

gct cct ttg agt acg ccc cca ggt gtg gcc gac gac ggc acc atc gga 2371
 Ala Pro Leu Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly
 745 750 755

caa att ttg gag ctt ttg ggc cga gca atg gag ccg ttc tac ggt ttc 2419
 Gln Ile Leu Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe
 760 765 770

cgt tcc ctc gct gcg tcc aag aac aaa ttc cac cca gaa cac cac ggt 2467
 Arg Ser Leu Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly
 775 780 785

tgg tac ttg tgt tac cgc gat gaa tta tcg tta cca agc att ggc ctt 2515
 Trp Tyr Leu Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu
 790 795 800 805

gcc gtt gct gcc tgc tac ctc aac gag ttt ccg ctg ccg aat tgg ctg 2563
 Ala Val Ala Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu
 810 815 820

aaa aag acc gcc act tcc gcc cca agc cac agc tagaaaaacg cgtaaccttg 2616
 Lys Lys Thr Ala Thr Ser Ala Pro Ser His Ser
 825 830

gtg 2619

<210> 356

<211> 832

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

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Gly Arg Ser Leu Arg Phe Ala Pro Leu Ser Leu Leu Met Ile Val Val
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Met Arg Gly Leu Arg Glu Val Phe Gly Ala Glu Asp Pro Ala Asn Ser
35 40 45
Ser Leu Val Asp Asn Leu Gly Leu Thr Leu Pro Trp Ser Leu Asn Asp
50 55 60
Pro His Phe Leu Thr Ala Gly Phe Ser Ala Ser Thr Thr Thr Ala Ala
65 70 75 80
Leu Met Ser Thr Leu Trp Ile Ile Val Phe Ala Val Pro Ser Glu Arg
85 90 95
Ile Leu Gly Ser Leu Lys Phe Ala Ile Thr Ala Ala Leu Ile His Ile
100 105 110
Thr Ser Ile Pro Leu Gly Ile Gly Ile Ala His Leu Ile Glu Glu Ala
115 120 125
Asp Leu Asn Arg Trp Gly Asn Asn Met Leu Ala Asp Val Leu Leu Thr
130 135 140
Pro Asp Phe Trp Val Phe Gly Val Ala Ala Phe Ala Ser Ala Ser Met
145 150 155 160
Pro Leu Leu Trp Arg Arg Arg Thr Arg Leu Phe Leu Phe Thr Ile Thr
165 170 175
Leu Thr Leu Leu Leu Tyr Thr Gly Thr Leu Ala Asp Val Thr Met Leu
180 185 190
Thr Ala Thr Ile Ile Gly Thr Val Ala Gly Glu Leu Asn Arg His Arg
195 200 205
Lys Thr Pro Gly Gly Arg Trp Leu Pro Gly Ser Leu Thr Val Arg Glu
210 215 220
Ala Arg Ile Met Thr Ala Ile Leu Val Thr Ala Val Ala Ala Gly Pro
225 230 235 240
Val Leu Ala Ala Leu Asn Pro Leu Thr His Gly Pro Phe Ser Ser Ala
245 250 255
Thr Lys Leu Ile Trp Gln Pro Leu Val Thr Glu Glu His Met His His
260 265 270
Leu Cys His Thr Asp Ser Thr Ser Asp Ala Cys Gln Gly Ala Leu Asp
275 280 285
Gln Leu Gln Gln His Gly Val Gly Pro Ser Val Ala Asn Leu Ile Pro
290 295 300

Leu Ile Leu Thr Val Val Leu Ala Met Gly Leu Ser Arg Gly Arg Arg
 305 310 315 320
 Leu Ala Trp Ile Leu Ala Val Leu Ala Gln Leu Ile Ser Ile Ala Val
 325 330 335
 Leu Met Phe Gln Leu Thr Lys Leu Ser Ala Asp Ser Thr Asp Leu Leu
 340 345 350
 Trp Ser Val Asn Ala Phe Ser Val Ile Val Pro Trp Leu Val Ala Leu
 355 360 365
 Ala Val Leu Val Phe Ser Arg Arg Ala Phe Gln Val Lys Ile Asp Thr
 370 375 380
 Thr Arg Ile Ser Lys Ser Leu Gly Ala Leu Met Val Thr Trp Leu Ala
 385 390 395 400
 Thr Ala Ala Leu Trp Ile Leu Ala Thr Leu Phe Leu Pro His Ala Phe
 405 410 415
 His Pro His Pro Thr Leu Gly Leu Ala Phe Lys Glu Leu Pro Phe Arg
 420 425 430
 Tyr Leu Pro Pro Thr Ile Glu Thr Val Leu Ser His Gln Leu Phe Pro
 435 440 445
 Arg Ser Pro Ala Gly Trp Ala Val Phe Glu Trp Thr Gly Thr Leu Phe
 450 455 460
 Trp Leu Val Val Ala Ala Thr Leu Tyr His Leu Leu Met Gly Val Pro
 465 470 475 480
 Ser Asn Lys Ala His Glu Asp Gln Glu Asn Ala Ala Thr Leu Leu Arg
 485 490 495
 Ser Gly Ser Gly Asp His Leu Ser Trp Met Thr Ile Trp Gly Gly Asn
 500 505 510
 Thr Tyr Trp Trp Ala Pro Glu Asn Ala Gly Tyr Val Ala Tyr Arg Val
 515 520 525
 Lys Arg Gly Ile Ala Ile Thr Leu Gly Glu Pro Ile Leu Gly Pro Asp
 530 535 540
 Ser Ser Val Ser Lys Ala Glu Leu Ala Ala Gln Phe Glu Glu Phe Ala
 545 550 555 560
 Ser Asn Gln Gly Trp Ile Val Ala Trp Tyr Ser Val Cys Glu Glu Phe
 565 570 575
 Ser Lys Glu Arg Ile Asn Ala Gly His His Thr Leu Arg Val Ala Glu
 580 585 590
 Glu Ala Val Leu Ser Ser Ala Asn Ala Asp Phe Lys Gly Lys His Phe
 595 600 605
 Gln Asn Val Arg Thr Ala Arg Asn Arg Ala Ala Lys Glu Gly Val Ser
 610 615 620
 Ser Ile Trp Thr Thr Trp Ala Asp Leu Ser Ala Glu Met Gln His Lys

625	630	635	640
Ile Ile Thr Leu Ser Glu Glu Trp Val Ser Asp Lys Ala Leu Pro Glu	645	650	655
Met Gly Phe Thr Leu Gly Thr Val Asn Glu Leu Ser Asp Pro Asp Thr	660	665	670
Tyr Leu Leu Leu Ala Ile Asp Glu Glu Glu His Leu His Gly Val Thr	675	680	685
Ser Trp Leu Pro Val Tyr Glu Lys Gly Arg Ile Val Gly Tyr Thr Leu	690	695	700
Asp Val Met Arg Arg Asp Pro Gln Gly Phe Lys Ser Val Ile Glu Phe	705	710	715
Leu Ile Ser Glu Ala Val Val Ile Ala Arg Asp His Asp Leu Glu Trp	725	730	735
Met Ser Met Ser Gly Ala Pro Leu Ser Thr Pro Pro Gly Val Ala Asp	740	745	750
Asp Gly Thr Ile Gly Gln Ile Leu Glu Leu Leu Gly Arg Ala Met Glu	755	760	765
Pro Phe Tyr Gly Phe Arg Ser Leu Ala Ala Ser Lys Asn Lys Phe His	770	775	780
Pro Glu His His Gly Trp Tyr Leu Cys Tyr Arg Asp Glu Leu Ser Leu	785	790	795
Pro Ser Ile Gly Leu Ala Val Ala Ala Cys Tyr Leu Asn Glu Phe Pro	805	810	815
Leu Pro Asn Trp Leu Lys Lys Thr Ala Thr Ser Ala Pro Ser His Ser	820	825	830

<210> 357

<211> 2495

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2472)

<223> FRXA00731

<400> 357

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1 5 10 15	
tta agc ctg ctc atg atc gtt gtc atg cgg ggt ttg agg gaa gtg ttt	96
Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg Glu Val Phe	
20 25 30	
ggc gcc gaa gat ccc gca aat agc tct ttg gta gac aac ctt ggg ctc	144
Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn Leu Gly Leu	
35 40 45	

acc ctg ccg tgg tct ctt aat gat ccg cat ttt ctc acc gca ggg ttt	192
Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr Ala Gly Phe	
50 55 60	
agc gct tcc acc acc aca gca gcg ctc atg tcc acg ttg tgg atc atc	240
Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu Trp Ile Ile	
65 70 75 80	
gtg ttt gcg gtg ccc tct gaa ccg att ctg ggc agc ctc aaa ttc gcg	288
Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu Lys Phe Ala	
85 90 95	
atc aca gca gcg ctt atc cac atc act tcc att ccg ctg ggc atc ggc	336
Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu Gly Ile Gly	
100 105 110	
atc gcc cac ctc atc gaa gaa gcc gat ctc aac cgc tgg ggc aac aac	384
Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp Gly Asn Asn	
115 120 125	
atg ttg gcc gat gtg ctg ctc acc cca gat ttc tgg gtc ttc ggc gtc	432
Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val Phe Gly Val	
130 135 140	
gcc gct ttc gca tcc gcc tcc atg cca ctg ctc tgg cga ccg cgc acc	480
Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg Arg Arg Thr	
145 150 155 160	
cga ttg ttc ctc ttt act atc acc ttg acg ctg ctg ctt tat acg ggc	528
Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu Tyr Thr Gly	
165 170 175	
acg ctt gcc gac gtc acc atg ctc acc gcg acc atc atc ggc acc gtt	576
Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile Gly Thr Val	
180 185 190	
gcc ggc gag ttg aac agg cat ccg aaa acc cca ggt ggc cgc tgg ctt	624
Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly Arg Trp Leu	
195 200 205	
ccc ggt tcc ctc acc gtg cgt gaa gcg cgc att atg acg gcc att ttg	672
Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr Ala Ile Leu	
210 215 220	
gtc act gcc gta gca gca ggt cca gtg ctt gct gcg ctt aat cca ctc	720
Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu Asn Pro Leu	
225 230 235 240	
acc cac ggc cct ttt tcc agt gca acg aaa ttg atc tgg cag ccc ctt	768
Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp Gln Pro Leu	
245 250 255	
gtc act gaa gaa cac atg cat cac ctc tgc cac aca gac agc acc tct	816
Val Thr Glu Glu His Met His His Leu Cys His Thr Asp Ser Thr Ser	
260 265 270	
gat gca tgc caa ggt gcg ctt gat cag ctc caa cag cac ggt gtt ggc	864
Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His Gly Val Gly	
275 280 285	

cct tcc gtt gcc aac ctg att cca ctg atc ctc acc gtg gtc ctt gcg Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val Val Leu Ala 290 295 300	912
atg ggg ctt agc cgc gga cgt cga ctt gca tgg att ttg gcg gtt ttg Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu Ala Val Leu 305 310 315 320	960
gcc cag ctc att tcc atc gca gtg ttg atg ttc cag ctg acc aaa cta Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu Thr Lys Leu 325 330 335	1008
tcg gct gat tcc acc gat ctt cta tgg tca gtc aat gcc ttt agc gtg Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala Phe Ser Val 340 345 350	1056
atc gtt cct tgg ctg gtg gcg ctc gcc gtc ttg gtg ttt tcc cgc cgt Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe Ser Arg Arg 355 360 365	1104
gca ttc cag gtg aag att gat acc acc cgg att tct aaa tcc tta ggc Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys Ser Leu Gly 370 375 380	1152
gct ctc atg gtt aca tgg ttg gca acg gca gca ttg tgg atc ctt gcc Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp Ile Leu Ala 385 390 395 400	1200
aca ttg ttc ctg cca cac gca ttc cac cca cat cca aca ttg ggg ctg Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr Leu Gly Leu 405 410 415	1248
gct ttc aaa gaa ctc ccc ttc cgc tat ctc cca cca act atc gaa acg Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr Ile Glu Thr 420 425 430	1296
gtg tta agc cat caa ctc ttc ccc aga agc cct gct ggg tgg gca gtg Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly Trp Ala Val 435 440 445	1344
ttt gaa tgg act gga acg cta ttc tgg ctg gtc gta gca gca act ctt Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala Ala Thr Leu 450 455 460	1392
tat cat ctg ctc atg ggt gtg ccc agc aac aaa gcg cac gag gac caa Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His Glu Asp Gln 465 470 475 480	1440
gaa aac gca gcg act ctc ctg cgc tct ggc agc ggc gat cac ttg tcc Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp His Leu Ser 485 490 495	1488
tgg atg acc att tgg ggt ggc aat acg tat tgg tgg gca cca gaa aat Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala Pro Glu Asn 500 505 510	1536
gca gga tat gtg gcc tac cgc gtg aaa agg ggc atc gca att aca ttg Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala Ile Thr Leu 515 520 525	1584
ggc gag cct att ctg ggt ccg gat tca tcc gtc tct aaa gca gag ctg	1632

Gly 530	Glu	Pro	Ile	Leu	Gly 535	Pro	Asp	Ser	Ser	Val	Ser 540	Lys	Ala	Glu	Leu	
gcc	gca	cag	ttt	gaa	gaa	ttt	gcc	agc	aac	caa	ggc	tgg	att	gtt	gcg	1680
Ala	Ala	Gln	Phe	Glu	Glu	Phe	Ala	Ser	Asn	Gln	Gly	Trp	Ile	Val	Ala	
545					550					555					560	
tgg	tat	tcc	gtt	tgt	gaa	gaa	ttc	tca	aag	gaa	cgc	atc	aac	gct	ggc	1728
Trp	Tyr	Ser	Val	Cys	Glu	Glu	Phe	Ser	Lys	Glu	Arg	Ile	Asn	Ala	Gly	
				565					570					575		
cac	cac	aca	ctt	cgt	gtg	gct	gag	gaa	gca	gtc	tta	agc	tca	gct	aat	1776
His	His	Thr	Leu	Arg	Val	Ala	Glu	Glu	Ala	Val	Leu	Ser	Ser	Ala	Asn	
			580					585					590			
gcg	gat	ttc	aaa	ggg	aag	cac	ttc	caa	aat	gtc	cgc	acc	gcc	cga	aac	1824
Ala	Asp	Phe	Lys	Gly	Lys	His	Phe	Gln	Asn	Val	Arg	Thr	Ala	Arg	Asn	
		595					600					605				
cgc	gcg	gcc	aaa	gag	ggc	gta	agt	tcc	atc	tgg	aca	acc	tgg	gct	gat	1872
Arg	Ala	Ala	Lys	Glu	Gly	Val	Ser	Ser	Ile	Trp	Thr	Thr	Trp	Ala	Asp	
	610					615					620					
ttg	agt	gcc	gaa	atg	cag	cac	aag	atc	atc	acg	ctg	tcg	gaa	gaa	tgg	1920
Leu	Ser	Ala	Glu	Met	Gln	His	Lys	Ile	Ile	Thr	Leu	Ser	Glu	Glu	Trp	
625					630					635					640	
gtc	tct	gat	aaa	gct	ctg	ccg	gag	atg	ggc	ttc	acg	ctt	ggc	act	gtc	1968
Val	Ser	Asp	Lys	Ala	Leu	Pro	Glu	Met	Gly	Phe	Thr	Leu	Gly	Thr	Val	
				645					650					655		
aac	gag	ctc	tca	gat	cca	gat	acc	tat	ctt	ctt	ctc	gcg	att	gat	gag	2016
Asn	Glu	Leu	Ser	Asp	Pro	Asp	Thr	Tyr	Leu	Leu	Leu	Ala	Ile	Asp	Glu	
			660					665					670			
gaa	gag	cat	ctg	cac	ggg	gtg	acc	agt	tgg	ttg	ccg	gtc	tat	gaa	aaa	2064
Glu	Glu	His	Leu	His	Gly	Val	Thr	Ser	Trp	Leu	Pro	Val	Tyr	Glu	Lys	
		675					680					685				
gga	cgc	atc	gtc	ggc	tac	aca	ctt	gat	gtg	atg	cgc	cgt	gat	ccg	caa	2112
Gly	Arg	Ile	Val	Gly	Tyr	Thr	Leu	Asp	Val	Met	Arg	Arg	Asp	Pro	Gln	
	690					695					700					
ggc	ttt	aaa	tct	gtc	atc	gag	ttt	ctc	att	tcc	gag	gcc	gtc	gtt	atc	2160
Gly	Phe	Lys	Ser	Val	Ile	Glu	Phe	Leu	Ile	Ser	Glu	Ala	Val	Val	Ile	
705					710					715					720	
gca	agg	gat	cac	gat	ctg	gaa	tgg	atg	tcg	atg	tcc	ggc	gct	cct	ttg	2208
Ala	Arg	Asp	His	Asp	Leu	Glu	Trp	Met	Ser	Met	Ser	Gly	Ala	Pro	Leu	
				725					730					735		
agt	acg	ccc	cca	ggg	gtg	gcc	gac	gac	ggc	acc	atc	gga	caa	att	ttg	2256
Ser	Thr	Pro	Pro	Gly	Val	Ala	Asp	Asp	Gly	Thr	Ile	Gly	Gln	Ile	Leu	
			740					745					750			
gag	ctt	ttg	ggc	cga	gca	atg	gag	ccg	ttc	tac	ggg	ttc	cgt	tcc	ctc	2304
Glu	Leu	Leu	Gly	Arg	Ala	Met	Glu	Pro	Phe	Tyr	Gly	Phe	Arg	Ser	Leu	
		755					760					765				
gct	gcg	tcc	aag	aac	aaa	ttc	cac	cca	gaa	cac	cac	ggg	tgg	tac	ttg	2352
Ala	Ala	Ser	Lys	Asn	Lys	Phe	His	Pro	Glu	His	His	Gly	Trp	Tyr	Leu	

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      770              775              780
tgt tac cgc gat gaa tta tcg tta cca agc att ggc ctt gcc gtt gct 2400
Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu Ala Val Ala
785              790              795              800

gcc tgc tac ctc aac gag ttt ccg ctg ccg aat tgg ctg aaa aag acc 2448
Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu Lys Lys Thr
      805              810              815

gcc act tcc gcc cca agc cac agc tagaaaaacg cgtaaccttg gtg 2495
Ala Thr Ser Ala Pro Ser His Ser
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<210> 358
 <211> 824
 <212> PRT
 <213> Corynebacterium glutamicum

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Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg Glu Val Phe
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Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn Leu Gly Leu
      35              40              45

Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr Ala Gly Phe
      50              55              60

Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu Trp Ile Ile
      65              70              75              80

Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu Lys Phe Ala
      85              90              95

Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu Gly Ile Gly
      100              105              110

Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp Gly Asn Asn
      115              120              125

Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val Phe Gly Val
      130              135              140

Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg Arg Arg Thr
      145              150              155              160

Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu Tyr Thr Gly
      165              170              175

Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile Gly Thr Val
      180              185              190

Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly Arg Trp Leu
      195              200              205

Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr Ala Ile Leu

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210	215	220
Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu Asn Pro Leu 225 230 235 240		
Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp Gln Pro Leu 245 250 255		
Val Thr Glu Glu His Met His His Leu Cys His Thr Asp Ser Thr Ser 260 265 270		
Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His Gly Val Gly 275 280 285		
Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val Val Leu Ala 290 295 300		
Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu Ala Val Leu 305 310 315 320		
Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu Thr Lys Leu 325 330 335		
Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala Phe Ser Val 340 345 350		
Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe Ser Arg Arg 355 360 365		
Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys Ser Leu Gly 370 375 380		
Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp Ile Leu Ala 385 390 395 400		
Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr Leu Gly Leu 405 410 415		
Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr Ile Glu Thr 420 425 430		
Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly Trp Ala Val 435 440 445		
Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala Ala Thr Leu 450 455 460		
Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His Glu Asp Gln 465 470 475 480		
Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp His Leu Ser 485 490 495		
Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala Pro Glu Asn 500 505 510		
Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala Ile Thr Leu 515 520 525		
Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys Ala Glu Leu 530 535 540		

Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp Ile Val Ala
 545 550 555 560
 Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile Asn Ala Gly
 565 570 575
 His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser Ser Ala Asn
 580 585 590
 Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr Ala Arg Asn
 595 600 605
 Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr Trp Ala Asp
 610 615 620
 Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser Glu Glu Trp
 625 630 635 640
 Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu Gly Thr Val
 645 650 655
 Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala Ile Asp Glu
 660 665 670
 Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val Tyr Glu Lys
 675 680 685
 Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg Asp Pro Gln
 690 695 700
 Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala Val Val Ile
 705 710 715 720
 Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly Ala Pro Leu
 725 730 735
 Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly Gln Ile Leu
 740 745 750
 Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe Arg Ser Leu
 755 760 765
 Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly Trp Tyr Leu
 770 775 780
 Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu Ala Val Ala
 785 790 795 800
 Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu Lys Lys Thr
 805 810 815
 Ala Thr Ser Ala Pro Ser His Ser
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<210> 359

<211> 386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(363)

<223> RXN00738

<400> 359

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Cys	Gln	Glu	Glu	Thr	Asp	Gly	Phe	Phe	Asp	Phe	Gly	Arg	Asp	Met	Arg	
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ccc	ggt	gag	cgc	cgg	tcg	tat	ggc	act	ttg	ctt	aac	gac	gcc	acg	acg	96
Pro	Gly	Glu	Arg	Arg	Ser	Tyr	Gly	Thr	Leu	Leu	Asn	Asp	Ala	Thr	Thr	
			20				25						30			

cag	gtg	tcg	cac	atc	ctc	ggc	aat	gcc	ttc	acc	cga	tct	ggg	ctc	aac	144
Gln	Val	Ser	His	Ile	Leu	Gly	Asn	Ala	Phe	Thr	Arg	Ser	Gly	Leu	Asn	
		35				40						45				

gct	gag	tac	gcg	aat	ctt	tat	ggt	cag	gcg	ttg	gtg	ggc	atg	gtg	tcg	192
Ala	Glu	Tyr	Ala	Asn	Leu	Tyr	Gly	Gln	Ala	Leu	Val	Gly	Met	Val	Ser	
	50					55					60					

atg	acg	gcg	caa	tgg	tgg	ttg	gat	gag	cgc	act	ccg	ccg	aag	gaa	gaa	240
Met	Thr	Ala	Gln	Trp	Trp	Leu	Asp	Glu	Arg	Thr	Pro	Pro	Lys	Glu	Glu	
	65				70				75					80		

gtt	gcc	gca	cat	att	gtt	aat	ctt	tgt	tgg	aat	ggt	ttg	acg	ggg	atg	288
Val	Ala	Ala	His	Ile	Val	Asn	Leu	Cys	Trp	Asn	Gly	Leu	Thr	Gly	Met	
			85					90						95		

gaa	gcc	gat	ccg	aag	tta	act	ccc	atc	agt	tct	gct	gag	ggt	gcg	att	336
Glu	Ala	Asp	Pro	Lys	Leu	Thr	Pro	Ile	Ser	Ser	Ala	Glu	Gly	Ala	Ile	
			100				105						110			

ttt	ggt	caa	gaa	aag	gag	agt	gaa	gcg	tgacacctat	gctcgcgggg	383
Phe	Gly	Gln	Glu	Lys	Glu	Ser	Glu	Ala			
	115						120				

ctg																386
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<210> 360

<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Cys	Gln	Glu	Glu	Thr	Asp	Gly	Phe	Phe	Asp	Phe	Gly	Arg	Asp	Met	Arg
1				5					10					15	

Pro	Gly	Glu	Arg	Arg	Ser	Tyr	Gly	Thr	Leu	Leu	Asn	Asp	Ala	Thr	Thr
			20				25						30		

Gln	Val	Ser	His	Ile	Leu	Gly	Asn	Ala	Phe	Thr	Arg	Ser	Gly	Leu	Asn
			35			40						45			

Ala	Glu	Tyr	Ala	Asn	Leu	Tyr	Gly	Gln	Ala	Leu	Val	Gly	Met	Val	Ser
	50					55					60				

Met	Thr	Ala	Gln	Trp	Trp	Leu	Asp	Glu	Arg	Thr	Pro	Pro	Lys	Glu	Glu
	65				70				75					80	

Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
85 90 95

Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
100 105 110

Phe Gly Gln Glu Lys Glu Ser Glu Ala
115 120

<210> 361

<211> 388

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (78)..(365)

<223> FRXA00738

<400> 361

catgcccccta ttagacggat ggcttttttg attttgggcg cgatatgcgg cccggtgagc 60

gccggtcgta tggcaact ttg ctt aac gac gcc acg acg cag gtg tcg cac atc 113
Leu Leu Asn Asp Ala Thr Thr Gln Val Ser His Ile
1 5 10

ctc ggc aat gcc ttc acc cga tct ggg ctc aac gct gag tac gcg aat 161
Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn Ala Glu Tyr Ala Asn
15 20 25

ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg atg acg gcg caa tgg 209
Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser Met Thr Ala Gln Trp
30 35 40

tgg ttg gat gag cgc act ccg ccg aag gaa gaa gtt gcc gca cat att 257
Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu Val Ala Ala His Ile
45 50 55 60

gtt aat ctt tgt tgg aat ggt ttg acg ggg atg gaa gcc gat ccg aag 305
Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met Glu Ala Asp Pro Lys
65 70 75

tta act ccc atc agt tct gct gag ggt gcg att ttt ggt caa gaa aag 353
Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile Phe Gly Gln Glu Lys
80 85 90

gag agt gaa gcg tgacacctat gctcgcgggg ctg 388
Glu Ser Glu Ala
95

<210> 362

<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

Leu Leu Asn Asp Ala Thr Thr Gln Val Ser His Ile Leu Gly Asn Ala
1 5 10 15

Phe Thr Arg Ser Gly Leu Asn Ala Glu Tyr Ala Asn Leu Tyr Gly Gln
 20 25 30
 Ala Leu Val Gly Met Val Ser Met Thr Ala Gln Trp Trp Leu Asp Glu
 35 40 45
 Arg Thr Pro Pro Lys Glu Glu Val Ala Ala His Ile Val Asn Leu Cys
 50 55 60
 Trp Asn Gly Leu Thr Gly Met Glu Ala Asp Pro Lys Leu Thr Pro Ile
 65 70 75 80
 Ser Ser Ala Glu Gly Ala Ile Phe Gly Gln Glu Lys Glu Ser Glu Ala
 85 90 95

<210> 363

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> RXN00750

<400> 363

ttttaaacaagcgcgataacaatgaaccgatggtgtctacgacagaaccga cccccccacc 60
 cactaacacc ccaccagaaaataacacctc gaccgaacct atg gac tgg tcg atc 115
 Met Asp Trp Ser Ile
 1 5
 att att aat gtg ctt gcc gtt gct act gtc gtg ata ctc acc ctt atc 163
 Ile Ile Asn Val Leu Ala Val Ala Thr Val Val Ile Leu Thr Leu Ile
 10 15 20
 atc gca gct gca tta tat agg ggt ttc aca cgc aac aaa ata aaa aaa 211
 Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg Asn Lys Ile Lys Lys
 25 30 35
 ctt gaa gct ata cga gaa gcc cag caa cac gaa cgc gac aat ccc act 259
 Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu Arg Asp Asn Pro Thr
 40 45 50
 atc cgc att gct gat ctt cgc ggc atc atg gat act cac cac tac atc 307
 Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp Thr His His Tyr Ile
 55 60 65
 tac acc gac gtc atg gtt aca cgt gca cat gaa ctc atg att act gca 355
 Tyr Thr Asp Val Met Val Thr Arg Ala His Glu Leu Met Ile Thr Ala
 70 75 80 85
 ccc gca ttc ttt gat gtc act ctc ccc gaa gca gtg ctc tac gaa gat 403
 Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala Val Leu Tyr Glu Asp
 90 95 100
 act aaa cgt gct gct cat gat gcc ctt aac ggc tat aaa gac acc act 451
 Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly Tyr Lys Asp Thr Thr
 105 110 115

gtc gct agt gca gag aag atc atg ctt gta gat gca gtc acc gca gca 499
Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp Ala Val Thr Ala Ala
120 125 130

tgg act ctc tat tcc aca aaa gca aac acc gga tcc acg tgatccgaga 548
Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly Ser Thr
135 140 145

gccgagtacc gct 561

<210> 364

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Met Asp Trp Ser Ile Ile Ile Asn Val Leu Ala Val Ala Thr Val Val
1 5 10 15

Ile Leu Thr Leu Ile Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg
20 25 30

Asn Lys Ile Lys Lys Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu
35 40 45

Arg Asp Asn Pro Thr Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp
50 55 60

Thr His His Tyr Ile Tyr Thr Asp Val Met Val Thr Arg Ala His Glu
65 70 75 80

Leu Met Ile Thr Ala Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala
85 90 95

Val Leu Tyr Glu Asp Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly
100 105 110

Tyr Lys Asp Thr Thr Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp
115 120 125

Ala Val Thr Ala Ala Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly
130 135 140

Ser Thr
145

<210> 365

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA00750

<400> 365

tttaaaca aa agcgataaca atgaaccgat ggtgtctacg acagaaccga ctccccacc 60

Thr His His Tyr Ile Tyr Thr Asp Val Met Val Thr Arg Ala His Glu
65 70 75 80

Leu Met Ile Thr Ala Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala
85 90 95

Val Leu Tyr Glu Asp Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly
100 105 110

Tyr Lys Asp Thr Thr Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp
115 120 125

Ala Val Thr Ala Ala Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly
130 135 140

Ser Thr
145

<210> 367

<211> 999

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(976)

<223> RXN00762

<400> 367

gatgctgcga tggtcacaag tcgttttctg gattttttcca catctatatc tttacccac 60

gttcctgcaa gagattcaaa cttggggcta acctggggac atg aat act tcc gat 115
Met Asn Thr Ser Asp
1 5

cgt att aaa agc act caa atc gcg ctg gat cgt gac ctc cgt gag cag 163
Arg Ile Lys Ser Thr Gln Ile Ala Leu Asp Arg Asp Leu Arg Glu Gln
10 15 20

gca cta ttg ctt ttg aag gag gtt cgc gca gtt gat ggc gtg gat gct 211
Ala Leu Leu Leu Leu Lys Glu Val Arg Ala Val Asp Gly Val Asp Ala
25 30 35

tta tca gaa caa ttt gtc cgt ggg ctt gca gaa ccc gga ctt gtt cac 259
Leu Ser Glu Gln Phe Val Arg Gly Leu Ala Glu Pro Gly Leu Val His
40 45 50

tcc cat tta ata gtc acg ctc aat agc gag ctg gtt ggc ctc gcg gcc 307
Ser His Leu Ile Val Thr Leu Asn Ser Glu Leu Val Gly Leu Ala Ala
55 60 65

gcg gat gag gaa acc acg gaa ctg gct gtc cac ccg gcg cac agg cgt 355
Ala Asp Glu Glu Thr Thr Glu Leu Ala Val His Pro Ala His Arg Arg
70 75 80 85

cag gga atc ggt aag gcg ctt atc gac gcc gcc ccc acc tca tca atc 403
Gln Gly Ile Gly Lys Ala Leu Ile Asp Ala Ala Pro Thr Ser Ser Ile
90 95 100

tgg gcg cat gga aat aca gca ggt gca caa gcg ttg gca tcc acc ctg 451

Trp	Ala	His	Gly	Asn	Thr	Ala	Gly	Ala	Gln	Ala	Leu	Ala	Ser	Thr	Leu		
			105					110					115				
cgt	atg	aag	aag	act	cgc	gag	ctt	ctg	gtg	atg	gag	att	tcc	gac	agg	499	
Arg	Met	Lys	Lys	Thr	Arg	Glu	Leu	Leu	Val	Met	Glu	Ile	Ser	Asp	Arg		
		120					125					130					
gcg	ctc	gat	gac	tct	gca	gca	tac	aaa	gat	cca	gat	gga	att	aca	cac	547	
Ala	Leu	Asp	Asp	Ser	Ala	Ala	Tyr	Lys	Asp	Pro	Asp	Gly	Ile	Thr	His		
		135					140					145					
agt	agt	ttg	gcg	aat	gcc	cct	gtg	gag	aaa	tca	gta	gct	gag	gct	aaa	595	
Ser	Ser	Leu	Ala	Asn	Ala	Pro	Val	Glu	Lys	Ser	Val	Ala	Glu	Ala	Lys		
150					155				160						165		
tgg	ctt	caa	tcc	aac	aac	gaa	gca	ttc	gac	tgg	cat	ccc	gag	cag	ggc	643	
Trp	Leu	Gln	Ser	Asn	Asn	Glu	Ala	Phe	Asp	Trp	His	Pro	Glu	Gln	Gly		
				170					175					180			
gga	tgg	aca	act	cat	cgg	ttg	gcg	cag	gct	cag	aaa	gcc	gat	tgg	tac	691	
Gly	Trp	Thr	Thr	His	Arg	Leu	Ala	Gln	Ala	Gln	Lys	Ala	Asp	Trp	Tyr		
			185					190					195				
aag	gac	tct	gac	gtg	tta	ttc	ctc	tgg	gac	ggc	gaa	gag	atc	gtt	ggc	739	
Lys	Asp	Ser	Asp	Val	Leu	Phe	Leu	Trp	Asp	Gly	Glu	Glu	Ile	Val	Gly		
		200					205					210					
ttc	cac	tgg	gta	aag	cag	cac	agt	cca	gaa	tta	caa	gag	att	tac	gta	787	
Phe	His	Trp	Val	Lys	Gln	His	Ser	Pro	Glu	Leu	Gln	Glu	Ile	Tyr	Val		
		215				220					225						
gtt	ggc	ctt	tct	tca	gcc	tac	cgt	ggt	cgc	ggc	ttg	gga	gat	ccg	ctt	835	
Val	Gly	Leu	Ser	Ser	Ala	Tyr	Arg	Gly	Arg	Gly	Leu	Gly	Asp	Pro	Leu		
230					235				240						245		
gtt	cgc	ctc	gga	ctg	cat	cac	atg	agg	gct	cat	ggt	gct	cga	aaa	gtg	883	
Val	Arg	Leu	Gly	Leu	His	His	Met	Arg	Ala	His	Gly	Ala	Arg	Lys	Val		
				250				255						260			
att	ctt	tat	gtg	gaa	gct	ggc	aac	act	ccg	gca	gtc	gcg	gca	tac	gaa	931	
Ile	Leu	Tyr	Val	Glu	Ala	Gly	Asn	Thr	Pro	Ala	Val	Ala	Ala	Tyr	Glu		
			265					270					275				
aaa	ctg	gga	ttc	act	gtc	gcg	gaa	agc	cac	gta	gtt	tac	gaa	aag		976	
Lys	Leu	Gly	Phe	Thr	Val	Ala	Glu	Ser	His	Val	Val	Tyr	Glu	Lys			
		280					285					290					
taaaaaagag acttgctaaa aac																999	

<210> 368

<211> 292

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

Met	Asn	Thr	Ser	Asp	Arg	Ile	Lys	Ser	Thr	Gln	Ile	Ala	Leu	Asp	Arg
1				5					10					15	

Asp	Leu	Arg	Glu	Gln	Ala	Leu	Leu	Leu	Lys	Glu	Val	Arg	Ala	Val
			20					25				30		

Asp Gly Val Asp Ala Leu Ser Glu Gln Phe Val Arg Gly Leu Ala Glu
35 40 45

Pro Gly Leu Val His Ser His Leu Ile Val Thr Leu Asn Ser Glu Leu
50 55 60

Val Gly Leu Ala Ala Ala Asp Glu Glu Thr Thr Glu Leu Ala Val His
65 70 75 80

Pro Ala His Arg Arg Gln Gly Ile Gly Lys Ala Leu Ile Asp Ala Ala
85 90 95

Pro Thr Ser Ser Ile Trp Ala His Gly Asn Thr Ala Gly Ala Gln Ala
100 105 110

Leu Ala Ser Thr Leu Arg Met Lys Lys Thr Arg Glu Leu Leu Val Met
115 120 125

Glu Ile Ser Asp Arg Ala Leu Asp Asp Ser Ala Ala Tyr Lys Asp Pro
130 135 140

Asp Gly Ile Thr His Ser Ser Leu Ala Asn Ala Pro Val Glu Lys Ser
145 150 155 160

Val Ala Glu Ala Lys Trp Leu Gln Ser Asn Asn Glu Ala Phe Asp Trp
165 170 175

His Pro Glu Gln Gly Gly Trp Thr Thr His Arg Leu Ala Gln Ala Gln
180 185 190

Lys Ala Asp Trp Tyr Lys Asp Ser Asp Val Leu Phe Leu Trp Asp Gly
195 200 205

Glu Glu Ile Val Gly Phe His Trp Val Lys Gln His Ser Pro Glu Leu
210 215 220

Gln Glu Ile Tyr Val Val Gly Leu Ser Ser Ala Tyr Arg Gly Arg Gly
225 230 235 240

Leu Gly Asp Pro Leu Val Arg Leu Gly Leu His His Met Arg Ala His
245 250 255

Gly Ala Arg Lys Val Ile Leu Tyr Val Glu Ala Gly Asn Thr Pro Ala
260 265 270

Val Ala Ala Tyr Glu Lys Leu Gly Phe Thr Val Ala Glu Ser His Val
275 280 285

Val Tyr Glu Lys
290

<210> 369

<211> 1242

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1219)

<400> 369

cacttgcgct tttggaagga ataacccttc ctgtcagatt gtg ggt act atc gaa 115
Val Gly Thr Ile Glu
1 5

gac gtg gct aac gaa caa atc gag gtc gcg aac aac act gat cag att 163
Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn Asn Thr Asp Gln Ile
10 15 20

cct gca gga tac aag tcc cct ctt ctt tct aga agt ggt gcg gca gaa 211
Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg Ser Gly Ala Ala Glu
25 30 35

gcg cag ggc gct gct gct caa gca ggt act gaa ggt gtc gcg tgg cat 259
Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu Gly Val Ala Trp His
40 45 50

tac ggt tcc cct ctg gtc gag caa cgc atc ttc gaa act ggc acg ggc 307
Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe Glu Thr Gly Thr Gly
 55 60 65

tta	ggt	gac	cgt	tct	aat	cg	aag	gtg	atc	aaa	gtc	gaa	ggg	cct	gat	355
Leu	Val	Asp	Arg	Ser	Asn	Arg	Lys	Val	Ile	Lys	Val	Glu	Gly	Pro	Asp	
70					75					80					85	

gcc ccc acg ttc ctc aat aat att ttg tcc caa aag gtt gat tcc gtt 403
Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln Lys Val Asp Ser Val
90 95 100

gaa aac ggc ttt act gcc ggt gcc ctg gat ttg gat gcg cag ggt cgt 451
Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu Asp Ala Gln Gly Arg
105 110 115

att caa cac aca atg cag gta act gtc gtc gat ggg gtt ttc tac ctc 499
Ile Gln His Thr Met Gln Val Thr Val Val Asp Gly Val Phe Tyr Leu
120 125 130

gac acg tcc gcg gcg gag ttt gat acc ctc atc ggt ttc ttg acc aag 547
Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile Gly Phe Leu Thr Lys
135 140 145

atg att ttc tgg tgc gaa gtc acc gtc cag gaa gcc gat ctg gcg atc 595
Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu Ala Asp Leu Ala Ile
150 155 160 165

atc	act	ctg	ctc	ggc	cag	gaa	att	gcc	ctt	ccg	gac	gcg	gtc	ttt	gcc	643
Ile	Thr	Leu	Leu	Gly	Gln	Glu	Ile	Ala	Leu	Pro	Asp	Ala	Val	Phe	Ala	
				170					175					180		

cgt agg gtc gat tgg aat ggg cca tcg cgt atc gac gtc gcc atc cgg 691
Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile Asp Val Ala Ile Arg
185 190 195

cgt gaa aac ctg gag gag ggc gtc gac aag ctc tta gaa gct ggc gca 739
Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu Leu Glu Ala Gly Ala
200 205 210

aag ctc acc ggt ctc atg gct tac acg gcc gag cgc gtg aag gcg ttg 787
Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Glu Arg Val Lys Ala Leu
215 220 225
gag ccc gct gcg ggc gtg gat ttg gat gat aag acc att ccc cat gaa 835
Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr Ile Pro His Glu
230 235 240 245
atc ccc cat tgg att ggc cgt ggc gaa cat tta ggc gct gtg cat ttg 883
Ile Pro His Trp Ile Gly Arg Gly Glu His Leu Gly Ala Val His Leu
250 255 260
acc aag ggt tgc tac cgc ggc cag gaa act gtc gcg cgc gtt gat aat 931
Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala Arg Val Asp Asn
265 270 275
ctt ggg cgt tcc ccg cgc gtg ctg gtt ctg ctt cat ctt gac ggt tcc 979
Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu His Leu Asp Gly Ser
280 285 290
gca ccg ctg gat cct gtg act ggc gct gaa atc aag gcc ggt gcg cgc 1027
Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys Ala Gly Ala Arg
295 300 305
acc gtt ggt cgt ctg ggc acc gtt gtc cat gac gcc gat tac ggg ccg 1075
Thr Val Gly Arg Leu Gly Thr Val Val His Asp Ala Asp Tyr Gly Pro
310 315 320 325
atc gct ctc ggg ctg gtt aag cgc agc gct ttg gat aaa gaa ctt cac 1123
Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp Lys Glu Leu His
330 335 340
atc gat gat gtc tct gta aac gtc gac cgc gat ctg ctt cct gcg gag 1171
Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu Leu Pro Ala Glu
345 350 355
gaa agt gaa caa cgc gga cgc gca gcg atc aat aag ctc aag ggt ctt 1219
Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys Leu Lys Gly Leu
360 365 370
taactaaaac gatttatagc gaa 1242

<210> 370

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Val Gly Thr Ile Glu Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn
1 5 10 15
Asn Thr Asp Gln Ile Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg
20 25 30
Ser Gly Ala Ala Glu Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu
35 40 45
Gly Val Ala Trp His Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe
50 55 60

Glu Thr Gly Thr Gly Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys
65 70 75 80

Val Glu Gly Pro Asp Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln
85 90 95

Lys Val Asp Ser Val Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu
100 105 110

Asp Ala Gln Gly Arg Ile Gln His Thr Met Gln Val Thr Val Val Asp
115 120 125

Gly Val Phe Tyr Leu Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile
130 135 140

Gly Phe Leu Thr Lys Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu
145 150 155 160

Ala Asp Leu Ala Ile Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro
165 170 175

Asp Ala Val Phe Ala Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile
180 185 190

Asp Val Ala Ile Arg Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu
195 200 205

Leu Glu Ala Gly Ala Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Glu
210 215 220

Arg Val Lys Ala Leu Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys
225 230 235 240

Thr Ile Pro His Glu Ile Pro His Trp Ile Gly Arg Gly Glu His Leu
245 250 255

Gly Ala Val His Leu Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val
260 265 270

Ala Arg Val Asp Asn Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu
275 280 285

His Leu Asp Gly Ser Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile
290 295 300

Lys Ala Gly Ala Arg Thr Val Gly Arg Leu Gly Thr Val Val His Asp
305 310 315 320

Ala Asp Tyr Gly Pro Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu
325 330 335

Asp Lys Glu Leu His Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp
340 345 350

Leu Leu Pro Ala Glu Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn
355 360 365

Lys Leu Lys Gly Leu
370

<210> 371
 <211> 567
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(544)
 <223> FRXA00768

<400> 371
 gacgtcgcca tccggcgtga aaacctggag gagggcgctcg acaagctctt agaagctggc 60
 gcaaagctca ccggtctcat ggcttacacg gcccgagcgc gtg aag gcg ttg gag 115
 Val Lys Ala Leu Glu
 1 5
 ccc gct gcg ggc gtg gat ttg gat gat aag acc att ccc cat gaa atc 163
 Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr Ile Pro His Glu Ile
 10 15 20
 ccc cat tgg att ggc cgt ggc gaa cat tta ggc gct gtg cat ttg acc 211
 Pro His Trp Ile Gly Arg Gly Glu His Leu Gly Ala Val His Leu Thr
 25 30 35
 aag ggt tgc tac cgc ggc cag gaa act gtc gcg cgc gtt gat aat ctt 259
 Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala Arg Val Asp Asn Leu
 40 45 50
 ggg cgt tcc ccg cgc gtg ctg gtt ctg ctt cat ctt gac ggt tcc gca 307
 Gly Arg Ser Pro Arg Val Leu Val Leu Leu His Leu Asp Gly Ser Ala
 55 60 65
 ccg ctg gat cct gtg act ggc gct gaa atc aag gcc ggt gcg cgc acc 355
 Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys Ala Gly Ala Arg Thr
 70 75 80 85
 gtt ggt cgt ctg ggc acc gtt gtc cat gac gcc gat tac ggg ccg atc 403
 Val Gly Arg Leu Gly Thr Val Val His Asp Ala Asp Tyr Gly Pro Ile
 90 95 100
 gct ctc ggg ctg gtt aag cgc agc gct ttg gat aaa gaa ctt cac atc 451
 Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp Lys Glu Leu His Ile
 105 110 115
 gat gat gtc tct gta aac gtc gac cgc gat ctg ctt cct gcg gag gaa 499
 Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu Leu Pro Ala Glu Glu
 120 125 130
 agt gaa caa cgc gga cgc gca gcg atc aat aag ctc aag ggt ctt 544
 Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys Leu Lys Gly Leu
 135 140 145
 taactaaaac gatttatagc gaa 567

<210> 372
 <211> 148
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 372

Val Lys Ala Leu Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr
 1 5 10 15

Ile Pro His Glu Ile Pro His Trp Ile Gly Arg Gly Glu His Leu Gly
 20 25 30

Ala Val His Leu Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala
 35 40 45

Arg Val Asp Asn Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu His
 50 55 60

Leu Asp Gly Ser Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys
 65 70 75 80

Ala Gly Ala Arg Thr Val Gly Arg Leu Gly Thr Val Val His Asp Ala
 85 90 95

Asp Tyr Gly Pro Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp
 100 105 110

Lys Glu Leu His Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu
 115 120 125

Leu Pro Ala Glu Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys
 130 135 140

Leu Lys Gly Leu
 145

<210> 373

<211> 837

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(814)

<223> FRXA00767

<400> 373

tcaagcgcca taacgcctga ttatgcacgg ttaaggcgca tctcgctcac tgggtgctaac 60

cacttgcgct tttggaagga ataacccttc ctgtcagatt gtg ggt act atc gaa 115
 Val Gly Thr Ile Glu
 1 5

gac gtg gct aac gaa caa atc gag gtc gcg aac aac act gat cag att 163
 Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn Asn Thr Asp Gln Ile
 10 15 20

cct gca gga tac aag tcc cct ctt ctt tct aga agt ggt gcg gca gaa 211
 Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg Ser Gly Ala Ala Glu
 25 30 35

gcg cag ggc gct gct gct caa gca ggt act gaa ggt gtc gcg tgg cat 259
 Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu Gly Val Ala Trp His
 40 45 50

tac ggt tcc cct ctc gtc gag caa cgc atc ttc gaa act ggc acg ggc 307
 Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe Glu Thr Gly Thr Gly
 55 60 65
 tta gtt gac cgt tct aat cgc aag gtg atc aaa gtc gaa ggg cct gat 355
 Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys Val Glu Gly Pro Asp
 70 75 80 85
 gcc ccc acg ttc ctc aat aat att ttg tcc caa aag gtt gat tcc gtt 403
 Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln Lys Val Asp Ser Val
 90 95 100
 gaa aac ggc ttt act gcc ggt gcc ctg gat ttg gat gcg cag ggt cgt 451
 Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu Asp Ala Gln Gly Arg
 105 110 115
 att caa cac aca atg cag gta act gtc gtc gat ggg gtt ttc tac ctc 499
 Ile Gln His Thr Met Gln Val Thr Val Val Asp Gly Val Phe Tyr Leu
 120 125 130
 gac acg tcc gcg gcg gag ttt gat acc ctc atc ggt ttc ttg acc aag 547
 Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile Gly Phe Leu Thr Lys
 135 140 145
 atg att ttc tgg tgg gaa gtc acc gtc cag gaa gcc gat ctg gcg atc 595
 Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu Ala Asp Leu Ala Ile
 150 155 160 165
 atc act ctg ctc ggc cag gaa att gcc ctt ccg gac gcg gtc ttt gcc 643
 Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro Asp Ala Val Phe Ala
 170 175 180
 cgt agg gtc gat tgg aat ggg cca tgg cgt atc gac gtc gcc atc cgg 691
 Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile Asp Val Ala Ile Arg
 185 190 195
 cgt gaa aac ctg gag gag ggc gtc gac aag ctc tta gaa gct ggc gca 739
 Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu Leu Glu Ala Gly Ala
 200 205 210
 aag ctc acc ggt ctc atg gct tac acg gcc cga gcg cgt gaa ggc gtt 787
 Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Arg Ala Arg Glu Gly Val
 215 220 225
 gga gcc cgc tgc ggg cgt gga ttt gga tgataagacc attccccatg 834
 Gly Ala Arg Cys Gly Arg Gly Phe Gly
 230 235
 aaa 837

<210> 374

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

Val Gly Thr Ile Glu Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn
 1 5 10 15

Asn Thr Asp Gln Ile Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg

20	25	30
Ser Gly Ala Ala Glu Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu 35 40 45		
Gly Val Ala Trp His Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe 50 55 60		
Glu Thr Gly Thr Gly Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys 65 70 75 80		
Val Glu Gly Pro Asp Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln 85 90 95		
Lys Val Asp Ser Val Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu 100 105 110		
Asp Ala Gln Gly Arg Ile Gln His Thr Met Gln Val Thr Val Val Asp 115 120 125		
Gly Val Phe Tyr Leu Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile 130 135 140		
Gly Phe Leu Thr Lys Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu 145 150 155 160		
Ala Asp Leu Ala Ile Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro 165 170 175		
Asp Ala Val Phe Ala Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile 180 185 190		
Asp Val Ala Ile Arg Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu 195 200 205		
Leu Glu Ala Gly Ala Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Arg 210 215 220		
Ala Arg Glu Gly Val Gly Ala Arg Cys Gly Arg Gly Phe Gly 225 230 235		

<210> 375

<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(313)

<223> RXN00769

<400> 375

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attcccagga tcggcccgct cactccaagg gggtcaggca atg ggt cgc ggt cgc	115
Met Gly Arg Gly Arg	
1 5	

gcg aag gca aaa cag acc aaa gtt gct cgc cag ttg aag tac agc tct	163
Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln Leu Lys Tyr Ser Ser	

10	15	20	
cca gac atg gat ctc gat tcg ctg cag cgg gag ctg gct aac cag tct			211
Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu Leu Ala Asn Gln Ser			
25	30	35	
cct agg cgt tcc tac tcc gat acc cct gat gat gag gac cag tac gca			259
Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp Glu Asp Gln Tyr Ala			
40	45	50	
gag tat gcg gac tgg gat gag gac gac acc gac aat cgt gcc tac ggc			307
Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp Asn Arg Ala Tyr Gly			
55	60	65	
aca aac tgatttcgtg tgtccttaac tct			336
Thr Asn			
70			

<210> 376

<211> 71

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Met Gly Arg Gly Arg Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln			
1	5	10	15
Leu Lys Tyr Ser Ser Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu			
20	25	30	
Leu Ala Asn Gln Ser Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp			
35	40	45	
Glu Asp Gln Tyr Ala Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp			
50	55	60	
Asn Arg Ala Tyr Gly Thr Asn			
65	70		

<210> 377

<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(313)

<223> FRXA00769

<400> 377

ggctattgtg tctatcagga atacagttaa tacatcttga aaagcccatg ggccatccga	60	
attcccagga tcggcccgt cactccaagg gggtcaggca atg ggt cgc ggt cgc	115	
Met Gly Arg Gly Arg		
1	5	
gcg aag gca aaa cag acc aaa gtt gct cgc cag ttg aag tac agc tct	163	
Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln Leu Lys Tyr Ser Ser		
10	15	20

acc ttt tgg gaa tgg gaa aac aaa agg gtt cac att gca agg aga cgt	211
Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His Ile Ala Arg Arg Arg	
25 30 35	
cga gaa gcg ccc gtc cgc gtt atc gtg gtg cat ggg cta ggc acc cat	259
Arg Glu Ala Pro Val Arg Val Ile Val Val His Gly Leu Gly Thr His	
40 45 50	
agt ggc gcc ctc tgg ccc ctc gtc gcg gcc att gag ggc gcg gac ctc	307
Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile Glu Gly Ala Asp Leu	
55 60 65	
gcc gcg atc gac ctg cct aaa act ccg ctt tac gac gat tgg ctg cgc	355
Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr Asp Asp Trp Leu Arg	
70 75 80 85	
ctt tta gaa tct ttc atc tcg tcc gaa gac gac ggt cgg cca ctc atc	403
Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp Gly Arg Pro Leu Ile	
90 95 100	
ctg atc ggt gca ggc acc gga ggc ttg ctt tgc gca gaa gct gca cac	451
Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys Ala Glu Ala Ala His	
105 110 115	
cgc aca gga ctg gtc gca cac gtc att gcc acc tgc ctg ctc aac ccc	499
Arg Thr Gly Leu Val Ala His Val Ile Ala Thr Cys Leu Leu Asn Pro	
120 125 130	
tcc gac cag ccg acg cgc cgg gca ctg ttc agg ttt tca ccg ctg act	547
Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg Phe Ser Pro Leu Thr	
135 140 145	
cgg ttg atc caa ggc cgc ttg cgc aac cgc gaa att ccc gtg acc aga	595
Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu Ile Pro Val Thr Arg	
150 155 160 165	
gtg ttg aac ttc agc aaa atc agc cgc agc cca gcc ctg agc aaa ttg	643
Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro Ala Leu Ser Lys Leu	
170 175 180	
tgc gcg gcc gat gaa ttt agc gga gca tcc aaa ata acc tgg ggt ttc	691
Cys Ala Ala Asp Glu Phe Ser Gly Ala Ser Lys Ile Thr Trp Gly Phe	
185 190 195	
ctc gcg tca tat gtg caa cac aag gcc aaa ctg ggt gca gtt ccc gtc	739
Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu Gly Ala Val Pro Val	
200 205 210	
act ctg atg cac cct gac cac gac ctt ctg act ccc gtt gag ctc agt	787
Thr Leu Met His Pro Asp His Asp Leu Leu Thr Pro Val Glu Leu Ser	
215 220 225	
ctg cgt acg ctt tcg cgc ctc aaa gcg ccc act gac gtg gtt atg ctc	835
Leu Arg Thr Leu Ser Arg Leu Lys Ala Pro Thr Asp Val Val Met Leu	
230 235 240 245	
aag gac tgc ggg cat ttt ccc atc gaa gaa ccc ggc ttc acc acc atg	883
Lys Asp Cys Gly His Phe Pro Ile Glu Glu Pro Gly Phe Thr Thr Met	
250 255 260	
ctc gaa acc gtc aca tca gtt atc gcg cgg aat agt tagcgggcgc	929

Leu Glu Thr Val Thr Ser Val Ile Ala Arg Asn Ser
 265 270

atgtgggttg gat

942

<210> 380

<211> 273

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 380

Met Thr Asn Pro Tyr Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly
 1 5 10 15

Ile Glu Pro Glu His Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His
 20 25 30

Ile Ala Arg Arg Arg Arg Glu Ala Pro Val Arg Val Ile Val Val His
 35 40 45

Gly Leu Gly Thr His Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile
 50 55 60

Glu Gly Ala Asp Leu Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr
 65 70 75 80

Asp Asp Trp Leu Arg Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp
 85 90 95

Gly Arg Pro Leu Ile Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys
 100 105 110

Ala Glu Ala Ala His Arg Thr Gly Leu Val Ala His Val Ile Ala Thr
 115 120 125

Cys Leu Leu Asn Pro Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg
 130 135 140

Phe Ser Pro Leu Thr Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu
 145 150 155 160

Ile Pro Val Thr Arg Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro
 165 170 175

Ala Leu Ser Lys Leu Cys Ala Ala Asp Glu Phe Ser Gly Ala Ser Lys
 180 185 190

Ile Thr Trp Gly Phe Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu
 195 200 205

Gly Ala Val Pro Val Thr Leu Met His Pro Asp His Asp Leu Leu Thr
 210 215 220

Pro Val Glu Leu Ser Leu Arg Thr Leu Ser Arg Leu Lys Ala Pro Thr
 225 230 235 240

Asp Val Val Met Leu Lys Asp Cys Gly His Phe Pro Ile Glu Glu Pro
 245 250 255

Gly Phe Thr Thr Met Leu Glu Thr Val Thr Ser Val Ile Ala Arg Asn

260

265

270

Ser

<210> 381

<211> 801

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(778)

<223> FRXA00771

<400> 381

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gctgctgaga	aaaatgaaga	ccttttggtta	ggttgggagt	atg	acc	aac	cca	tac	115
				Met	Thr	Asn	Pro	Tyr	
				1				5	

gag gcc ttc ata ccg ctc aag cat cgt acg ggg att gaa ccc gag cac	163
Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly Ile Glu Pro Glu His	
10 15 20	

acc ttt tgg gaa tgg gaa aac aaa agg gtt cac att gca agg aga cgt	211
Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His Ile Ala Arg Arg Arg	
25 30 35	

cga gaa gcg ccc gtc cgc gtt atc gtg gtg cat ggg cta ggc acc cat	259
Arg Glu Ala Pro Val Arg Val Ile Val Val His Gly Leu Gly Thr His	
40 45 50	

agt ggc gcc ctc tgg ccc ctc gtc gcg gcc att gag ggc gcg gac ctc	307
Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile Glu Gly Ala Asp Leu	
55 60 65	

gcc gcg atc gac ctg cct aaa act ccg ctt tac gac gat tgg ctg cgc	355
Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr Asp Asp Trp Leu Arg	
70 75 80 85	

ctt tta gaa tct ttc atc tcg tcc gaa gac gac ggt cgg cca ctc atc	403
Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp Gly Arg Pro Leu Ile	
90 95 100	

ctg atc ggt gca ggc acc gga ggc ttg ctt tgc gca gaa gct gca cac	451
Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys Ala Glu Ala Ala His	
105 110 115	

cgc aca gga ctg gtc gca cac gtc att gcc acc tgc ctg ctc aac ccc	499
Arg Thr Gly Leu Val Ala His Val Ile Ala Thr Cys Leu Leu Asn Pro	
120 125 130	

tcc gac cag ccg acg cgc cgg gca ctg ttc agg ttt tca ccg ctg act	547
Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg Phe Ser Pro Leu Thr	
135 140 145	

cgg ttg atc caa ggc cgc ttg cgc aac cgc gaa att ccc gtg acc aga	595
Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu Ile Pro Val Thr Arg	

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150          155          160          165
gtg ttg aac ttc agc aaa atc agc cgc agc cca gcc ctg agc aaa ttg   643
Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro Ala Leu Ser Lys Leu
          170          175          180

tgc gcg gcc gat gaa ttt aac gga gca ttc aaa ata acc tgg ggt ttc   691
Cys Ala Ala Asp Glu Phe Asn Gly Ala Phe Lys Ile Thr Trp Gly Phe
          185          190          195

ctc gcg tca tat gtg caa cac aag gcc aaa ctg ggt gca gtt ccc ctc   739
Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu Gly Ala Val Pro Leu
          200          205          210

act ctg atg cac cct gac cac gac ctt ttt gac tcc cgt tgagctcaaa   788
Thr Leu Met His Pro Asp His Asp Leu Phe Asp Ser Arg
          215          220          225

tctgcgtacg ctt   801

<210> 382
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 382
Met Thr Asn Pro Tyr Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly
  1          5          10          15

Ile Glu Pro Glu His Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His
          20          25          30

Ile Ala Arg Arg Arg Arg Glu Ala Pro Val Arg Val Ile Val Val His
          35          40          45

Gly Leu Gly Thr His Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile
          50          55          60

Glu Gly Ala Asp Leu Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr
          65          70          75          80

Asp Asp Trp Leu Arg Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp
          85          90          95

Gly Arg Pro Leu Ile Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys
          100          105          110

Ala Glu Ala Ala His Arg Thr Gly Leu Val Ala His Val Ile Ala Thr
          115          120          125

Cys Leu Leu Asn Pro Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg
          130          135          140

Phe Ser Pro Leu Thr Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu
          145          150          155          160

Ile Pro Val Thr Arg Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro
          165          170          175

Ala Leu Ser Lys Leu Cys Ala Ala Asp Glu Phe Asn Gly Ala Phe Lys

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180

185

190

Ile Thr Trp Gly Phe Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu
 195 200 205

Gly Ala Val Pro Leu Thr Leu Met His Pro Asp His Asp Leu Phe Asp
 210 215 220

Ser Arg
 225

<210> 383

<211> 680

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(657)

<223> RXN00785

<400> 383

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 1 5 10 15

ttc ttg acg gtt gcg tcc att ccc att ctg ttt ggt att ttc aca cca 96
 Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
 20 25 30

ctg act tcg tgg ttt gtg tcc caa caa ggc gtg gct gcg aat gtg tcc 144
 Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
 35 40 45

cct ggt gtt tcc gtc acg gaa atc ctc acg gct gtt tat cct ttg gcg 192
 Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
 50 55 60

cag ttg ttc ccc acc ctg atc atg gtc act ttg gtg gcg gca ttg atc 240
 Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65 70 75 80

gct gtg gtg cgg att att ctg ctg cgc agg aac cag gaa tct cgt cag 288
 Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
 85 90 95

gtt tct ggg gaa ctt acc cgg cgc gcg cag cgt gag gct gag gaa gct 336
 Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
 100 105 110

aat cag aat gct gct cgt cgt gct cgc gca cag agc acg agg gta caa 384
 Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
 115 120 125

agt tct aaa aca cgt aac cgt cgc gcg caa cca acc ggc gat acc ggt 432
 Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
 130 135 140

tca caa gtc acg gtt gat gag ttg atc agg cgt agc cag gag cgc cgg 480
 Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg

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145              150              155              160
caa act gtt gcg cag cgc caa act gag cgc ggt gtg ccg ttt act cca 528
Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
              165              170              175

act ccg ggt cct gtg gtg gcc ccc aag ccg cgc ccg agc gcc cct gag 576
Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
              180              185              190

gcg ccg gct cct acg gat gtg ggt gag cgt cga caa gca gcc cct aaa 624
Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro Lys
              195              200              205

cgc cgc acc tcg ctc gac gat gat ctg tac agc taaaaaatcc ccgctcatgt 677
Arg Arg Thr Ser Leu Asp Asp Asp Leu Tyr Ser
              210              215

ggc 680

<210> 384
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 384
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1              5              10              15

Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
  20              25              30

Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
  35              40              45

Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
  50              55              60

Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
  65              70              75              80

Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
  85              90              95

Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
  100             105             110

Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
  115             120             125

Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
  130             135             140

Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
  145             150             155             160

Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
  165             170             175

Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu

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180	185	190
Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro Lys		
195	200	205
Arg Arg Thr Ser Leu Asp Asp Asp Leu Tyr Ser		
210	215	

<210> 385

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(621)

<223> FRXA00785

<400> 385

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Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu	
1 5 10 15	
ttc ttg acg gtt gcg tcc att ccc att ctg ttt ggt att ttc aca cca	96
Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro	
20 25 30	
ctg act tcg tgg ttt gtg tcc caa caa ggc gtg gct gcg aat gtg tcc	144
Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser	
35 40 45	
cct ggt gtt tcc gtc acg gaa atc ctc acg gct gtt tat cct ttg gcg	192
Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala	
50 55 60	
cag ttg ttc ccc acc ctg atc atg gtc act ttg gtg gcg gca ttg atc	240
Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile	
65 70 75 80	
gct gtg gtg cgg att att ctg ctg cgc agg aac cag gaa tct cgt cag	288
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln	
85 90 95	
gtt tct ggg gaa ctt acc cgg cgc gcg cag cgt gag gct gag gaa gct	336
Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala	
100 105 110	
aat cag aat gct gct cgt cgt gct cgc gca cag agc acg agg gta caa	384
Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln	
115 120 125	
agt tct aaa aca cgt aac cgt cgc gcg caa cca acc ggc gat acc ggt	432
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly	
130 135 140	
tca caa gtc acg gtt gat gag ttg atc agg cgt agc cag gag cgc cgg	480
Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg	
145 150 155 160	
caa act gtt gcg cag cgc caa act gag cgc ggt gtg ccg ttt act cca	528

Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
 165 170 175

act ccg ggt cct gtg gtg gcc ccc aag ccg cgc ccg agc gcc cct gag 576
 Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
 180 185 190

gcg ccg gct cct acg gat gtg ggt gag cgt cga caa gca gcc cct 621
 Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro
 195 200 205

<210> 386
 <211> 207
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 386
 Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
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Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
 20 25 30

Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
 35 40 45

Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
 50 55 60

Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65 70 75 80

Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
 85 90 95

Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
 100 105 110

Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
 115 120 125

Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
 130 135 140

Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
 145 150 155 160

Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
 165 170 175

Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
 180 185 190

Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro
 195 200 205

<210> 387
 <211> 651
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXN00795

<400> 387

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ggctgagaaaa cgaccgaaaa tttttgatgg cagtcgagac atg att atc tcg ttg 115
                                         Met Ile Ile Ser Leu
                                         1 5

gta gtc tcc gcg atc atc atg ttg gta gcg gtg gga ttc acg gga atg 163
Val Val Ser Ala Ile Ile Met Leu Val Ala Val Gly Phe Thr Gly Met
                        10 15 20

tgt tct ttc aat aca gga tcc cct gaa aat ggg cag gta cct gaa gtt 211
Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly Gln Val Pro Glu Val
                        25 30 35

gat gct tcc act ttt atg tca atg gaa gcg cgc gca atg act gat cat 259
Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg Ala Met Thr Asp His
                        40 45 50

gca act agg ttg ccg gaa act cct gaa ggc tgg acc aca aat tca gct 307
Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp Thr Thr Asn Ser Ala
                        55 60 65

cga cgc acc atg gtg gat gac acc ccg gca tct gta gtt gga tat gtc 355
Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser Val Val Gly Tyr Val
                        70 75 80 85

acc gca gat gag ggc tat att cag ctc act caa act ggt gaa acc gtt 403
Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln Thr Gly Glu Thr Val
                        90 95 100

gag gat gct gtg gct ggt tat gat act cgc tgg cgt gat ctt tct gag 451
Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp Arg Asp Leu Ser Glu
                        105 110 115

tct tat gat ctt gat ggc cac gac gtg gga att tac acc tca cag gaa 499
Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile Tyr Thr Ser Gln Glu
                        120 125 130

tct gat gtg cgt gat ctg cgt gtg atg gat ctg ggc gat gcc cgc gtc 547
Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu Gly Asp Ala Arg Val
                        135 140 145

atg gtc tcg ggt gct gct acc gat gaa gaa ttc aat gat ctg ctt cgc 595
Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe Asn Asp Leu Leu Arg
                        150 155 160 165

gca gtt gcg aat tcg gag cca ctg cct acc aat taagaattgg tcgaaccacc 648
Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
                        170 175

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aaa

651

<210> 388
 <211> 176
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 388

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Met Ile Ile Ser Leu Val Val Ser Ala Ile Ile Met Leu Val Ala Val
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Gly Phe Thr Gly Met Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly
      20             25             30

Gln Val Pro Glu Val Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg
      35             40             45

Ala Met Thr Asp His Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp
 50             55             60

Thr Thr Asn Ser Ala Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser
 65             70             75             80

Val Val Gly Tyr Val Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln
      85             90             95

Thr Gly Glu Thr Val Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp
      100            105            110

Arg Asp Leu Ser Glu Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile
      115            120            125

Tyr Thr Ser Gln Glu Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu
      130            135            140

Gly Asp Ala Arg Val Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe
      145            150            155            160

Asn Asp Leu Leu Arg Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
      165            170            175

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<210> 389
 <211> 651
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> FRXA00795

<400> 389

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ggctgagaaa cgaccgaaaa tttttgatgg cagtcgagac atg att atc tcg ttg      115
                                   Met Ile Ile Ser Leu
                                   1             5

gta gtc tcc gcg atc atc atg ttg gta gcg gtg gga ttc acg gga atg      163
Val Val Ser Ala Ile Ile Met Leu Val Ala Val Gly Phe Thr Gly Met
      10             15             20

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tgt tct ttc aat aca gga tcc cct gaa aat ggg cag gta cct gaa gtt 211
 Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly Gln Val Pro Glu Val
 25 30 35

gat gct tcc act ttt atg tca atg gaa gcg cgc gca atg act gat cat 259
 Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg Ala Met Thr Asp His
 40 45 50

gca act agg ttg ccg gaa act cct gaa ggc tgg acc aca aat tca gct 307
 Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp Thr Thr Asn Ser Ala
 55 60 65

cga cgc acc atg gtg gat gac acc ccg gca tct gta gtt gga tat gtc 355
 Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser Val Val Gly Tyr Val
 70 75 80 85

acc gca gat gag ggc tat att cag ctc act caa act ggt gaa acc gtt 403
 Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln Thr Gly Glu Thr Val
 90 95 100

gag gat gct gtg gct ggt tat gat act cgc tgg cgt gat ctt tct gag 451
 Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp Arg Asp Leu Ser Glu
 105 110 115

tct tat gat ctt gat ggc cac gac gtg gga att tac acc tca cag gaa 499
 Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile Tyr Thr Ser Gln Glu
 120 125 130

tct gat gtg cgt gat ctg cgt gtg atg gat ctg ggc gat gcc cgc gtc 547
 Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu Gly Asp Ala Arg Val
 135 140 145

atg gtc tcg ggt gct gct acc gat gaa gaa ttc aat gat ctg ctt cgc 595
 Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe Asn Asp Leu Leu Arg
 150 155 160 165

gca gtt gcg aat tcg gag cca ctg cct acc aat taagaattgg tcgaaccacc 648
 Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
 170 175

aaa 651

<210> 390

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

Met Ile Ile Ser Leu Val Val Ser Ala Ile Ile Met Leu Val Ala Val
 1 5 10 15

Gly Phe Thr Gly Met Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly
 20 25 30

Gln Val Pro Glu Val Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg
 35 40 45

Ala Met Thr Asp His Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp
 50 55 60

Thr Thr Asn Ser Ala Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser
 65 70 75 80
 Val Val Gly Tyr Val Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln
 85 90 95
 Thr Gly Glu Thr Val Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp
 100 105 110
 Arg Asp Leu Ser Glu Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile
 115 120 125
 Tyr Thr Ser Gln Glu Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu
 130 135 140
 Gly Asp Ala Arg Val Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe
 145 150 155 160
 Asn Asp Leu Leu Arg Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
 165 170 175

<210> 391
 <211> 825
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(802)
 <223> RXN00831

<400> 391
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 atgatgagca tgttcgcctg atttaggtag cctgggtggga atg agt gca ctt gag 115
 Met Ser Ala Leu Glu
 1 5
 aca ttg caa tgg cag gac tgg tca agc gtc tta att gtg gta gct cac 163
 Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu Ile Val Val Ala His
 10 15 20
 cca gat gat ccg gag tat ggg ctt tcc gcg gct gtt aaa gaa tgg aca 211
 Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala Val Lys Glu Trp Thr
 25 30 35
 gac gcc ggg gtg gag gtg tct tac ctg ctg ctc acc cac ggg gag gca 259
 Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu Thr His Gly Glu Ala
 40 45 50
 ggt atc caa ggt tta gac cct aaa gaa acc ggg tca ttg cgc gca gcg 307
 Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly Ser Leu Arg Ala Ala
 55 60 65
 gaa cag cgg gct gca tgt gat gtg gta gga gtt aga aat ctc acc att 355
 Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val Arg Asn Leu Thr Ile
 70 75 80 85
 ttg aat cac cca gat tcc atg ttg gtg tac aat ctg gta ctg cgc aaa 403
 Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn Leu Val Leu Arg Lys

90	95	100	
gat att gct cgg gaa atc cgg atc cgt aaa cca aat gct gtg gtg gta Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro Asn Ala Val Val Val 105 110 115			451
tcc aat ttt gat gta gag gcc tac ggt ggt ttg aac cag gcg gat cac Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu Asn Gln Ala Asp His 120 125 130			499
cgc gtg gcg gga tta gcc gca att gat gcg acc cgc gat gcc gct aat Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr Arg Asp Ala Ala Asn 135 140 145			547
ccg tgg gcg cag cca gag ctg ttg cag gag gat ctg cag ccg tgg gga Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp Leu Gln Pro Trp Gly 150 155 160 165			595
gct gaa gtc atc atc att gcc gga cac cca gag ccc acc cac acc atg Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu Pro Thr His Thr Met 170 175 180			643
gat ctg gct aaa gat tct gtt gat gcc gga gtt gca tcc ctt caa gct Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val Ala Ser Leu Gln Ala 185 190 195			691
cac aag gaa tac ttg gcc gct ctt cca gat ccc ccg aag ccg gag gag His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro Pro Lys Pro Glu Glu 200 205 210			739
ttc att ccg gcg ttt ctc gag gta gag ggc ggt tac gca gcg gcc ttc Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly Tyr Ala Ala Ala Phe 215 220 225			787
cga gtt ttc gga cgg taagcagggc gatacgtgat agg Arg Val Phe Gly Arg 230			825

<210> 392
 <211> 234
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 392
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 Ile Val Val Ala His Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala
 20 25 30
 Val Lys Glu Trp Thr Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu
 35 40 45
 Thr His Gly Glu Ala Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly
 50 55 60
 Ser Leu Arg Ala Ala Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val
 65 70 75 80
 Arg Asn Leu Thr Ile Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn

85	90	95
Leu Val Leu Arg Lys Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro 100 105 110		
Asn Ala Val Val Val Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu 115 120 125		
Asn Gln Ala Asp His Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr 130 135 140		
Arg Asp Ala Ala Asn Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp 145 150 155 160		
Leu Gln Pro Trp Gly Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu 165 170 175		
Pro Thr His Thr Met Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val 180 185 190		
Ala Ser Leu Gln Ala His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro 195 200 205		
Pro Lys Pro Glu Glu Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly 210 215 220		
Tyr Ala Ala Ala Phe Arg Val Phe Gly Arg 225 230		

<210> 393

<211> 825

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(802)

<223> FRXA00831

<400> 393

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atgatgagca tgttcgcctg atttaggtag cctgggtggga	atg agt gca ctt gag	115
	Met Ser Ala Leu Glu	
	1 5	

aca ttg caa tgg cag gac tgg tca agc gtc tta att gtg gta gct cac	163
Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu Ile Val Val Ala His	
10 15 20	

cca gat gat ccg gag tat ggg ctt tcc gcg gct gtt aaa gaa tgg aca	211
Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala Val Lys Glu Trp Thr	
25 30 35	

gac gcc ggg gtg gag gtg tct tac ctg ctg ctc acc cac ggg gag gca	259
Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu Thr His Gly Glu Ala	
40 45 50	

ggg atc caa ggt tta gac cct aaa gaa acc ggg tca ttg cgc gca gcg	307
Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly Ser Leu Arg Ala Ala	

55	60	65	
gaa cag cgg gct gca tgt gat gtg gta gga gtt aga aat ctc acc att			355
Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val Arg Asn Leu Thr Ile			
70	75	80	85
ttg aat cac cca gat tcc atg ttg gtg tac aat ctg gta ctg cgc aaa			403
Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn Leu Val Leu Arg Lys			
	90	95	100
gat att gct cgg gaa atc cgg atc cgt aaa cca aat gct gtg gtg gta			451
Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro Asn Ala Val Val Val			
	105	110	115
tcc aat ttt gat gta gag gcc tac ggt ggt ttg aac cag gcg gat cac			499
Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu Asn Gln Ala Asp His			
	120	125	130
cgc gtg gcg gga tta gcc gca att gat gcg acc cgc gat gcc gct aat			547
Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr Arg Asp Ala Ala Asn			
	135	140	145
ccg tgg gcg cag cca gag ctg ttg cag gag gat ctg cag ccg tgg gga			595
Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp Leu Gln Pro Trp Gly			
	150	155	160
gct gaa gtc atc atc att gcc gga cac cca gag ccc acc cac acc atg			643
Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu Pro Thr His Thr Met			
	170	175	180
gat ctg gct aaa gat tct gtt gat gcc gga gtt gca tcc ctt caa gct			691
Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val Ala Ser Leu Gln Ala			
	185	190	195
cac aag gaa tac ttg gcc gct ctt cca gat ccc ccg aag ccg gag gag			739
His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro Pro Lys Pro Glu Glu			
	200	205	210
ttc att ccg gcg ttt ctc gag gta gag ggc ggt tac gca gcg gcc ttc			787
Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly Tyr Ala Ala Ala Phe			
	215	220	225
cga gtt ttc gga cgg taagcagggc gatacgtgat agg			825
Arg Val Phe Gly Arg			
230			

<210> 394

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

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Ile	Val	Val	Ala	His	Pro	Asp	Asp	Pro	Glu	Tyr	Gly	Leu	Ser	Ala	Ala
			20					25					30		

Val	Lys	Glu	Trp	Thr	Asp	Ala	Gly	Val	Glu	Val	Ser	Tyr	Leu	Leu	Leu
		35					40					45			

Thr His Gly Glu Ala Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly
 50 55 60
 Ser Leu Arg Ala Ala Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val
 65 70 75 80
 Arg Asn Leu Thr Ile Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn
 85 90 95
 Leu Val Leu Arg Lys Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro
 100 105 110
 Asn Ala Val Val Val Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu
 115 120 125
 Asn Gln Ala Asp His Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr
 130 135 140
 Arg Asp Ala Ala Asn Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp
 145 150 155 160
 Leu Gln Pro Trp Gly Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu
 165 170 175
 Pro Thr His Thr Met Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val
 180 185 190
 Ala Ser Leu Gln Ala His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro
 195 200 205
 Pro Lys Pro Glu Glu Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly
 210 215 220
 Tyr Ala Ala Ala Phe Arg Val Phe Gly Arg
 225 230

<210> 395
 <211> 1077
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1054)
 <223> RXN00835

<400> 395
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 gatttgtaag cactaccocct tctctacaaa ggagtcacatca atg gcc ggt gga ttg 115
 Met Ala Gly Gly Leu
 1 5
 gca gca cta tta gac gat gtc gca gca att act cga gcg gct gca gcc 163
 Ala Ala Leu Leu Asp Asp Val Ala Ala Ile Thr Arg Ala Ala Ala Ala
 10 15 20
 agc ctc gat gat gtc acg gcg atg gct gga aaa acc agc gtt aaa gcc 211
 Ser Leu Asp Asp Val Thr Ala Met Ala Gly Lys Thr Ser Val Lys Ala

25										30					35					
gca ggc gtg gtt gta gat gac acg gca gtt acc ccg caa tat gtt caa	259																			
Ala Gly Val Val Val Asp Asp Thr Ala Val Thr Pro Gln Tyr Val Gln																				
40	45	50																		
ggt gtc aaa cct gca cgc gaa ctg ccc atg att tgg cgg atc gct aag	307																			
Gly Val Lys Pro Ala Arg Glu Leu Pro Met Ile Trp Arg Ile Ala Lys																				
55	60	65																		
ggc tct ttg gta aac aag atc atc atc att ttg ccc atc gcg ttg ctt	355																			
Gly Ser Leu Val Asn Lys Ile Ile Ile Ile Leu Pro Ile Ala Leu Leu																				
70	75	80	85																	
ctt tcc gcg ttt gct ccg tgg gct ctc aca cca att ttg atg ctg ggc	403																			
Leu Ser Ala Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly																				
90	95	100																		
ggc tcc tac ctg tgc ttc gaa ggt gca gaa aag atc tgg cac tcc ctc	451																			
Gly Ser Tyr Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu																				
105	110	115																		
cac agg cgc atc aaa ggt gaa cag cac agc acc gaa ccc aag tcg cag	499																			
His Arg Arg Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln																				
120	125	130																		
gaa agc cca aag tca gag gat cag ctg gtc aaa agt gcc atc aca act	547																			
Glu Ser Pro Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr																				
135	140	145																		
gac ctc atc ctt tcc gca gag atc atg gtt att tca ctc aat cag att	595																			
Asp Leu Ile Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile																				
150	155	160	165																	
gca gat caa act atc tgg atg cag gct gcg gtt ctt ttc gtc gta ggt	643																			
Ala Asp Gln Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly																				
170	175	180																		
att ggc atc acc gcg ctc gtg tac ggc gta gtc ggt gtt ctt gtg aaa	691																			
Ile Gly Ile Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys																				
185	190	195																		
atg gat gac gtc gga ctt aca ctt tca aag cgt gac tcc gca ggt atc	739																			
Met Asp Asp Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile																				
200	205	210																		
cag aaa ttt ggc cgc ggc ttg gtc aaa gcg atg ccc atc gtt ctt caa	787																			
Gln Lys Phe Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln																				
215	220	225																		
gtt att tct gtt gtc ggc gtt ttt gcc atg ctg tgg gtt ggt ggc cac	835																			
Val Ile Ser Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His																				
230	235	240	245																	
atc atg gtc gtt gga act gaa gag tta gga tgg gaa ctt ccc tac cac	883																			
Ile Met Val Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His																				
250	255	260																		
ctt gtt cac gga cta gag tcc tgg gct aac ggt atc gga ggc agt gct	931																			
Leu Val His Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala																				
265	270	275																		

Asp Ser Ala Gly Ile Gln Lys Phe Gly Arg Gly Leu Val Lys Ala Met
 210 215 220
 Pro Ile Val Leu Gln Val Ile Ser Val Val Gly Val Phe Ala Met Leu
 225 230 235 240
 Trp Val Gly Gly His Ile Met Val Val Gly Thr Glu Glu Leu Gly Trp
 245 250 255
 Glu Leu Pro Tyr His Leu Val His Gly Leu Glu Ser Trp Ala Asn Gly
 260 265 270
 Ile Gly Gly Ser Ala Leu Gly Trp Val Gly Asn Thr Phe Gly Ser Leu
 275 280 285
 Val Phe Gly Leu Ile Trp Gly Ala Ile Ile Thr Val Val Val Ser Val
 290 295 300
 Ile Lys Lys Phe Ile Pro Gln Arg Ala Gln Asn Ser Ser His
 305 310 315

<210> 397
 <211> 713
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(690)
 <223> FRXA00835

<400> 397
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 ctg tgc ttc gaa ggt gca gaa aag atc tgg cac tcc ctc cac agg cgc 96
 Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu His Arg Arg
 20 25 30
 atc aaa ggt gaa cag cac agc acc gaa ccc aag tcg cag gaa agc cca 144
 Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln Glu Ser Pro
 35 40 45
 aag tca gag gat cag ctg gtc aaa agt gcc atc aca act gac ctc atc 192
 Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr Asp Leu Ile
 50 55 60
 ctt tcc gca gag atc atg gtt att tca ctc aat cag att gca gat caa 240
 Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile Ala Asp Gln
 65 70 75 80
 act atc tgg atg cag gct gcg gtt ctt ttc gtc gta ggt att ggc atc 288
 Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly Ile Gly Ile
 85 90 95
 acc gcg ctc gtg tac ggc gta gtc ggt gtt ctt gtg aaa atg gat gac 336
 Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys Met Asp Asp
 100 105 110

gtc gga ctt aca ctt tca aag cgt gac tcc gca ggt atc cag aaa ttt 384
 Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile Gln Lys Phe
 115 120 125
 ggc cgc ggc ttg gtc aaa gcg atg ccc atc gtt ctt caa gtt att tct 432
 Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln Val Ile Ser
 130 135 140
 gtt gtc ggc gtt ttt gcc atg ctg tgg gtt ggt ggc cac atc atg gtc 480
 Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His Ile Met Val
 145 150 155 160
 gtt gga act gaa gag tta gga tgg gaa ctt ccc tac cac ctt gtt cac 528
 Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His Leu Val His
 165 170 175
 gga cta gag tcc tgg gct aac ggt atc gga ggc agt gct ctg gga tgg 576
 Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala Leu Gly Trp
 180 185 190
 gtt ggc aat act ttc ggg tca ctt gtg ttc ggc ctc att tgg ggc gcg 624
 Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile Trp Gly Ala
 195 200 205
 att atc acc gtt gtg gtc agt gtg atc aag aag ttc att cca cag cgt 672
 Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile Pro Gln Arg
 210 215 220
 gcg caa aac tcg tct cat tagtggagag ttgttcgctg taa 713
 Ala Gln Asn Ser Ser His
 225 230

<210> 398

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly Gly Ser Tyr
 1 5 10 15
 Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu His Arg Arg
 20 25 30
 Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln Glu Ser Pro
 35 40 45
 Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr Asp Leu Ile
 50 55 60
 Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile Ala Asp Gln
 65 70 75 80
 Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly Ile Gly Ile
 85 90 95
 Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys Met Asp Asp
 100 105 110
 Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile Gln Lys Phe

115	120	125
Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln Val Ile Ser		
130	135	140
Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His Ile Met Val		
145	150	155 160
Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His Leu Val His		
	165	170 175
Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala Leu Gly Trp		
	180	185 190
Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile Trp Gly Ala		
	195	200 205
Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile Pro Gln Arg		
210	215	220
Ala Gln Asn Ser Ser His		
225	230	

<210> 399
 <211> 1816
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1816)
 <223> RXN00836

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 Met Tyr Thr His Ser
 1 5
 aca ggc act cct cag ctt gat ttc gac ggt gac atc tat ccc ctt cac 163
 Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp Ile Tyr Pro Leu His
 10 15 20
 ctc ttc ttc tct gca cag act gcc caa cat ttc gct ctc gag cgc gtc 211
 Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe Ala Leu Glu Arg Val
 25 30 35
 aat tgg cat gtc tta cgc gct att gtg aaa cct gag caa ggc gaa ctc 259
 Asn Trp His Val Leu Arg Ala Ile Val Lys Pro Glu Gln Gly Glu Leu
 40 45 50
 atc gtc gaa gcg ctt ctc gca cca ata gaa tcc gca aca aaa atc ggt 307
 Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser Ala Thr Lys Ile Gly
 55 60 65
 gtt tgg gtt caa gat gaa ttt ctc ggg gtg att gca gag tcc cag ttc 355
 Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile Ala Glu Ser Gln Phe
 70 75 80 85

ctg ttg aat tct caa ttg tct cga att ttt gcc tct ggc cac ctg att	403
Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala Ser Gly His Leu Ile	
90 95 100	
tcc agc caa cta ctt ctc aca ccg agt aaa gga tct ctc gct tca gtt	451
Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly Ser Leu Ala Ser Val	
105 110 115	
ctt ctt cca aac cta aaa ttc ggg ctc atc agc aat gat cct cca cga	499
Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser Asn Asp Pro Pro Arg	
120 125 130	
gct gat tcc cac ctc tta ccg cta ggc aga atg tgg cgc gtt gag ccc	547
Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met Trp Arg Val Glu Pro	
135 140 145	
acc gtt cat gct ctg ttt gag gat ttc tca ctt ggc tcc acg att ctt	595
Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu Gly Ser Thr Ile Leu	
150 155 160 165	
ttt ggg ctg agg ctt gat tta gaa gcc cta att gtc tcc tat aac gga	643
Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile Val Ser Tyr Asn Gly	
170 175 180	
ata gaa tgt ggc atc tta aac ttt gat gac gcc tca gca cta agc tct	691
Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala Ser Ala Leu Ser Ser	
185 190 195	
gct gtg aaa ttc tca aat gca aat ggt ctc acc ccc acg gtg ctc ggc	739
Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr Pro Thr Val Leu Gly	
200 205 210	
cac gta gtc cgg gag aac ggt gaa aca tcc ttc gag att gac gtt ctc	787
His Val Val Arg Glu Asn Gly Glu Thr Ser Phe Glu Ile Asp Val Leu	
215 220 225	
cca ctg gag ttg tgg tcg aag aag cag cat cgc ctt gag gtt tta aaa	835
Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg Leu Glu Val Leu Lys	
230 235 240 245	
atc cct cgg ttg ata cct aaa gag gca gat tcc caa aat tat gtg aag	883
Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser Gln Asn Tyr Val Lys	
250 255 260	
gcg aca gcg ctc ctt tca gac gag att ctg cga cca caa acg ctg tcc	931
Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg Pro Gln Thr Leu Ser	
265 270 275	
aaa aag gca ctg tct ttg tcg gac acc gca gtt aag tac agc cct cat	979
Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val Lys Tyr Ser Pro His	
280 285 290	
gtt gct tgt ggc gtg ggg atg ttt agt ctt ttc gcc gtt att ccc ttt	1027
Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe Ala Val Ile Pro Phe	
295 300 305	
gac aag ttg agt gat cat agt gcg atg ctg ctc gca gtc att agc ttg	1075
Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu Ala Val Ile Ser Leu	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 400

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35 40 45

Glu Gln Gly Glu Leu Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser
50 55 60

Ala Thr Lys Ile Gly Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile
65 70 75 80

Ala Glu Ser Gln Phe Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala
85 90 95

Ser Gly His Leu Ile Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly
100 105 110

Ser Leu Ala Ser Val Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser
115 120 125

Asn Asp Pro Pro Arg Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met
130 135 140

Trp Arg Val Glu Pro Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu
145 150 155 160

Gly Ser Thr Ile Leu Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile
165 170 175

Val Ser Tyr Asn Gly Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala
180 185 190

Ser Ala Leu Ser Ser Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr
195 200 205

Pro Thr Val Leu Gly His Val Val Arg Glu Asn Gly Glu Thr Ser Phe
210 215 220

Glu Ile Asp Val Leu Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg
225 230 235 240

Leu Glu Val Leu Lys Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser
245 250 255

Gln Asn Tyr Val Lys Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg
260 265 270

Pro Gln Thr Leu Ser Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val

275					280					285					
Lys	Tyr	Ser	Pro	His	Val	Ala	Cys	Gly	Val	Gly	Met	Phe	Ser	Leu	Phe
290						295					300				
Ala	Val	Ile	Pro	Phe	Asp	Lys	Leu	Ser	Asp	His	Ser	Ala	Met	Leu	Leu
305					310					315					320
Ala	Val	Ile	Ser	Leu	Met	Leu	Phe	Val	Leu	Ala	Leu	Val	Ile	Leu	Phe
				325					330					335	
Lys	Arg	Ile	Gln	Ser	Thr	Asn	Thr	Gln	Arg	Trp	Asn	Leu	Ala	Ser	Ser
			340					345					350		
Val	Gly	Leu	Leu	Ala	Thr	Leu	Pro	Ile	Ile	Ile	Phe	Leu	Val	Ala	Asp
			355				360					365			
Thr	Leu	Ile	Pro	Gln	Gly	Ser	Leu	Glu	Asn	His	Ala	Gln	Pro	Asp	Val
	370					375					380				
Gln	Val	Thr	Thr	Leu	Ala	Asn	Arg	Arg	Pro	Ser	Ser	Pro	Thr	Ser	Leu
385					390					395					400
Asp	Ser	Leu	Gly	Ala	Leu	Asn	Ser	Pro	Ser	Ser	Pro	Asn	Ser	Pro	Ser
				405					410					415	
Ser	Ser	Met	Leu	Gln	Asn	Ser	Glu	Met	Phe	Ala	Ser	Pro	Pro	Ile	Ala
			420					425					430		
Ser	Gly	Gln	Ser	Pro	Val	Ser	Thr	Phe	Arg	Ser	Trp	Leu	Asp	Arg	Ser
			435				440					445			
Ile	Leu	Pro	Leu	Thr	Arg	Glu	Asn	Ser	Ala	Ser	Glu	Ser	Ala	Val	Thr
	450					455					460				
Ala	Leu	Gly	Pro	Ser	Ile	Val	Gln	Pro	Ala	Ser	Glu	Ser	Ile	Thr	Thr
465					470					475					480
Pro	Ala	Gln	Thr	Ser	Gln	Ser	Arg	His	Ala	Ile	Asp	Asp	Gly	Asp	Asp
			485						490				495		
Ser	Lys	Thr	Ser	Thr	Gly	Arg	Pro	Ala	Pro	Thr	Thr	Asn	Ser	Pro	Ile
			500					505					510		
Ile	Ala	Leu	Pro	Pro	Thr	Trp	Ile	Ile	Gly	Pro	Glu	Asp	Pro	Glu	Ser
	515					520						525			
Thr	Asp	Pro	Thr	Ala	Pro	Thr	Glu	Pro	Thr	Glu	Pro	Ser	Glu	Pro	Val
	530					535					540				
Ala	Thr	Asp	Glu	Pro	Ser	Glu	Thr	Ser	Glu	Gln	Thr	Ser	Pro	Leu	Leu
545					550					555					560
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<211> 1771

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1771)

<223> FRXA00836

<400> 401

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 Met Tyr Thr His Ser
 1 5

aca ggc act cct cag ctt gat ttc gac ggt gac atc tat ccc ctt cac 163
 Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp Ile Tyr Pro Leu His
 10 15 20

ctc ttc ttc tct gca cag act gcc caa cat ttc gct ctc gag cgc gtc 211
 Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe Ala Leu Glu Arg Val
 25 30 35

aat tgg cat gtc tta cgc gct att gtg aaa cct gag caa ggc gaa ctc 259
 Asn Trp His Val Leu Arg Ala Ile Val Lys Pro Glu Gln Gly Glu Leu
 40 45 50

atc gtc gaa gcg ctt ctc gca cca ata gaa tcc gca aca aaa atc ggt 307
 Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser Ala Thr Lys Ile Gly
 55 60 65

gtt tgg gtt caa gat gaa ttt ctc ggg gtg att gca gag tcc cag ttc 355
 Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile Ala Glu Ser Gln Phe
 70 75 80 85

ctg ttg aat tct caa ttg tct cga att ttt gcc tct ggc cac ctg att 403
 Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala Ser Gly His Leu Ile
 90 95 100

tcc agc caa cta ctt ctc aca ccg agt aaa gga tct ctc gct tca gtt 451
 Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly Ser Leu Ala Ser Val
 105 110 115

ctt ctt cca aac cta aaa ttc ggg ctc atc agc aat gat cct cca cga 499
 Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser Asn Asp Pro Pro Arg
 120 125 130

gct gat tcc cac ctc tta ccg cta ggc aga atg tgg cgc gtt gag ccc 547
 Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met Trp Arg Val Glu Pro
 135 140 145

acc gtt cat gct ctg ttt gag gat ttc tca ctt ggc tcc acg att ctt 595
 Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu Gly Ser Thr Ile Leu
 150 155 160 165

ttt ggg ctg agg ctt gat tta gaa gcc cta att gtc tcc tat aac gga 643
 Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile Val Ser Tyr Asn Gly
 170 175 180

ata gaa tgt ggc atc tta aac ttt gat gac gcc tca gca cta agc tct 691
 Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala Ser Ala Leu Ser Ser
 185 190 195

gct gta aaa ttc tca aat gca aat ggt ctc acc ccc acg gtg ctc ggc	739
Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr Pro Thr Val Leu Gly	
200 205 210	
cac gta gtc cgg gag aac ggt gaa aca tcc ttc gag att gac gtt ctc	787
His Val Val Arg Glu Asn Gly Glu Thr Ser Phe Glu Ile Asp Val Leu	
215 220 225	
cca ctg gag ttg tgg tgc aag aag cag cat cgc ctt gag gtt tta aaa	835
Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg Leu Glu Val Leu Lys	
230 235 240 245	
atc cct cgg ttg ata cct aaa gag gca gat tcc caa aat tat gtg aag	883
Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser Gln Asn Tyr Val Lys	
250 255 260	
gcg aca gcg ctc ctt tca gac gag att ctg cga cca caa acg ctg tcc	931
Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg Pro Gln Thr Leu Ser	
265 270 275	
aaa aag gca ctg tct ttg tgc gac acc gca gtt aag tac agc cct cat	979
Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val Lys Tyr Ser Pro His	
280 285 290	
gtt gct tgt ggc gtg ggg atg ttt agt ctt ttc gcc gtt att ccc ttt	1027
Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe Ala Val Ile Pro Phe	
295 300 305	
gac aag ttg agt gat cat agt gcg atg ctg ctc gca gtc att agc ttg	1075
Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu Ala Val Ile Ser Leu	
310 315 320 325	
atg ctt ttt gtg ctg gca tta gta att ctt ttc aag aga att cag tca	1123
Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe Lys Arg Ile Gln Ser	
330 335 340	
act aat act cag cgt tgg aac ttg gcc tgc tca gtc gga tta ctc gcg	1171
Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser Val Gly Leu Leu Ala	
345 350 355	
aca ctt ccg att atc ata ttc ctg gtt gct gat aca ttg att cct cag	1219
Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp Thr Leu Ile Pro Gln	
360 365 370	
ggc agc ctg gaa aac cat gct caa ccc gac gta cag gta aca acg tta	1267
Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val Gln Val Thr Thr Leu	
375 380 385	
gct aac agg cgg cca agt tca cct acc tca ctg gac tca cta ggc gca	1315
Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu Asp Ser Leu Gly Ala	
390 395 400 405	
ctg aat tca cca agt tgc ccg aat tcc ccg agc tca tca atg ctg caa	1363
Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser Ser Ser Met Leu Gln	
410 415 420	
aac tct gaa atg ttc gcc tca cca ccg atc gcc tct ggg cag tca ccg	1411
Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala Ser Gly Gln Ser Pro	
425 430 435	
gtt tgc acg ttc cgc tca tgg cta gat cga tcc att ctg cca ctc aca	1459

Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser Ile Leu Pro Leu Thr
 440 445 450
 cga gaa aat tcc gct tca gaa agc gca gtg aca gct ctt gga ccg tcg 1507
 Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr Ala Leu Gly Pro Ser
 455 460 465
 ata gtg cag cct gca tct gaa tcg att aca act cca gct caa acg tcg 1555
 Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr Pro Ala Gln Thr Ser
 470 475 480 485
 caa agt cgc cac gca att gac gat ggt gac gac agt aaa acc tca acg 1603
 Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp Ser Lys Thr Ser Thr
 490 495 500
 gga aga cca gct ccc act act aac tcg ccg atc att gct ctt ccc cca 1651
 Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile Ile Ala Leu Pro Pro
 505 510 515
 acg tgg att atc ggg ccg gaa gat cca gaa tcc acc gac cct aca gca 1699
 Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser Thr Asp Pro Thr Ala
 520 525 530
 cca acc gag ccc acc gag cca agc gaa cct gtc gca acc gac gaa ccc 1747
 Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val Ala Thr Asp Glu Pro
 535 540 545
 tca gag acc tct gaa caa act tca 1771
 Ser Glu Thr Ser Glu Gln Thr Ser
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<210> 402

<211> 557

<212> PRT

<213> Corynebacterium glutamicum

<400> 402

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 Ile Tyr Pro Leu His Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe
 20 25 30
 Ala Leu Glu Arg Val Asn Trp His Val Leu Arg Ala Ile Val Lys Pro
 35 40 45
 Glu Gln Gly Glu Leu Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser
 50 55 60
 Ala Thr Lys Ile Gly Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile
 65 70 75 80
 Ala Glu Ser Gln Phe Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala
 85 90 95
 Ser Gly His Leu Ile Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly
 100 105 110
 Ser Leu Ala Ser Val Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser
 115 120 125

Asn Asp Pro Pro Arg Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met
 130 135 140
 Trp Arg Val Glu Pro Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu
 145 150 155 160
 Gly Ser Thr Ile Leu Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile
 165 170 175
 Val Ser Tyr Asn Gly Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala
 180 185 190
 Ser Ala Leu Ser Ser Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr
 195 200 205
 Pro Thr Val Leu Gly His Val Val Arg Glu Asn Gly Glu Thr Ser Phe
 210 215 220
 Glu Ile Asp Val Leu Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg
 225 230 235 240
 Leu Glu Val Leu Lys Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser
 245 250 255
 Gln Asn Tyr Val Lys Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg
 260 265 270
 Pro Gln Thr Leu Ser Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val
 275 280 285
 Lys Tyr Ser Pro His Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe
 290 295 300
 Ala Val Ile Pro Phe Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu
 305 310 315 320
 Ala Val Ile Ser Leu Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe
 325 330 335
 Lys Arg Ile Gln Ser Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser
 340 345 350
 Val Gly Leu Leu Ala Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp
 355 360 365
 Thr Leu Ile Pro Gln Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val
 370 375 380
 Gln Val Thr Thr Leu Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu
 385 390 395 400
 Asp Ser Leu Gly Ala Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser
 405 410 415
 Ser Ser Met Leu Gln Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala
 420 425 430
 Ser Gly Gln Ser Pro Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser
 435 440 445

Ile Leu Pro Leu Thr Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr
 450 455 460

Ala Leu Gly Pro Ser Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr
 465 470 475 480

Pro Ala Gln Thr Ser Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp
 485 490 495

Ser Lys Thr Ser Thr Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile
 500 505 510

Ile Ala Leu Pro Pro Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser
 515 520 525

Thr Asp Pro Thr Ala Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val
 530 535 540

Ala Thr Asp Glu Pro Ser Glu Thr Ser Glu Gln Thr Ser
 545 550 555

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(814)
 <223> RXN00840

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tccctccgca ttgtctcggt gaaaggtaag taaaactcaa gtg aca aag aca ctc 115
 Val Thr Lys Thr Leu
 1 5

ccc cga ctg ctt aca gtc gct gcc gct cta gcc att gca ctc ccg gca 163
 Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala Ile Ala Leu Pro Ala
 10 15 20

acc ccg gta gca tcg gct gtc aca cca gtt gaa caa gct ttc aac gcc 211
 Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu Gln Ala Phe Asn Ala
 25 30 35

tca tcg aat ctc tcc agc ggt ctc ccc gta gac caa tgg gga cgc ccc 259
 Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp Gln Trp Gly Arg Pro
 40 45 50

aac gag cag ttc cgc caa caa atc gaa cag gca gta aac caa ccg tgg 307
 Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala Val Asn Gln Pro Trp
 55 60 65

gtc ccg cag gaa atc aag aac atc gtt tct cag gcc atg ggt ttt atc 355
 Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln Ala Met Gly Phe Ile
 70 75 80 85

acc ggt gac ggc agc gaa ggt ggg gac att gaa atc ccc gac aac gca 403
 Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu Ile Pro Asp Asn Ala

90	95	100	
cca cgc atc gcg cag ttc ttc tgg ccc acc cga tca gaa aac tgc atc			451
Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg Ser Glu Asn Cys Ile			
105	110	115	
aac gga aat tct gca gcc gta gga tct gcc ttc gca gtt cca gga cca			499
Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe Ala Val Pro Gly Pro			
120	125	130	
gca gat ctc ccc ctc ccc ggc gca ggt gtc ggc caa acc tcc ttc gtg			547
Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly Gln Thr Ser Phe Val			
135	140	145	
ttc acc gca ctg gga act ggc ccc ctc gca gaa cag caa agc acc gca			595
Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu Gln Gln Ser Thr Ala			
150	155	160	165
atg act gtt caa tgg gca aac tta agc aac ttc acc cat ggc acc acg			643
Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe Thr His Gly Thr Thr			
170	175	180	
acg ttg agc aac acc gga atc aac ccc gat ggc ccc tca acg att tcc			691
Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly Pro Ser Thr Ile Ser			
185	190	195	
ggt gtg gca gac aca gga cgc ggc atc atc gtc gcc tcc atg tca ggc			739
Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val Ala Ser Met Ser Gly			
200	205	210	
ggc ctc acc aca tcc acc gaa aac ggt tca gcg aac tgt aat ttc atc			787
Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala Asn Cys Asn Phe Ile			
215	220	225	
ccg act gcc gtc gta ttc gat gtg agg taagaaaaca atgactgac			834
Pro Thr Ala Val Val Phe Asp Val Arg			
230	235		
ttc			837
<210> 404			
<211> 238			
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<213> Corynebacterium glutamicum			
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Ile Ala Leu Pro Ala Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu			
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Gln Ala Phe Asn Ala Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp			
35	40	45	
Gln Trp Gly Arg Pro Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala			
50	55	60	
Val Asn Gln Pro Trp Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln			
65	70	75	80

aac gag cag ttc cgc caa caa atc gaa cag gca gta aac caa ccg tgg 307
 Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala Val Asn Gln Pro Trp
 55 60 65

gtc ccg cag gaa atc aag aac atc gtt tct cag gcc atg ggt ttt atc 355
 Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln Ala Met Gly Phe Ile
 70 75 80 85

acc ggt gac ggc agc gaa ggt ggg gac att gaa atc ccc gac aac gca 403
 Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu Ile Pro Asp Asn Ala
 90 95 100

cca cgc atc gcg cag ttc ttc tgg ccc acc cga tca gaa aac tgc atc 451
 Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg Ser Glu Asn Cys Ile
 105 110 115

aac gga aat tct gca gcc gta gga tct gcc ttc gca gtt cca gga cca 499
 Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe Ala Val Pro Gly Pro
 120 125 130

gca gat ctc ccc ctc ccc ggc gca ggt gtc ggc caa acc tcc ttc gtg 547
 Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly Gln Thr Ser Phe Val
 135 140 145

ttc acc gca ctg gga act ggc ccc ctc gca gaa cag caa agc acc gca 595
 Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu Gln Gln Ser Thr Ala
 150 155 160 165

atg act gtt caa tgg gca aac tta agc aac ttc acc cat ggc acc acg 643
 Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe Thr His Gly Thr Thr
 170 175 180

acg ttg agc aac acc gga atc aac ccc gat ggc ccc tca acg att tcc 691
 Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly Pro Ser Thr Ile Ser
 185 190 195

ggt gtg gca gac aca gga cgc ggc atc atc gtc gcc tcc atg tca ggc 739
 Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val Ala Ser Met Ser Gly
 200 205 210

ggc ctc acc aca tcc acc gaa aac ggt tca gcg aac tgt aat ttc atc 787
 Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala Asn Cys Asn Phe Ile
 215 220 225

ccg act gcc gtc gta ttc gat gtg agg taagaaaaca atgactgac 834
 Pro Thr Ala Val Val Phe Asp Val Arg
 230 235

ttc 837

<210> 406
 <211> 238
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 406
 Val Thr Lys Thr Leu Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala
 1 5 10 15
 Ile Ala Leu Pro Ala Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu

20 25 30
 Gln Ala Phe Asn Ala Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp
 35 40 45
 Gln Trp Gly Arg Pro Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala
 50 55 60
 Val Asn Gln Pro Trp Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln
 65 70 75 80
 Ala Met Gly Phe Ile Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu
 85 90 95
 Ile Pro Asp Asn Ala Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg
 100 105 110
 Ser Glu Asn Cys Ile Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe
 115 120 125
 Ala Val Pro Gly Pro Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly
 130 135 140
 Gln Thr Ser Phe Val Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu
 145 150 155 160
 Gln Gln Ser Thr Ala Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe
 165 170 175
 Thr His Gly Thr Thr Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly
 180 185 190
 Pro Ser Thr Ile Ser Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val
 195 200 205
 Ala Ser Met Ser Gly Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala
 210 215 220
 Asn Cys Asn Phe Ile Pro Thr Ala Val Val Phe Asp Val Arg
 225 230 235

<210> 407
 <211> 660
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(637)
 <223> RXN00841

<400> 407
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 atcccgactg ccgtcgtatt cgatgtgagg taagaaaaca atg act gat ctt cat 115
 Met Thr Asp Leu His
 1 5
 ccc gta aag cag gaa att ttc aac act gct gaa tcc ata aac aca gat 163
 Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu Ser Ile Asn Thr Asp

10	15	20	
ccc aag ggg ttt ctc cgc gag gta gac acc ttc aaa gta acc gac ttc			211
Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe Lys Val Thr Asp Phe			
25	30	35	
ggc ctg tac atg gct cgt ggt gca aac cac ccc aag ttc gga tac ttg			259
Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro Lys Phe Gly Tyr Leu			
40	45	50	
gaa agc tgg ctc ctc cca gaa ctt gga ttg cgt gcc aac att ttc cac			307
Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg Ala Asn Ile Phe His			
55	60	65	
ttc cgc aaa ggc gtg gat gaa cgt cag gat tac tac atc gat gtc gct			355
Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr Tyr Ile Asp Val Ala			
70	75	80	85
gaa att cgc gtc gaa gac aac atc tgg acc acc cgc gac ctc tac gtg			403
Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr Arg Asp Leu Tyr Val			
90	95	100	
gat ctc atc tct gtc tgc gga gaa cca gta aca gtc atg gac atc gac			451
Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr Val Met Asp Ile Asp			
105	110	115	
gaa cta gct gca gca acc tca gca ggg ctt atc act gca gat gac gct			499
Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile Thr Ala Asp Asp Ala			
120	125	130	
gag cgc gca att gat gcc acc ttg aat gct gtt gaa gga atc acc cgc			547
Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val Glu Gly Ile Thr Arg			
135	140	145	
cac ggc gac gat cct atg cag tgg ctg cgc tcc aag gga atc gaa ctc			595
His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser Lys Gly Ile Glu Leu			
150	155	160	165
acc tgg gct gac gcc agc cag gta gag ctc gtc cct gca gag			637
Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val Pro Ala Glu			
170	175		
taactacttc ctaaccgctg ctt			660

<210> 408

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

Met Thr Asp Leu His Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu
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Ser Ile Asn Thr Asp Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe
20 25 30

Lys Val Thr Asp Phe Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro
35 40 45

Lys Phe Gly Tyr Leu Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg

Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr Tyr Ile Asp Val Ala
 70 75 80 85
 gaa att cgc gtc gaa gac aac atc tgg acc acc cgc gac ctc tac gtg 403
 Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr Arg Asp Leu Tyr Val
 90 95 100
 gat ctc atc tct gtc tgc gga gaa cca gta aca gtc atg gac atc gac 451
 Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr Val Met Asp Ile Asp
 105 110 115
 gaa cta gct gca gca acc tca gca ggg ctt atc act gca gat gac gct 499
 Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile Thr Ala Asp Asp Ala
 120 125 130
 gag cgc gca att gat gcc acc ttg aat gct gtt gaa gga atc acc cgc 547
 Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val Glu Gly Ile Thr Arg
 135 140 145
 cac ggc gac gat cct atg cag tgg ctg cgc tcc aag gga atc gaa ctc 595
 His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser Lys Gly Ile Glu Leu
 150 155 160 165
 acc tgg gct gac gcc agc cag gta gag ctc gtc cct gca gag 637
 Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val Pro Ala Glu
 170 175
 taactacttc ctaaccgctg ctt 660

<210> 410
 <211> 179
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 410
 Met Thr Asp Leu His Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu
 1 5 10 15
 Ser Ile Asn Thr Asp Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe
 20 25 30
 Lys Val Thr Asp Phe Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro
 35 40 45
 Lys Phe Gly Tyr Leu Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg
 50 55 60
 Ala Asn Ile Phe His Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr
 65 70 75 80
 Tyr Ile Asp Val Ala Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr
 85 90 95
 Arg Asp Leu Tyr Val Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr
 100 105 110
 Val Met Asp Ile Asp Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile
 115 120 125
 Thr Ala Asp Asp Ala Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val

cat ctt ttg atc acc tat ggc cct gac ggc ggc tat ggg cac ccc gat 547
 His Leu Leu Ile Thr Tyr Gly Pro Asp Gly Gly Tyr Gly His Pro Asp
 135 140 145

cac att cgt gcg cat gaa atc acc cac gca gca gcc ggc gag caa cgc 595
 His Ile Arg Ala His Glu Ile Thr His Ala Ala Ala Gly Glu Gln Arg
 150 155 160 165

att ctg tgg gct gtg agc gac cgt gag gag ctc gag gac ggt cta aag 643
 Ile Leu Trp Ala Val Ser Asp Arg Glu Glu Leu Glu Asp Gly Leu Lys
 170 175 180

gca atc act ggg ctt cct gaa ggt tgg ggc agg gga gag ctc tct gcg 691
 Ala Ile Thr Gly Leu Pro Glu Gly Trp Gly Arg Gly Glu Leu Ser Ala
 185 190 195

gtc gat tcc gtg gac ctc tct gtt gag ctg aac gat gaa gtg tat gcc 739
 Val Asp Ser Val Asp Leu Ser Val Glu Leu Asn Asp Glu Val Tyr Ala
 200 205 210

acc aag gtg gaa tcc atg cgc gcg cat gcg aca caa ttg tgg atc gct 787
 Thr Lys Val Glu Ser Met Arg Ala His Ala Thr Gln Leu Trp Ile Ala
 215 220 225

gac ggt tcc gta tct cgc acc aac ccg gtt gcc gca cac gca gtg aca 835
 Asp Gly Ser Val Ser Arg Thr Asn Pro Val Ala Ala His Ala Val Thr
 230 235 240 245

cag cag gac aat gtg aag gtg tgg gcg cta tct aat ttg att gca caa 883
 Gln Gln Asp Asn Val Lys Val Trp Ala Leu Ser Asn Leu Ile Ala Gln
 250 255 260

ccc atc atg cgc cac gag cac tac caa ctc ggc gcc gga aca cca ctg 931
 Pro Ile Met Arg His Glu His Tyr Gln Leu Gly Ala Gly Thr Pro Leu
 265 270 275

cct gaa ggt gca act gga gtg ctt gac gga ctg gag ttc tgacacgggtt 980
 Pro Glu Gly Ala Thr Gly Val Leu Asp Gly Leu Glu Phe
 280 285 290

atggcagaat cta 993

<210> 412

<211> 290

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

Met Leu Lys Asn Asp Leu Ser Gly Ala Arg Val Val Ala Val His Ala
 1 5 10 15

His Pro Asp Asp Glu Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu
 20 25 30

Ala Ala Arg Gly Ala Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu
 35 40 45

Gln Gly Glu Val Ile Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp
 50 55 60

Ala Asp Gln Leu Gly Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu
 65 70 75 80
 Glu Ile Leu Gly Val Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp
 85 90 95
 Arg Asp Ser Gly Met Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala
 100 105 110
 Phe Ile His Ser Gly Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu
 115 120 125
 Ala Glu Leu Lys Pro His Leu Leu Ile Thr Tyr Gly Pro Asp Gly Gly
 130 135 140
 Tyr Gly His Pro Asp His Ile Arg Ala His Glu Ile Thr His Ala Ala
 145 150 155 160
 Ala Gly Glu Gln Arg Ile Leu Trp Ala Val Ser Asp Arg Glu Glu Leu
 165 170 175
 Glu Asp Gly Leu Lys Ala Ile Thr Gly Leu Pro Glu Gly Trp Gly Arg
 180 185 190
 Gly Glu Leu Ser Ala Val Asp Ser Val Asp Leu Ser Val Glu Leu Asn
 195 200 205
 Asp Glu Val Tyr Ala Thr Lys Val Glu Ser Met Arg Ala His Ala Thr
 210 215 220
 Gln Leu Trp Ile Ala Asp Gly Ser Val Ser Arg Thr Asn Pro Val Ala
 225 230 235 240
 Ala His Ala Val Thr Gln Gln Asp Asn Val Lys Val Trp Ala Leu Ser
 245 250 255
 Asn Leu Ile Ala Gln Pro Ile Met Arg His Glu His Tyr Gln Leu Gly
 260 265 270
 Ala Gly Thr Pro Leu Pro Glu Gly Ala Thr Gly Val Leu Asp Gly Leu
 275 280 285
 Glu Phe
 290

<210> 413

<211> 487

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(487)

<223> FRXA00846

<400> 413

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 cctgggggaa tttcaagtgc tgcaagttgg aggaaaaacg atg ttg aag aat gat 115
 Met Leu Lys Asn Asp

1

5

. ctg tct ggt gct cga gtt gta gct gtg cat gcg cac cct gac gat gag 163
 Leu Ser Gly Ala Arg Val Val Ala Val His Ala His Pro Asp Asp Glu
 10 15 20

 gcg att acc acc ggt ggt gtg ctt gcg gat ctt gct gct cgt ggc gcc 211
 Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu Ala Ala Arg Gly Ala
 25 30 35

 gat gtc acg gta att acc tgc acg ttg ggc gag cag ggt gag gtt atc 259
 Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu Gln Gly Glu Val Ile
 40 45 50

 ggt gag aca ttc gcg cag cta gtc aac ggt gat gcg gat cag ctt ggc 307
 Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp Ala Asp Gln Leu Gly
 55 60 65

 ggg ttt agg atc cat gag ctt tac gcc tgc ctg gag att ctg ggc gtg 355
 Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu Glu Ile Leu Gly Val
 70 75 80 85

 cgt ggc att cat ctg ggt ggc gct ggc tgc tgg agg gat tcc ggt atg 403
 Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp Arg Asp Ser Gly Met
 90 95 100

 gtt ggt gat cct gca aat gag cat ccg cgt gcg ttt att cac tct ggt 451
 Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala Phe Ile His Ser Gly
 105 110 115

 gac cgt gca gtg gag caa ttg aaa gaa ctt ctt gcg 487
 Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu Ala
 120 125

<210> 414

<211> 129

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

Met Leu Lys Asn Asp Leu Ser Gly Ala Arg Val Val Ala Val His Ala
 1 5 10 15

 His Pro Asp Asp Glu Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu
 20 25 30

 Ala Ala Arg Gly Ala Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu
 35 40 45

 Gln Gly Glu Val Ile Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp
 50 55 60

 Ala Asp Gln Leu Gly Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu
 65 70 75 80

 Glu Ile Leu Gly Val Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp
 85 90 95

 Arg Asp Ser Gly Met Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala
 100 105 110

Phe Ile His Ser Gly Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu
 115 120 125

Ala

<210> 415
 <211> 951
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(928)
 <223> RXN00850

<400> 415
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 attacctgtt tcagatatatt aggaaggctc acttttcaac atg gct aat cca ttc 115
 Met Ala Asn Pro Phe
 1 5
 tcc aag gca tgg aag tac ctc atg gcg ttg ttc gac tcc aag att gag 163
 Ser Lys Ala Trp Lys Tyr Leu Met Ala Leu Phe Asp Ser Lys Ile Glu
 10 15 20
 gag aac gcg gat cct aag gta cag atc cag caa gcc atc gaa gat gct 211
 Glu Asn Ala Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Asp Ala
 25 30 35
 cag cgc cag cat cag gag ctc tcc cag cag gca gca gct gtt att ggt 259
 Gln Arg Gln His Gln Glu Leu Ser Gln Gln Ala Ala Ala Val Ile Gly
 40 45 50
 aac cag cgt cag ctt gaa atg cag ctg aac cgc cgt ctg gct gaa att 307
 Asn Gln Arg Gln Leu Glu Met Gln Leu Asn Arg Arg Leu Ala Glu Ile
 55 60 65
 gag aag ctg cag ggc aac acc cgc cag gct atc cag ctg gct gac aag 355
 Glu Lys Leu Gln Gly Asn Thr Arg Gln Ala Ile Gln Leu Ala Asp Lys
 70 75 80 85
 gct cgc gct gac ggt gat gtc aag aag gct act gag tac gaa aac gcc 403
 Ala Arg Ala Asp Gly Asp Val Lys Lys Ala Thr Glu Tyr Glu Asn Ala
 90 95 100
 gct gag gct ttc gct gca cag ctg gtt act gct gag cag tcc gtt gaa 451
 Ala Glu Ala Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu
 105 110 115
 gat acc aag cag ctc cac gac cag gct ctg cag cag gct gat cag gct 499
 Asp Thr Lys Gln Leu His Asp Gln Ala Leu Gln Gln Ala Asp Gln Ala
 120 125 130
 aag aag gct gtg gag cgt aac tcc atg gct ttg cag cag aag gtt gct 547
 Lys Lys Ala Val Glu Arg Asn Ser Met Ala Leu Gln Gln Lys Val Ala
 135 140 145

gag cgc acc aag ctt ctg agc cag ctg gag cag gcg aag atg cag gaa 595
 Glu Arg Thr Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu
 150 155 160 165
 aag gtt tcc gag tcc ctg aag tcc atg gat tct ttg acc tcc ggc agc 643
 Lys Val Ser Glu Ser Leu Lys Ser Met Asp Ser Leu Thr Ser Gly Ser
 170 175 180
 act cct aac ctg gat caa gtt cgt gag aag att gag cgt cgt tac gct 691
 Thr Pro Asn Leu Asp Gln Val Arg Glu Lys Ile Glu Arg Arg Tyr Ala
 185 190 195
 aac gcg ctt ggc cag gct gag ctt gcg tcc aac tct gtt gag ggc cgc 739
 Asn Ala Leu Gly Gln Ala Glu Leu Ala Ser Asn Ser Val Glu Gly Arg
 200 205 210
 atg gct gag gtt gag cag gct ggc gtt cag atg gct gga cac tcc cgc 787
 Met Ala Glu Val Glu Gln Ala Gly Val Gln Met Ala Gly His Ser Arg
 215 220 225
 ctt gag cag atc cgc gct gag atg gct ggt ggt tcc ctg acc gct ggt 835
 Leu Glu Gln Ile Arg Ala Glu Met Ala Gly Gly Ser Leu Thr Ala Gly
 230 235 240 245
 aac aag cag gag tcc att gag gct cct gca gcg ggc aac aac gtc act 883
 Asn Lys Gln Glu Ser Ile Glu Ala Pro Ala Ala Gly Asn Asn Val Thr
 250 255 260
 gat gac gca gtt gca cag cgc atg cgt gag ctg cgc ggc gag gct 928
 Asp Asp Ala Val Ala Gln Arg Met Arg Glu Leu Arg Gly Glu Ala
 265 270 275
 taaacctgcc acagcagact aaa 951

<210> 416
 <211> 276
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 416
 Met Ala Asn Pro Phe Ser Lys Ala Trp Lys Tyr Leu Met Ala Leu Phe
 1 5 10 15
 Asp Ser Lys Ile Glu Glu Asn Ala Asp Pro Lys Val Gln Ile Gln Gln
 20 25 30
 Ala Ile Glu Asp Ala Gln Arg Gln His Gln Glu Leu Ser Gln Gln Ala
 35 40 45
 Ala Ala Val Ile Gly Asn Gln Arg Gln Leu Glu Met Gln Leu Asn Arg
 50 55 60
 Arg Leu Ala Glu Ile Glu Lys Leu Gln Gly Asn Thr Arg Gln Ala Ile
 65 70 75 80
 Gln Leu Ala Asp Lys Ala Arg Ala Asp Gly Asp Val Lys Lys Ala Thr
 85 90 95
 Glu Tyr Glu Asn Ala Ala Glu Ala Phe Ala Ala Gln Leu Val Thr Ala
 100 105 110

Glu Gln Ser Val Glu Asp Thr Lys Gln Leu His Asp Gln Ala Leu Gln
 115 120 125
 Gln Ala Asp Gln Ala Lys Lys Ala Val Glu Arg Asn Ser Met Ala Leu
 130 135 140
 Gln Gln Lys Val Ala Glu Arg Thr Lys Leu Leu Ser Gln Leu Glu Gln
 145 150 155 160
 Ala Lys Met Gln Glu Lys Val Ser Glu Ser Leu Lys Ser Met Asp Ser
 165 170 175
 Leu Thr Ser Gly Ser Thr Pro Asn Leu Asp Gln Val Arg Glu Lys Ile
 180 185 190
 Glu Arg Arg Tyr Ala Asn Ala Leu Gly Gln Ala Glu Leu Ala Ser Asn
 195 200 205
 Ser Val Glu Gly Arg Met Ala Glu Val Glu Gln Ala Gly Val Gln Met
 210 215 220
 Ala Gly His Ser Arg Leu Glu Gln Ile Arg Ala Glu Met Ala Gly Gly
 225 230 235 240
 Ser Leu Thr Ala Gly Asn Lys Gln Glu Ser Ile Glu Ala Pro Ala Ala
 245 250 255
 Gly Asn Asn Val Thr Asp Asp Ala Val Ala Gln Arg Met Arg Glu Leu
 260 265 270
 Arg Gly Glu Ala
 275

<210> 417
 <211> 336
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(313)
 <223> RXN00854

<400> 417
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 ggacacgtaa cttctgtgct tgcgctgtat tatcgcccc atg cgt tta tcg gag 115
 Met Arg Leu Ser Glu
 1 5
 ttt cgg caa ctc att gaa gat gaa ttc gga gaa gcc aaa ggg gag tgg 163
 Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu Ala Lys Gly Glu Trp
 10 15 20
 att gca cac tcg cat gtg att ggt gcc ctc ggc gtc act gca gat gtt 211
 Ile Ala His Ser His Val Ile Gly Ala Leu Gly Val Thr Ala Asp Val
 25 30 35
 gca gta gat acc ggg gtt gat ctg cgc gat gta tgg gaa caa ctg tgc 259

Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val Trp Glu Gln Leu Cys
 40 45 50

att gat ttc agt gtt ccc gaa gag cga cga ctt ggt aaa gat gaa cca 307
 Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu Gly Lys Asp Glu Pro
 55 60 65

ggg ttc tagcttggtc gagggggttc gca 336
 Gly Phe
 70

<210> 418

<211> 71

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

Met Arg Leu Ser Glu Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu
 1 5 10 15

Ala Lys Gly Glu Trp Ile Ala His Ser His Val Ile Gly Ala Leu Gly
 20 25 30

Val Thr Ala Asp Val Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val
 35 40 45

Trp Glu Gln Leu Cys Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu
 50 55 60

Gly Lys Asp Glu Pro Gly Phe
 65 70

<210> 419

<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(313)

<223> FRXA00854

<400> 419

ttcatccgcc ctggaagacg gtcgatgacgg ggacccttct tagggtcgct gtcggagatt 60

ggacacgtaa cttctgtgct tgcgctgtat tatcgcccc atg cgt tta tcg gag 115
 Met Arg Leu Ser Glu
 1 5

ttt cgg caa ctc att gaa gat gaa ttc gga gaa gcc aaa ggg gag tgg 163
 Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu Ala Lys Gly Glu Trp
 10 15 20

att gca cac tcg cat gtg att ggt gcc ctc ggc gtc act gca gat gtt 211
 Ile Ala His Ser His Val Ile Gly Ala Leu Gly Val Thr Ala Asp Val
 25 30 35

gca gta gat acc ggg gtt gat ctg cgc gat gta tgg gaa caa ctg tgc 259
 Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val Trp Glu Gln Leu Cys

40 45 50
 att gat ttc agt gtt ccc gaa gag cga cga ctt ggt aaa gat gaa cca 307
 Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu Gly Lys Asp Glu Pro
 55 60 65

ggg ttc tagcttggtc gaggggggttc gca 336
 Gly Phe
 70

<210> 420
 <211> 71
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 420
 Met Arg Leu Ser Glu Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu
 1 5 10 15
 Ala Lys Gly Glu Trp Ile Ala His Ser His Val Ile Gly Ala Leu Gly
 20 25 30
 Val Thr Ala Asp Val Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val
 35 40 45
 Trp Glu Gln Leu Cys Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu
 50 55 60
 Gly Lys Asp Glu Pro Gly Phe
 65 70

<210> 421
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> RXN00855

<400> 421
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 ttccgttttag tgtacgtcta gacgcctaaa cttacctggt atg act tat ttt gcc 115
 Met Thr Tyr Phe Ala
 1 5
 gtg ctt tac aca tac aac cca gac agc gag aaa gtc gct gaa gtt cgt 163
 Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys Val Ala Glu Val Arg
 10 15 20
 acc gtc cac cgc gag ttc att gcc aac ctt cat gcg gag ggc aaa atc 211
 Thr Val His Arg Glu Phe Ile Ala Asn Leu His Ala Glu Gly Lys Ile
 25 30 35
 gtt ggc tcc ggt cct ttc gtg gac ggc gac ggt ggc gcg ctg att gtc 259
 Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly Gly Ala Leu Ile Val
 40 45 50

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atc aag ttg gaa gaa ggc tcc aac ctt gtt gat gct gaa acc ctg atg 307
Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp Ala Glu Thr Leu Met
    55                      60                      65

aac aat gat cca ttc cac gta gaa aac gtg ctg gac aac cgc gtc atc 355
Asn Asn Asp Pro Phe His Val Glu Asn Val Leu Asp Asn Arg Val Ile
    70                      75                      80                      85

cgt agc tgg aac cct gtg acc aaa gat ttc taggcaactt tttctttaac 405
Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
                90                      95

aat 408

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<210> 422
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 422
Met Thr Tyr Phe Ala Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys
  1                      5                      10                      15

Val Ala Glu Val Arg Thr Val His Arg Glu Phe Ile Ala Asn Leu His
                20                      25                      30

Ala Glu Gly Lys Ile Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly
    35 .                      40                      45

Gly Ala Leu Ile Val Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp
    50                      55                      60

Ala Glu Thr Leu Met Asn Asn Asp Pro Phe His Val Glu Asn Val Leu
    65                      70                      75                      80

Asp Asn Arg Val Ile Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
                85                      90                      95

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<210> 423
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> FRXA00855

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<400> 423
taaaaacctc tcgacggacg aagcgccaca aaagcaagag aagaatataa gtgaacccaaa 60

ttccgttttag tgtacgtcta gacgcctaaa cttacctgtt atg act tat ttt gcc 115
                                Met Thr Tyr Phe Ala
                                1                      5

gtg ctt tac aca tac aac cca gac agc gag aaa gtc gct gaa gtt cgt 163
Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys Val Ala Glu Val Arg
                10                      15                      20

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acc gtc cac cgc gag ttc att gcc aac ctt cat gcg gag ggc aaa atc 211
 Thr Val His Arg Glu Phe Ile Ala Asn Leu His Ala Glu Gly Lys Ile
 25 30 35

gtt ggc tcc ggt cct ttc gtg gac ggc gac ggt ggc gcg ctg att gtc 259
 Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly Gly Ala Leu Ile Val
 40 45 50

atc aag ttg gaa gaa ggc tcc aac ctt gtt gat gct gaa acc ctg atg 307
 Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp Ala Glu Thr Leu Met
 55 60 65

aac aat gat cca ttc cac gta gaa aac gtg ctg gac aac cgc gtc atc 355
 Asn Asn Asp Pro Phe His Val Glu Asn Val Leu Asp Asn Arg Val Ile
 70 75 80 85

cgt agc tgg aac cct gtg acc aaa gat ttc taggcaactt tttctttaac 405
 Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
 90 95

aat 408

<210> 424
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 424
 Met Thr Tyr Phe Ala Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys
 1 5 10 15

Val Ala Glu Val Arg Thr Val His Arg Glu Phe Ile Ala Asn Leu His
 20 25 30

Ala Glu Gly Lys Ile Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly
 35 40 45

Gly Ala Leu Ile Val Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp
 50 55 60

Ala Glu Thr Leu Met Asn Asn Asp Pro Phe His Val Glu Asn Val Leu
 65 70 75 80

Asp Asn Arg Val Ile Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
 85 90 95

<210> 425
 <211> 1044
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1021)
 <223> RXN00869

<400> 425
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accgatgagg tggaagcctc cctcaaccag aaagtctgat	atg act cct ccg att	115
	Met Thr Pro Pro Ile	
	1 5	
atc tcc cca gag agc ttt gaa gcc cta agg cgg atg cgt gcg gct gaa	163	
Ile Ser Pro Glu Ser Phe Glu Ala Leu Arg Arg Met Arg Ala Ala Glu		
10 15 20		
ccc acg atg gtg gcg gaa cgt ttc aag cag cgc cgt aag cgt gaa ctg	211	
Pro Thr Met Val Ala Glu Arg Phe Lys Gln Arg Arg Lys Arg Glu Leu		
25 30 35		
ctc ggt gag gac ggc aag ctg ttt atc gtg gct gcc gac cac cca gcg	259	
Leu Gly Glu Asp Gly Lys Leu Phe Ile Val Ala Ala Asp His Pro Ala		
40 45 50		
cgc ggc gca ctt gct gtt ggc gac aat gaa acc gcc atg gct aac cgc	307	
Arg Gly Ala Leu Ala Val Gly Asp Asn Glu Thr Ala Met Ala Asn Arg		
55 60 65		
tat gaa ctg ctc gaa cgc atg gct atc gca ctg tct cgc ccg ggt gtg	355	
Tyr Glu Leu Leu Glu Arg Met Ala Ile Ala Leu Ser Arg Pro Gly Val		
70 75 80 85		
gat ggt gtg ctg gga act cca gac atc att gat gat ctg gcg gcg ctc	403	
Asp Gly Val Leu Gly Thr Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu		
90 95 100		
gga ctg ctc gat gac aag atc gtg gtt ggc tcc atg aac cgt ggt ggc	451	
Gly Leu Leu Asp Asp Lys Ile Val Val Gly Ser Met Asn Arg Gly Gly		
105 110 115		
ctg cgt ggc gct tcc ttt gaa atg gat gat cgc tac acc ggc tac aac	499	
Leu Arg Gly Ala Ser Phe Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn		
120 125 130		
gtg tcc tcc atg gtt gat cgt ggc gtg gat ttc gcg aaa acc cta gtg	547	
Val Ser Ser Met Val Asp Arg Gly Val Asp Phe Ala Lys Thr Leu Val		
135 140 145		
cgc atc aac ttg agc gac gcc gga acc gcc ccg acc ttg gaa gcc acc	595	
Arg Ile Asn Leu Ser Asp Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr		
150 155 160 165		
gcg cat gca gtc aat gag gct gca gca gca cag ctg ccc atc atg ctc	643	
Ala His Ala Val Asn Glu Ala Ala Ala Ala Gln Leu Pro Ile Met Leu		
170 175 180		
gag ccg ttc atg agt aac tgg gta aac ggc aag gtg gtc aat gat ctt	691	
Glu Pro Phe Met Ser Asn Trp Val Asn Gly Lys Val Val Asn Asp Leu		
185 190 195		
tcc acc gat gca gtt atc caa tct gtc gcc att gct gct ggt ctg ggc	739	
Ser Thr Asp Ala Val Ile Gln Ser Val Ala Ile Ala Ala Gly Leu Gly		
200 205 210		
aat gat tct tcc tat acc tgg atg aag ctt cca gtg gtg gag gag atg	787	
Asn Asp Ser Ser Tyr Thr Trp Met Lys Leu Pro Val Val Glu Glu Met		
215 220 225		

gag cgc gtc atg gaa tcc acc acc atg cca acc ctg ttg ttg ggc ggc 835
 Glu Arg Val Met Glu Ser Thr Thr Met Pro Thr Leu Leu Leu Gly Gly
 230 235 240 245
 gaa ggc ggc aac gat cca gat gcc acc ttc gca tcc tgg gag cat gca 883
 Glu Gly Gly Asn Asp Pro Asp Ala Thr Phe Ala Ser Trp Glu His Ala
 250 255 260
 ctc acc ctg ccg ggt gtg cgt ggc ctg acc gtg gga cgc act ctg ctg 931
 Leu Thr Leu Pro Gly Val Arg Gly Leu Thr Val Gly Arg Thr Leu Leu
 265 270 275
 tat ccg caa gac ggc gat gtc gcc gcc gct gtt gat acc gca gcg cga 979
 Tyr Pro Gln Asp Gly Asp Val Ala Ala Ala Val Asp Thr Ala Ala Arg
 280 285 290
 ctt gtt cac aca gat att caa caa ttc act tcg cag agc att 1021
 Leu Val His Thr Asp Ile Gln Phe Thr Ser Gln Ser Ile
 295 300 305
 taaggaattt acacacatgt ctg 1044

<210> 426
 <211> 307
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 426
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 Met Arg Ala Ala Glu Pro Thr Met Val Ala Glu Arg Phe Lys Gln Arg
 20 25 30
 Arg Lys Arg Glu Leu Leu Gly Glu Asp Gly Lys Leu Phe Ile Val Ala
 35 40 45
 Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val Gly Asp Asn Glu Thr
 50 55 60
 Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg Met Ala Ile Ala Leu
 65 70 75 80
 Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr Pro Asp Ile Ile Asp
 85 90 95
 Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys Ile Val Val Gly Ser
 100 105 110
 Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe Glu Met Asp Asp Arg
 115 120 125
 Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp Arg Gly Val Asp Phe
 130 135 140
 Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp Ala Gly Thr Ala Pro
 145 150 155 160
 Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu Ala Ala Ala Ala Gln
 165 170 175

Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn Trp Val Asn Gly Lys
 180 185 190
 Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile Gln Ser Val Ala Ile
 195 200 205
 Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr Trp Met Lys Leu Pro
 210 215 220
 Val Val Glu Glu Met Glu Arg Val Met Glu Ser Thr Thr Met Pro Thr
 225 230 235 240
 Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro Asp Ala Thr Phe Ala
 245 250 255
 Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val Arg Gly Leu Thr Val
 260 265 270
 Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp Val Ala Ala Ala Val
 275 280 285
 Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile Gln Gln Phe Thr Ser
 290 295 300
 Gln Ser Ile
 305

<210> 427
 <211> 815
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(792)
 <223> FRXA00869

<400> 427
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 Leu Phe Ile Val Ala Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val
 1 5 10 15
 ggc gac aat gaa ccc gcc atg gct aac cgc tat gaa ctg ctc gaa cgc 96
 Gly Asp Asn Glu Pro Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg
 20 25 30
 atg gct atc gca ctg tct cgc ccg ggt gtg gat ggt gtg ctg gga act 144
 Met Ala Ile Ala Leu Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr
 35 40 45
 cca gac atc att gat gat ctg gcg gcg ctc gga ctg ctc gat gac aag 192
 Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys
 50 55 60
 atc gtg gtt ggc tcc atg aac cgt ggt ggc ctg cgt ggc gct tcc ttt 240
 Ile Val Val Gly Ser Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe
 65 70 75 80
 gaa atg gat gat cgc tac acc ggc tac aac gtg tcc tcc atg gtt gat 288

Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp
 85 90 95

 cgt ggc gtg gat ttc gcg aaa acc cta gtg cgc atc aac ttg agc gac 336
 Arg Gly Val Asp Phe Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp
 100 105 110

 gcc gga acc gcc ccg acc ttg gaa gcc acc gcg cat gca gtc aat gag 384
 Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu
 115 120 125

 gct gca gca gca cag ctg ccc atc atg ctc gag ccg ttc atg agt aac 432
 Ala Ala Ala Ala Gln Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn
 130 135 140

 tgg gta aac ggc aag gtg gtc aat gat ctt tcc acc gat gca gtt atc 480
 Trp Val Asn Gly Lys Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile
 145 150 155 160

 caa tct gtc gcc att gct gct ggt ctg ggc aat gat tct tcc tat acc 528
 Gln Ser Val Ala Ile Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr
 165 170 175

 tgg atg aag ctt cca gtg gtg gag gag atg gag cgc gtc atg gaa tcc 576
 Trp Met Lys Leu Pro Val Val Glu Glu Met Glu Arg Val Met Glu Ser
 180 185 190

 acc acc atg cca acc ctg ttg ttg ggc ggc gaa ggc ggc aac gat cca 624
 Thr Thr Met Pro Thr Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro
 195 200 205

 gat gcc acc ttc gca tcc ttg gag cat gca ctc acc ctg ccg ggt gtg 672
 Asp Ala Thr Phe Ala Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val
 210 215 220

 cgt ggc ctg acc gtg gga cgc act ctg ctg tat ccg caa gac ggc gat 720
 Arg Gly Leu Thr Val Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp
 225 230 235 240

 gtc gcc gcc gct gtt gat acc gca gcg cga ctt gtt cac aca gat att 768
 Val Ala Ala Ala Val Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile
 245 250 255

 caa caa ttc act tcg cag agc att taaggaattt acacacatgt ctg 815
 Gln Gln Phe Thr Ser Gln Ser Ile
 260

<210> 428

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

Leu Phe Ile Val Ala Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val
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Gly Asp Asn Glu Pro Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg
 20 25 30

Met Ala Ile Ala Leu Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr

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<400> 429  
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ttcttcagga ccttctctac ctggtgaggg tgagttctaa atg tcc gcc gcc tat 115  
Met Ser Ala Ala Tyr  
1 5
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tcg cag gac acc att ttg acg gtg ttt ctg ggg agg ggt ctg acc gct 163
 Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly Arg Gly Leu Thr Ala
 10 15 20

gaa ggg atc cga cag acc cta gaa gac ttc gca gaa acc ggc cta gtc 211
 Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala Glu Thr Gly Leu Val
 25 30 35

cgc aac ctg gtg tgg att gat gcc gat agt ttc cac gag tct tca tct 259
 Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe His Glu Ser Ser Ser
 40 45 50

gaa gtc acc cac ttg gca acc aac caa gac ggt ctt ccg gag ctt cag 307
 Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly Leu Pro Glu Leu Gln
 55 60 65

cga cga cct ttc aat gag ttg gtg tcc cgg tca cga acc acc aag ctt 355
 Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser Arg Thr Thr Lys Leu
 70 75 80 85

cac atc ggt gtc atc aac gtc att gat ggc agc gaa ggc atg ctt cat 403
 His Ile Gly Val Ile Asn Val Ile Asp Gly Ser Glu Gly Met Leu His
 90 95 100

gca gaa gaa ctc aac cca ttg gtt ggg atc atc gac agt gtc tgt tca 451
 Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile Asp Ser Val Cys Ser
 105 110 115

cac cac caa att cac cga tcc aac gtg atg atc ggt gcg gtg gct gcc 499
 His His Gln Ile His Arg Ser Asn Val Met Ile Gly Ala Val Ala Ala
 120 125 130

aca ctt gat gag gaa ctt cca att ctt cgt ggt tat gtg aac ctg atg 547
 Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly Tyr Val Asn Leu Met
 135 140 145

ctg gca cct gaa gat agc cac agc cca ggc acc gca aca gtg acc tac 595
 Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr Ala Thr Val Thr Tyr
 150 155 160 165

cgt cat ggt ttc agc gat cac cgt tta ccc tgc act gcg tgg cta ata 643
 Arg His Gly Phe Ser Asp His Arg Leu Pro Cys Thr Ala Trp Leu Ile
 170 175 180

tcg cca gct tgt acg gac tgt ggg aag gca gca cat cca cac caa tcg 691
 Ser Pro Ala Cys Thr Asp Cys Gly Lys Ala Ala His Pro His Gln Ser
 185 190 195

aac agc tcg tac ctg cga aag gtt cca gct ttc gtt tgg tgaggtcttt 740
 Asn Ser Ser Tyr Leu Arg Lys Val Pro Ala Phe Val Trp
 200 205 210

ttacaggcga att 753

<210> 430

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

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Met Ser Ala Ala Tyr Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly
 1           5           10           15
Arg Gly Leu Thr Ala Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala
          20           25           30
Glu Thr Gly Leu Val Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe
          35           40           45
His Glu Ser Ser Ser Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly
          50           55           60
Leu Pro Glu Leu Gln Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser
          65           70           75           80
Arg Thr Thr Lys Leu His Ile Gly Val Ile Asn Val Ile Asp Gly Ser
          85           90           95
Glu Gly Met Leu His Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile
          100          105          110
Asp Ser Val Cys Ser His His Gln Ile His Arg Ser Asn Val Met Ile
          115          120          125
Gly Ala Val Ala Ala Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly
          130          135          140
Tyr Val Asn Leu Met Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr
          145          150          155          160
Ala Thr Val Thr Tyr Arg His Gly Phe Ser Asp His Arg Leu Pro Cys
          165          170          175
Thr Ala Trp Leu Ile Ser Pro Ala Cys Thr Asp Cys Gly Lys Ala Ala
          180          185          190
His Pro His Gln Ser Asn Ser Ser Tyr Leu Arg Lys Val Pro Ala Phe
          195          200          205
Val Trp
          210

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<210> 431

<211> 610

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(610)

<223> FRXA00915

<400> 431

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ttcttcagga ccttctctac ctgggtgaggg tgagttctaa atg tcc gcc gcc tat 115
                                     Met Ser Ala Ala Tyr
                                     1           5

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tcg cag gac acc att ttg acg gtg ttt ctg ggg agg ggt ctg acc gct 163
 Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly Arg Gly Leu Thr Ala
 10 15 20

gaa ggg atc cga cag acc cta gaa gac ttc gca gaa acc ggc cta gtc 211
 Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala Glu Thr Gly Leu Val
 25 30 35

cgc aac ctg gtg tgg att gat gcc gat agt ttc cac gag tct tca tct 259
 Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe His Glu Ser Ser Ser
 40 45 50

gaa gtc acc cac ttg gca acc aac caa gac ggt ctt ccg gag ctt cag 307
 Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly Leu Pro Glu Leu Gln
 55 60 65

cga cga cct ttc aat gag ttg gtg tcc cgg tca cga acc acc aag ctt 355
 Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser Arg Thr Thr Lys Leu
 70 75 80 85

cac atc ggt gtc atc aac gtc att gat ggc agc gaa ggc atg ctt cat 403
 His Ile Gly Val Ile Asn Val Ile Asp Gly Ser Glu Gly Met Leu His
 90 95 100

gca gaa gaa ctc aac cca ttg gtt ggg atc atc gac agt gtc tgt tca 451
 Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile Asp Ser Val Cys Ser
 105 110 115

cac cac caa att cac cga tcc aac gtg atg atc ggt gcg gtg gct gcc 499
 His His Gln Ile His Arg Ser Asn Val Met Ile Gly Ala Val Ala Ala
 120 125 130

aca ctt gat gag gaa ctt cca att ctt cgt ggt tat gtg aac ctg atg 547
 Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly Tyr Val Asn Leu Met
 135 140 145

ctg gca cct gaa gat agc cac agc cca ggc acc gca aca gtg acc tac 595
 Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr Ala Thr Val Thr Tyr
 150 155 160 165

cgt cat ggt ttc agc 610
 Arg His Gly Phe Ser
 170

<210> 432

<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Ser Ala Ala Tyr Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly
 1 5 10 15

Arg Gly Leu Thr Ala Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala
 20 25 30

Glu Thr Gly Leu Val Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe
 35 40 45

His Glu Ser Ser Ser Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly

50	55	60
Leu Pro Glu Leu Gln Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser		
65	70	75 80
Arg Thr Thr Lys Leu His Ile Gly Val Ile Asn Val Ile Asp Gly Ser		
	85	90 95
Glu Gly Met Leu His Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile		
	100	105 110
Asp Ser Val Cys Ser His His Gln Ile His Arg Ser Asn Val Met Ile		
	115	120 125
Gly Ala Val Ala Ala Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly		
	130	135 140
Tyr Val Asn Leu Met Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr		
	145	150 155 160
Ala Thr Val Thr Tyr Arg His Gly Phe Ser		
	165	170

<210> 433
 <211> 2802
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2779)
 <223> RXN00917

<400> 433
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 ggtcggcctt ggatattgcc ctgtgggtag gaaagcagtc atg gtg aac acg ttg 115
 Met Val Asn Thr Leu
 1 5
 aac tct aaa acc gtg aat gta ccc cgt ttt gcc aga ggc gtt gtt gct 163
 Asn Ser Lys Thr Val Asn Val Pro Arg Phe Ala Arg Gly Val Val Ala
 10 15 20
 gca gcc aca gcg cta ttt ttt ggc gct ttg gta agc ctc gcg cct agt 211
 Ala Ala Thr Ala Leu Phe Phe Gly Ala Leu Val Ser Leu Ala Pro Ser
 25 30 35
 gcg ttg gcg cag gaa cca cct gca gtt gag gcc gga gcg tca ggt tct 259
 Ala Leu Ala Gln Glu Pro Pro Ala Val Glu Ala Gly Ala Ser Gly Ser
 40 45 50
 ttg agc aac ctg ggt gcc tgc atc gct gat aaa ggc act ctt gat gtc 307
 Leu Ser Asn Leu Gly Ala Cys Ile Ala Asp Lys Gly Thr Leu Asp Val
 55 60 65
 atc atc atg atc gat gag aca gaa tcc ttg atc cat gaa gct cgt gac 355
 Ile Ile Met Ile Asp Glu Thr Glu Ser Leu Ile His Glu Ala Arg Asp
 70 75 80 85

ggc gtg gtc aac gcc aat gaa cca ggc gcg gac gca cag cac cac cgt Gly Val Val Asn Ala Asn Glu Pro Gly Ala Asp Ala Gln His His Arg 90 95 100	403
gtt cct gca gca cag agc ttt gtg gat gag ctt cta gcc aag caa agc Val Pro Ala Ala Gln Ser Phe Val Asp Glu Leu Leu Ala Lys Gln Ser 105 110 115	451
gat ggt gat ctg aac acc cgc atc cgt gtt gct ggt ttc ggc cag acg Asp Gly Asp Leu Asn Thr Arg Ile Arg Val Ala Gly Phe Gly Gln Thr 120 125 130	499
tac aaa tct ggt gcc act gat cca gac aat tac gga gca tgg acg caa Tyr Lys Ser Gly Ala Thr Asp Pro Asp Asn Tyr Gly Ala Trp Thr Gln 135 140 145	547
cta gat gcc tcc acc gtt ggc gga gta caa gat gaa atc tcc cgc ttc Leu Asp Ala Ser Thr Val Gly Gly Val Gln Asp Glu Ile Ser Arg Phe 150 155 160 165	595
gct gac cgc acc cag gag cag tac acc aac tac gcc tcc gcg att gag Ala Asp Arg Thr Gln Glu Gln Tyr Thr Asn Tyr Ala Ser Ala Ile Glu 170 175 180	643
ggc gct tac cag gac ttc act agg tcc ggc tct gag gac gcc tgc cgc Gly Ala Tyr Gln Asp Phe Thr Arg Ser Gly Ser Glu Asp Ala Cys Arg 185 190 195	691
atg ctg gtg acc ttc acc gac ggc gca ctg acc gct caa gaa ggc gcc Met Leu Val Thr Phe Thr Asp Gly Ala Leu Thr Ala Gln Glu Gly Ala 200 205 210	739
gat gtt gca gaa gca gca ctg tgc gcg ccg ggt ggc gtc acc gat cga Asp Val Ala Glu Ala Ala Leu Cys Ala Pro Gly Gly Val Thr Asp Arg 215 220 225	787
ctg cgc agt gct ggc atc acc cac atc ggc atc ggt tta tcg gca cct Leu Arg Ser Ala Gly Ile Thr His Ile Gly Ile Gly Leu Ser Ala Pro 230 235 240 245	835
acc aac cca tct gat ttc agc ctg ctg cgc gga acc acc gca ggt ggc Thr Asn Pro Ser Asp Phe Ser Leu Leu Arg Gly Thr Thr Ala Gly Gly 250 255 260	883
gga aca tgt ggt gtc gaa cca gct aac ggt gca ttc ttc cca gca gat Gly Thr Cys Gly Val Glu Pro Ala Asn Gly Ala Phe Phe Pro Ala Asp 265 270 275	931
aac gtg ggc gga ctt ttc gca gca ttc cgt gaa gcc ctt gcg att ggt Asn Val Gly Gly Leu Phe Ala Ala Phe Arg Glu Ala Leu Ala Ile Gly 280 285 290	979
ggt gaa aca att ggt gaa acc cga gct ggt gat cct ttc agc ttc acc Gly Glu Thr Ile Gly Glu Thr Arg Ala Gly Asp Pro Phe Ser Phe Thr 295 300 305	1027
ctg gac aac tcg gtg aac tct gtg cgt ttc acc gcg atc gcc aag gat Leu Asp Asn Ser Val Asn Ser Val Arg Phe Thr Ala Ile Ala Lys Asp 310 315 320 325	1075
gat ctc ggc ccg aac gcc cac ttg gtg ctc acc gca ccc aac ggc gaa	1123

Asp Leu Gly Pro Asn Ala His Leu Val	Leu Thr Ala Pro Asn Gly Glu	
330	335	340
acg gtt gag ctc aaa gat tct gga agc agc gtc gcc aac agc act gac		1171
Thr Val Glu Leu Lys Asp Ser Gly Ser Ser Val Ala Asn Ser Thr Asp		
345	350	355
gtg agt tgg gaa gcc gaa agc agc cca gta aaa atg gct gat ggt tcc		1219
Val Ser Trp Glu Ala Glu Ser Ser Pro Val Lys Met Ala Asp Gly Ser		
360	365	370
ctc aac ctg cag caa ggt ggg gat tgg aag ggt gtc tgg cag att cag		1267
Leu Asn Leu Gln Gln Gly Gly Asp Trp Lys Gly Val Trp Gln Ile Gln		
375	380	385
ttc caa gga att gat cct gca gcg gtt gat gga cgc gta ttc aac tca		1315
Phe Gln Gly Ile Asp Pro Ala Ala Val Asp Gly Arg Val Phe Asn Ser		
390	395	400
gtg gag atc cag cct gac ctc cag ctt gtg ttc agt ggc ggt gat tcg		1363
Val Glu Ile Gln Pro Asp Leu Gln Leu Val Phe Ser Gly Gly Asp Ser		
410	415	420
acg tca ggt gca ctt aac ctt cgc gat gat cag cag ctg aat atg cag		1411
Thr Ser Gly Ala Leu Asn Leu Arg Asp Asp Gln Gln Leu Asn Met Gln		
425	430	435
ctg gtg ggc cgt gat ggt cag cca cgc atc ctt gag ggg tcc gcg ctg		1459
Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu Glu Gly Ser Ala Leu		
440	445	450
gtc gat ctt ggt ttc acc cgc gca gat acc ggc gag ttc gcc cct ttg		1507
Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly Glu Phe Ala Pro Leu		
455	460	465
gct caa gga att gat att tct ggc ggc gaa tta agc ttc ccg ctg gat		1555
Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu Ser Phe Pro Leu Asp		
470	475	480
acg att tcg cag ctc cca gcc atc ggc acg gtg gaa gcg cgt acc acg		1603
Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val Glu Ala Arg Thr Thr		
490	495	500
atc acc acc gca ggc gtc gat gat ctc ccc ggc acc acg ttg agc cca		1651
Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly Thr Thr Leu Ser Pro		
505	510	515
att ctc aac acc acg cgc atc acc atc act cag cgc gat atg cct cag		1699
Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln Arg Asp Met Pro Gln		
520	525	530
ctg cca gcg tcg gtt cgc ttc aca gcg gat gag gac gtt gtt acc gta		1747
Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu Asp Val Val Thr Val		
535	540	545
gac atc ccc atc acc ggc ccc ggc aag gta tgg att gca ccg gga acc		1795
Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp Ile Ala Pro Gly Thr		
550	555	560
cag ctc agc gga gtg ctt cca gac ggc gtg gac ggc att gca gca tca		1843
Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp Gly Ile Ala Ala Ser		

570	575	580	
agt act ttc gac agc cca gat aat gct ttg gtg ctc gga ctg gat gag Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val Leu Gly Leu Asp Glu 585 590 595			1891
cag ggc acg att cct gtt gaa cta acc gtg agc gat ctt cgt gac gga Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser Asp Leu Arg Asp Gly 600 605 610			1939
ctg gtc aac ggc tcg att cca ctc cag atc tcc aac gct gag ggc gcc Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser Asn Ala Glu Gly Ala 615 620 625			1987
aat gaa acc agc gtg gat ctg ccg aca gaa ggc acg ttg agc gtt ccc Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly Thr Leu Ser Val Pro 630 635 640 645			2035
att aac gcc tcc act ttc gca ttg gca ttc att ttg gcc ctt gtg ctt Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile Leu Ala Leu Val Leu 650 655 660			2083
tcc ctc ctg att ccg ctg ctc att ttg tat att gtg cgt ttc ctc tcc Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile Val Arg Phe Leu Ser 665 670 675			2131
gca aag gtt ccg tcc tct gcg atg agt ggc gtg cgc att cca gtg gaa Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val Arg Ile Pro Val Glu 680 685 690			2179
ttc tcc ggt gaa gct ctg cgc tat gcg ggc agc act atg cct gat ctc Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser Thr Met Pro Asp Leu 695 700 705			2227
gca tcg caa acc acc gcc acc aag cag gtc gtt gtt cat gga gac acc Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val Val His Gly Asp Thr 710 715 720 725			2275
ttc aat gtg gaa ggc cac aaa ctt aaa gtc cag cgc ttc cag ctg aac Phe Asn Val Glu Gly His Lys Leu Lys Val Gln Arg Phe Gln Leu Asn 730 735 740			2323
ccg att gcg tct cct gca gtg atc gtg cag acc gac ccg tcg atc agc Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr Asp Pro Ser Ile Ser 745 750 755			2371
ttc gac ggc aaa caa aag ggc aca caa gct aaa ctc ccg ctg gcg gtc Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys Leu Pro Leu Ala Val 760 765 770			2419
caa ggc agt tgg ttc ctc act gca agc ggc gct gac cct tcc aag atg Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala Asp Pro Ser Lys Met 775 780 785			2467
gaa ctc atc gcc ctg aca aac ctg ccg ctc gag cag ggc caa atc gac Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu Gln Gly Gln Ile Asp 790 795 800 805			2515
cgc atg atc gca ggt atc acc agc aaa gcc cct gat agg gca cgc gaa Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro Asp Arg Ala Arg Glu 810 815 820			2563

cta caa aaa ttg ctt gac gac gcc gcg acc tcc cag ccc gca aag gtt 2611
Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser Gln Pro Ala Lys Val
825 830 835

cca ccg cgc gcc cca gcc gcg cag ggc cac gtc gaa aag caa gct cct 2659
Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val Glu Lys Gln Ala Pro
840 845 850

agt ttt ggc act ggt tcc ggt ggt ggt ttc ggc tcc agc aat ggt gga 2707
Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly Ser Ser Asn Gly Gly
855 860 865

ggc ttt ggc tcc ggt agc gga tcc aac gac aca aat ggt gga ttt ggt 2755
Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr Asn Gly Gly Phe Gly
870 875 880 885

tcc agc ggc ggc ttc ggc gcg cga taacctgtaa cttgcgatta aaa 2802
Ser Ser Gly Gly Phe Gly Ala Arg
890

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<212> PRT
<213> Corynebacterium glutamicum

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Arg Gly Val Val Ala Ala Ala Thr Ala Leu Phe Phe Gly Ala Leu Val
20 25 30

Ser Leu Ala Pro Ser Ala Leu Ala Gln Glu Pro Pro Ala Val Glu Ala
35 40 45

Gly Ala Ser Gly Ser Leu Ser Asn Leu Gly Ala Cys Ile Ala Asp Lys
50 55 60

Gly Thr Leu Asp Val Ile Ile Met Ile Asp Glu Thr Glu Ser Leu Ile
65 70 75 80

His Glu Ala Arg Asp Gly Val Val Asn Ala Asn Glu Pro Gly Ala Asp
85 90 95

Ala Gln His His Arg Val Pro Ala Ala Gln Ser Phe Val Asp Glu Leu
100 105 110

Leu Ala Lys Gln Ser Asp Gly Asp Leu Asn Thr Arg Ile Arg Val Ala
115 120 125

Gly Phe Gly Gln Thr Tyr Lys Ser Gly Ala Thr Asp Pro Asp Asn Tyr
130 135 140

Gly Ala Trp Thr Gln Leu Asp Ala Ser Thr Val Gly Gly Val Gln Asp
145 150 155 160

Glu Ile Ser Arg Phe Ala Asp Arg Thr Gln Glu Gln Tyr Thr Asn Tyr
165 170 175

Ala Ser Ala Ile Glu Gly Ala Tyr Gln Asp Phe Thr Arg Ser Gly Ser
180 185 190

Glu Asp Ala Cys Arg Met Leu Val Thr Phe Thr Asp Gly Ala Leu Thr
195 200 205

Ala Gln Glu Gly Ala Asp Val Ala Glu Ala Ala Leu Cys Ala Pro Gly
210 215 220

Gly Val Thr Asp Arg Leu Arg Ser Ala Gly Ile Thr His Ile Gly Ile
225 230 235 240

Gly Leu Ser Ala Pro Thr Asn Pro Ser Asp Phe Ser Leu Leu Arg Gly
245 250 255

Thr Thr Ala Gly Gly Gly Thr Cys Gly Val Glu Pro Ala Asn Gly Ala
260 265 270

Phe Phe Pro Ala Asp Asn Val Gly Gly Leu Phe Ala Ala Phe Arg Glu
275 280 285

Ala Leu Ala Ile Gly Gly Glu Thr Ile Gly Glu Thr Arg Ala Gly Asp
290 295 300

Pro Phe Ser Phe Thr Leu Asp Asn Ser Val Asn Ser Val Arg Phe Thr
305 310 315 320

Ala Ile Ala Lys Asp Asp Leu Gly Pro Asn Ala His Leu Val Leu Thr
325 330 335

Ala Pro Asn Gly Glu Thr Val Glu Leu Lys Asp Ser Gly Ser Ser Val
340 345 350

Ala Asn Ser Thr Asp Val Ser Trp Glu Ala Glu Ser Ser Pro Val Lys
355 360 365

Met Ala Asp Gly Ser Leu Asn Leu Gln Gln Gly Gly Asp Trp Lys Gly
370 375 380

Val Trp Gln Ile Gln Phe Gln Gly Ile Asp Pro Ala Ala Val Asp Gly
385 390 395 400

Arg Val Phe Asn Ser Val Glu Ile Gln Pro Asp Leu Gln Leu Val Phe
405 410 415

Ser Gly Gly Asp Ser Thr Ser Gly Ala Leu Asn Leu Arg Asp Asp Gln
420 425 430

Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
435 440 445

Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
450 455 460

Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
465 470 475 480

Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
485 490 495

Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly

500							505							510						
Thr	Thr	Leu	Ser	Pro	Ile	Leu	Asn	Thr	Thr	Arg	Ile	Thr	Ile	Thr	Gln					
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Arg	Asp	Met	Pro	Gln	Leu	Pro	Ala	Ser	Val	Arg	Phe	Thr	Ala	Asp	Glu					
	530					535					540									
Asp	Val	Val	Thr	Val	Asp	Ile	Pro	Ile	Thr	Gly	Pro	Gly	Lys	Val	Trp					
545					550					555					560					
Ile	Ala	Pro	Gly	Thr	Gln	Leu	Ser	Gly	Val	Leu	Pro	Asp	Gly	Val	Asp					
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Gly	Ile	Ala	Ala	Ser	Ser	Thr	Phe	Asp	Ser	Pro	Asp	Asn	Ala	Leu	Val					
			580					585					590							
Leu	Gly	Leu	Asp	Glu	Gln	Gly	Thr	Ile	Pro	Val	Glu	Leu	Thr	Val	Ser					
		595					600					605								
Asp	Leu	Arg	Asp	Gly	Leu	Val	Asn	Gly	Ser	Ile	Pro	Leu	Gln	Ile	Ser					
	610					615					620									
Asn	Ala	Glu	Gly	Ala	Asn	Glu	Thr	Ser	Val	Asp	Leu	Pro	Thr	Glu	Gly					
625					630					635					640					
Thr	Leu	Ser	Val	Pro	Ile	Asn	Ala	Ser	Thr	Phe	Ala	Leu	Ala	Phe	Ile					
				645					650					655						
Leu	Ala	Leu	Val	Leu	Ser	Leu	Leu	Ile	Pro	Leu	Leu	Ile	Leu	Tyr	Ile					
			660					665					670							
Val	Arg	Phe	Leu	Ser	Ala	Lys	Val	Pro	Ser	Ser	Ala	Met	Ser	Gly	Val					
		675					680					685								
Arg	Ile	Pro	Val	Glu	Phe	Ser	Gly	Glu	Ala	Leu	Arg	Tyr	Ala	Gly	Ser					
	690					695					700									
Thr	Met	Pro	Asp	Leu	Ala	Ser	Gln	Thr	Thr	Ala	Thr	Lys	Gln	Val	Val					
705					710					715					720					
Val	His	Gly	Asp	Thr	Phe	Asn	Val	Glu	Gly	His	Lys	Leu	Lys	Val	Gln					
				725					730					735						
Arg	Phe	Gln	Leu	Asn	Pro	Ile	Ala	Ser	Pro	Ala	Val	Ile	Val	Gln	Thr					
			740					745					750							
Asp	Pro	Ser	Ile	Ser	Phe	Asp	Gly	Lys	Gln	Lys	Gly	Thr	Gln	Ala	Lys					
		755					760					765								
Leu	Pro	Leu	Ala	Val	Gln	Gly	Ser	Trp	Phe	Leu	Thr	Ala	Ser	Gly	Ala					
	770					775					780									
Asp	Pro	Ser	Lys	Met	Glu	Leu	Ile	Ala	Leu	Thr	Asn	Leu	Pro	Leu	Glu					
785					790					795					800					
Gln	Gly	Gln	Ile	Asp	Arg	Met	Ile	Ala	Gly	Ile	Thr	Ser	Lys	Ala	Pro					
				805					810					815						
Asp	Arg	Ala	Arg	Glu	Leu	Gln	Lys	Leu	Leu	Asp	Asp	Ala	Ala	Thr	Ser					
			820					825					830							

Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
 835 840 845

Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
 850 855 860

Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
 865 870 875 880

Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
 885 890

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1383)
 <223> FRXA00917

<400> 435

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1				5				10						15		
gag	ggg	tcc	gcg	ctg	gtc	gat	ctt	ggt	ttc	acc	cgc	gca	gat	acc	ggc	96
Glu	Gly	Ser	Ala	Leu	Val	Asp	Leu	Gly	Phe	Thr	Arg	Ala	Asp	Thr	Gly	
			20					25					30			
gag	ttc	gcc	cct	ttg	gct	caa	gga	att	gat	att	tct	ggc	ggc	gaa	tta	144
Glu	Phe	Ala	Pro	Leu	Ala	Gln	Gly	Ile	Asp	Ile	Ser	Gly	Gly	Glu	Leu	
		35				40						45				
agc	ttc	ccg	ctg	gat	acg	att	tcg	cag	ctc	cca	gcc	atc	ggc	acg	gtg	192
Ser	Phe	Pro	Leu	Asp	Thr	Ile	Ser	Gln	Leu	Pro	Ala	Ile	Gly	Thr	Val	
		50				55				60						
gaa	gcg	cgt	acc	acg	atc	acc	acc	gca	ggc	gtc	gat	gat	ctc	ccc	ggc	240
Glu	Ala	Arg	Thr	Thr	Ile	Thr	Thr	Ala	Gly	Val	Asp	Asp	Leu	Pro	Gly	
65					70				75					80		
acc	acg	ttg	agc	cca	att	ctc	aac	acc	acg	cgc	atc	acc	atc	act	cag	288
Thr	Thr	Leu	Ser	Pro	Ile	Leu	Asn	Thr	Thr	Arg	Ile	Thr	Ile	Thr	Gln	
				85				90						95		
cgc	gat	atg	cct	cag	ctg	cca	gcg	tcg	gtt	cgc	ttc	aca	gcg	gat	gag	336
Arg	Asp	Met	Pro	Gln	Leu	Pro	Ala	Ser	Val	Arg	Phe	Thr	Ala	Asp	Glu	
			100					105					110			
gac	gtt	gtt	acc	gta	gac	atc	ccc	atc	acc	ggc	ccc	ggc	aag	gta	tgg	384
Asp	Val	Val	Thr	Val	Asp	Ile	Pro	Ile	Thr	Gly	Pro	Gly	Lys	Val	Trp	
		115				120						125				
att	gca	ccg	gga	acc	cag	ctc	agc	gga	gtg	ctt	cca	gac	ggc	gtg	gac	432
Ile	Ala	Pro	Gly	Thr	Gln	Leu	Ser	Gly	Val	Leu	Pro	Asp	Gly	Val	Asp	
		130				135					140					

ggc att gca gca tca agt act ttc gac agc cca gat aat gct ttg gtg Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val 145 150 155 160	480
ctc gga ctg gat gag cag ggc acg att cct gtt gaa cta acc gtg agc Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser 165 170 175	528
gat ctt cgt gac gga ctg gtc aac ggc tcg att cca ctc cag atc tcc Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser 180 185 190	576
aac gct gag ggc gcc aat gaa acc agc gtg gat ctg ccg aca gaa ggc Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly 195 200 205	624
acg ttg agc gtt ccc att aac gcc tcc act ttc gca ttg gca ttc att Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile 210 215 220	672
ttg gcc ctt gtg ctt tcc ctc ctg att ccg ctg ctc att ttg tat att Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile 225 230 235 240	720
gtg cgt ttc ctc tcc gca aag gtt ccg tcc tct gcg atg agt ggc gtg Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val 245 250 255	768
cgc att cca gtg gaa ttc tcc ggt gaa gct ctg cgc tat gcg ggc agc Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser 260 265 270	816
act atg cct gat ctc gca tcg caa acc acc gcc acc aag cag gtc gtt Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val 275 280 285	864
gtt cat gga gac acc ttc aat gtg gaa ggc cac aaa ctt aaa gtc cag Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln 290 295 300	912
cgc ttc cag ctg aac ccg att gcg tct cct gca gtg atc gtg cag acc Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr 305 310 315 320	960
gac ccg tcg atc agc ttc gac ggc aaa caa aag ggc aca caa gct aaa Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys 325 330 335	1008
ctc ccg ctg gcg gtc caa ggc agt tgg ttc ctc act gca agc ggc gct Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala 340 345 350	1056
gac cct tcc aag atg gaa ctc atc gcc ctg aca aac ctg ccg ctc gag Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu 355 360 365	1104
cag ggc caa atc gac cgc atg atc gca ggt atc acc agc aaa gcc cct Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro 370 375 380	1152
gat agg gca cgc gaa cta caa aaa ttg ctt gac gac gcc gcg acc tcc	1200

Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
 385 390 395 400
 cag ccc gca aag gtt cca ccg cgc gcc cca gcc gcg cag ggc cac gtc 1248
 Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
 405 410 415
 gaa aag caa gct cct agt ttt ggc act ggt tcc ggt ggt ggt ttc ggc 1296
 Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
 420 425 430
 tcc agc aat ggt gga ggc ttt ggc tcc ggt agc gga tcc aac gac aca 1344
 Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Ser Asn Asp Thr
 435 440 445
 aat ggt gga ttt ggt tcc agc ggc ggc ttc ggc gcg cga taacctgtaa 1393
 Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
 50 55 60
 Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
 65 70 75 80
 Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
 85 90 95
 Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
 100 105 110
 Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
 115 120 125
 Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
 130 135 140
 Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
 145 150 155 160
 Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
 165 170 175

Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
 180 185 190
 Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
 195 200 205
 Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
 210 215 220
 Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
 225 230 235 240
 Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
 245 250 255
 Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
 260 265 270
 Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
 275 280 285
 Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
 290 295 300
 Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
 305 310 315 320
 Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
 325 330 335
 Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
 340 345 350
 Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
 355 360 365
 Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
 370 375 380
 Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
 385 390 395 400
 Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
 405 410 415
 Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
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 Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
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<210> 437

<211> 536

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(513)

<223> RXN00921

<400> 437

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cgg tct ttg cca gac atc gaa gac tgg acg aga agc gat gaa gct cag 96
Arg Ser Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln
             20             25             30

cag atc ttt gca gga atc att gcg ggt gcg tct gtt caa act ggt aga 144
Gln Ile Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg
             35             40             45

agc cac ttc atg tgg gat ctt ttg cgg gcg tat ttt gga gtc gct ttg 192
Ser His Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu
             50             55             60

atc ggc gac gaa gat acc tac agg gct ttt act act ctc acg gtc gat 240
Ile Gly Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp
             65             70             75             80

tct gtt ctt agt ttc gtg cag tta act ctt caa gag ggc aga acg gaa 288
Ser Val Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu
             85             90             95

gac att aga cga ttc gag aaa tat ggt gag cag att gcc cga gag gat 336
Asp Ile Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp
             100             105             110

ttg ccg tcg att ctc acc aat gct cga gca gta cag caa tat ctc ggc 384
Leu Pro Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly
             115             120             125

tat atc gac caa gat atc atc aat aag aaa gtg tcc cgg tct agg gat 432
Tyr Ile Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp
             130             135             140

gtt aac cag att ttt act gag atg gcg cgc gct atc atc aga gca att 480
Val Asn Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile
             145             150             155             160

agc cgg aat aat att gga aag gac atg cgg tca tgaacgtgat tcgactggat 533
Ser Arg Asn Asn Ile Gly Lys Asp Met Arg Ser
             165             170

tcc 536

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<210> 438

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

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<212> DNA
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<222> (101)..(1999)  
<223> FRXA00921
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t	c	a	c	t	a	c	g	c	t	t	t	a	g	a	a	c	t	115
tcacctacgc gtcctttaga ggaactgcag gtaggggtgg																		
												Val	Glu	Gly	Gly	Thr		
												1				5		
t	g	g	t	c	t	g	c	t	a	a	a	a	a	a	a	a	a	163
tgg tct gct cag gcc act aaa gaa gac ctc caa ttt atc gcg gag gtt																		
Trp	Ser	Ala	Gln	Ala	Thr	Lys	Glu	Asp	Leu	Gln	Phe	Ile	Ala	Glu	Val			
				10					15					20				
g	c	g	c	c	c	a	c	t	a	t	t	a	a	c	a	t	a	211
gcg ccc act cat att gaa acg gtg acc cct ttt gat gat ttc atc tca																		
Ala	Pro	Thr	His	Ile	Glu	Thr	Val	Thr	Pro	Phe	Asp	Asp	Phe	Ile	Ser			
				25					30					35				
t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	259
tca gaa gat atc gat gcg ttg ccg agg agg ttt gag tac cgt cct ttg																		
Ser	Glu	Asp	Ile	Asp	Ala	Leu	Pro	Arg	Arg	Phe	Glu	Tyr	Arg	Pro	Leu			
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Pro	Asp	Leu	Leu	Thr	Pro	Phe	Arg	Ala	Ala	Ala	Val	Asn	Ala	Ala	Glu		
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Leu	Pro	Leu	Asp	Ala	Gly	Glu	Pro	Arg	Ile	Gly	Pro	Ile	Thr	Asp	Leu		
		120					125					130					
tcc	ttg	tcg	tgg	atg	atg	atc	gac	agc	atg	ttt	ggc	gat	cgc	aga	cag	547	
Ser	Leu	Ser	Trp	Met	Met	Ile	Asp	Ser	Met	Phe	Gly	Asp	Arg	Arg	Gln		
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cag	ttc	tac	cag	ctt	caa	gat	gct	ctc	caa	gct	gga	gat	aaa	gct	act	595	
Gln	Phe	Tyr	Gln	Leu	Gln	Asp	Ala	Leu	Gln	Ala	Gly	Asp	Lys	Ala	Thr		
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Glu	Ala	Arg	Ser	Leu	Phe	Val	Val	Pro	Gly	Ile	Asp	Arg	Glu	Leu	Leu		
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Gln	Pro	Phe	Gly	Pro	Gln	Gly	Ser	Trp	Ser	Arg	Met	Thr	Glu</				

295	300	305	
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 35 40 45
 Glu Tyr Arg Pro Leu Ala Gly Arg Ser Leu Ile Met Gln Ser Val Pro
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 Ala Gly Lys Asp Ala Thr Gly Arg Pro Gly Asn Val Phe Thr His Ala
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 Val Phe Asp Gly Asp Leu Glu Ser Pro Leu Glu Ser Val Tyr Pro Ile
 85 90 95
 Ser Leu Tyr Arg Ser Pro Asp Leu Leu Thr Pro Phe Arg Ala Ala Ala
 100 105 110
 Val Asn Ala Ala Glu Leu Pro Leu Asp Ala Gly Glu Pro Arg Ile Gly
 115 120 125
 Pro Ile Thr Asp Leu Ser Leu Ser Trp Met Met Ile Asp Ser Met Phe
 130 135 140
 Gly Asp Arg Arg Gln Gln Phe Tyr Gln Leu Gln Asp Ala Leu Gln Ala
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Gly Asp Lys Ala Thr Val Leu Val Leu Asn Ser Thr Asn Glu Ala Ala
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Tyr Trp Leu Gln Ala Leu Ser Ser Thr Leu Thr Pro Asn Glu Ala Arg
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Arg Leu Leu His Phe Ser Thr Phe Glu Arg Ala Ala Thr Leu Pro Ala
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Pro Asp Lys Ser Met Glu Ala Arg Ser Leu Phe Val Val Pro Gly Ile
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Asp Arg Glu Leu Leu Ala Glu His Ser Gly Ile Val Ile Ile Asp Pro
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Glu Ile Pro Gln Ser Gln Pro Phe Gly Pro Gln Gly Ser Trp Ser Arg
245 250 255

Met Thr Glu Gly Leu Phe Ser Asp Gly Phe Asp Ala Asp Glu Leu Val
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275 280 285

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Phe Ser Gly Thr His Pro Leu Arg Val Leu Ala Asp Gln His Met Phe
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Gly Lys Val Pro Asp Lys Pro Ala Pro Lys Val Glu Pro Val Ala Pro
325 330 335

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Tyr Leu Asp Phe Leu Leu Lys Thr Glu Leu Ala Thr Ser Ile Asn Ala
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Ser Asp Pro Phe Phe Arg Ser Ser Phe Ser Asp Phe Pro Ala Met Asp
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Asn Trp Arg His Ile Lys Phe Thr Glu Asp Ala His Pro Arg Leu Arg
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Glu Leu Leu Val Asp Ala Glu Arg Asp Ala Arg Asn Arg Ala Pro Ala
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Asn Asn Ile Gly Lys Asp Met Arg Ser
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gat cca gaa ttg gtc acc cgc gtc att ggc ggc acc aaa gtc ggt gcg 307

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Val	Thr	Glu	Tyr	Ala	Tyr	Thr	Ala	Gln	Asp	Phe	Val	Gly	Glu	Asn	Lys	195	
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Ser	Gly	Asp	Trp	Leu	Glu	Ala	Ala	Gln	Ala	Asn	Ala	Lys	Thr	Ala	Arg	245	
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Lys	Ser	Ala	Val	Lys	Ala	Ala	Gly	Lys	Ala	Gln	Glu	Lys	Ala	Asn	Phe	260	
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Ala	Leu	Gln	Val	Ala	Glu	Glu	Thr	Ser	Gly	Arg	Ala	Asn	Lys	Lys	Ala	275	
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1035

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Gln Val Val Leu Asp Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala
35 40 45

Lys Arg Ile Ser Arg Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly
50 55 60

Thr Lys Val Gly Ala Gly Ser Leu Leu Ala Ile Gly Arg Ala Pro Arg
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Thr Ser Ala Ala Thr Leu Ala Ile Leu Thr Ile Pro Asn Ile Leu Ala
85 90 95

Arg Asn Ala Phe Trp Glu Thr Gln Asp Ala Asp Glu Lys Arg Asn Arg
100 105 110

Arg Asn Gly Phe Leu Thr Asn Ile Ala Leu Leu Gly Gly Leu Phe Ile
115 120 125

Thr Ser Val Asp Thr Glu Gly Lys Pro Gly Val Lys Trp Arg Ala Thr
130 135 140

Asn Ala Thr Lys Arg Gly Lys Lys Gln Leu Gln Gln Ala Leu Pro Thr
145 150 155 160

Lys Ser Glu Thr Glu Lys Phe Gly Glu Lys Ala Ser Asp Trp Phe Asn
165 170 175

Asp Thr Ser Asp Lys Val Thr Glu Tyr Ala Tyr Thr Ala Gln Asp Phe
180 185 190

Val Gly Glu Asn Lys Asp Asp Trp Ile Lys Ser Ala Thr Glu Thr Ala
195 200 205

His Lys Val Ala Asp Thr Val Ser Asp Tyr Ala His Lys Ala Thr Ser
210 215 220

Tyr Leu Glu Glu Asn Ser Gly Asp Trp Leu Glu Ala Ala Gln Ala Asn
225 230 235 240

Ala Lys Thr Ala Arg Lys Ser Ala Val Lys Ala Ala Gly Lys Ala Gln
245 250 255

Glu Lys Ala Asn Phe Ala Leu Gln Val Ala Glu Glu Thr Ser Gly Arg
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Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys Val Thr	
35 40 45	
gag tac gcg tac acc gct cag gat ttt gtc ggt gag aac aag gat gac	192
Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys Asp Asp	
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tgg atc aag tcc gca acc gag act gct cac aag gtc gct gat act gtg	240
Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp Thr Val	
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agc gat tac gct cac aag gct acc tct tac ctt gag gag aac agc ggt	288
Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn Ser Gly	
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Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg Lys Ser	
100 105 110	
gca gtg aag gct gcc ggc aag gct cac gaa aag gct aac ttt gct ctt	384
Ala Val Lys Ala Ala Gly Lys Ala His Glu Lys Ala Asn Phe Ala Leu	
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cag gtc gca gag gaa acc tct ggt cgc gcc aac aag aag gca act aag	432
Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala Thr Lys	
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Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp Arg Ala	
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gag

530

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Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys Asp Asp
      50      55      60
Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp Thr Val
  65      70      75      80
Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn Ser Gly
      85      90      95
Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg Lys Ser
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Ala Val Lys Ala Ala Gly Lys Ala His Glu Lys Ala Asn Phe Ala Leu
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Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala Thr Lys
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Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val	
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Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg	
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Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly	
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Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala	
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Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala	
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Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met	
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Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe	
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Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val	
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Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile	
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gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc	739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala	
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Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile	
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Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe	
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Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile
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 Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu
 295 300 305

gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc 1072
 Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala
 310 315 320

taaaagtcct cagtagctag cca 1095

<210> 448
 <211> 324
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 448
 Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
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Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
 20 25 30

Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
 35 40 45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
 50 55 60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
 65 70 75 80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
 85 90 95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
 100 105 110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
 115 120 125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
 130 135 140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
 145 150 155 160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
 165 170 175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
 180 185 190
 Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
 195 200 205
 Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
 210 215 220
 Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
 225 230 235 240
 Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
 245 250 255
 Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
 260 265 270
 Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
 275 280 285
 Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
 290 295 300
 Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
 305 310 315 320
 Lys Ala Asn Ala

<210> 449
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXN00946

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 cgaaagcgta cattcgcagc aactaacgga aagcacactc atg act cac act ctg 115
 Met Thr His Thr Leu
 1 5
 cag gca act aat ccc ctt gat caa acc gct tgg cac gct tgg cat ttc 163
 Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp His Ala Trp His Phe
 10 15 20
 tcc cga aac aaa gag gcc atc agc cgc acc ggc gcc acc agc ctg agt 211
 Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly Ala Thr Ser Leu Ser
 25 30 35
 gcc aca gag tgg att agc gcc acc aca ctc aag gac gcg cac act ttt 259
 Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys Asp Ala His Thr Phe
 40 45 50
 cct tca ctt ccc ggg cga tgg tat aaa cga ggc ggc ggg gta gtg gga 307

Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly Gly Gly Val Val Gly
55 60 65

gca cat tta cca cca gct ttc gca aca act gga acg gtg caa ctg cgc 355
Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly Thr Val Gln Leu Arg
70 75 80 85

ccc ggt gag ctc ttg ata gcg gaa gat ttc acc ctc acc gtc att gaa 403
Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr Leu Thr Val Ile Glu
90 95 100

cgg ctt gga cag ttt gca ctt cag gtt ttt gat gca cgc aat ccg aag 451
Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp Ala Arg Asn Pro Lys
105 110 115

cgt ttt gaa ttc cac tcc atc gca gct ttc cca ccg tcc gag gaa tgg 499
Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro Pro Ser Glu Glu Trp
120 125 130

cgg att gag gct cgc ttc ttc ccg gaa cct gac act gtt aac acc gct 547
Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp Thr Val Asn Thr Ala
135 140 145

gca gct gat gga gtt atc gtt gcc acg cct act gcg ggt tgg gtg cac 595
Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr Ala Gly Trp Val His
150 155 160 165

ttt ttg aag ggc cgt ctg gat tac cgt ctt cgt gta acc gtt cag aaa 643
Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg Val Thr Val Gln Lys
170 175 180

aat aat cta cgg gca cta ttt agc gac aat tcc tcg acg ttg ggc gtt 691
Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser Ser Thr Leu Gly Val
185 190 195

tat cag cat cgt ttt gtc gac atc cca cgc cct gat gcc gag gga aac 739
Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro Asp Ala Glu Gly Asn
200 205 210

acc atc att gat ttc aac cgc gct tat ctt ccc cca aag gca ttg aac 787
Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro Pro Lys Ala Leu Asn
215 220 225

cga aag ttc ctg tgc cca tcg ccc agc ctg aac aac cac ctc aat ctc 835
Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn Asn His Leu Asn Leu
230 235 240 245

acc gtg gag gca ggg gag aag tgg gtg gtt gct gga gga taataacttgc 884
Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala Gly Gly
250 255

taaccgtcct aaa 897

<210> 450

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Thr His Thr Leu Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp

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His Ala Trp	His Phe Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly		
	20	25	30
Ala Thr Ser	Leu Ser Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys		
	35	40	45
Asp Ala His	Thr Phe Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly		
	50	55	60
Gly Gly Val	Val Gly Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly		
	65	70	75
Thr Val Gln	Leu Arg Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr		
	85	90	95
Leu Thr Val	Ile Glu Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp		
	100	105	110
Ala Arg Asn	Pro Lys Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro		
	115	120	125
Pro Ser Glu	Glu Trp Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp		
	130	135	140
Thr Val Asn	Thr Ala Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr		
	145	150	155
Ala Gly Trp	Val His Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg		
	165	170	175
Val Thr Val	Gln Lys Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser		
	180	185	190
Ser Thr Leu	Gly Val Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro		
	195	200	205
Asp Ala Glu	Gly Asn Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro		
	210	215	220
Pro Lys Ala	Leu Asn Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn		
	225	230	235
Asn His Leu	Asn Leu Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala		
	245	250	255

Gly Gly

<210> 451

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> FRXA00946

<400> 451

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cgaaagcgta cattcgcagc aactaacgga aagcacactc atg act cac act ctg 115
                                   Met Thr His Thr Leu
                                   1 5

cag gca act aat ccc ctt gat caa acc gct tgg cac gct tgg cat ttc 163
Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp His Ala Trp His Phe
              10              15              20

tcc cga aac aaa gag gcc atc agc cgc acc ggc gcc acc agc ctg agt 211
Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly Ala Thr Ser Leu Ser
              25              30              35

gcc aca gag tgg att agc gcc acc aca ctc aag gac gcg cac act ttt 259
Ala Thr Glu Trp Ile Ser Ala Thr Leu Lys Asp Ala His Thr Phe
              40              45              50

cct tca ctt ccc ggg cga tgg tat aaa cga ggc ggc ggc gta gtg gga 307
Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly Gly Gly Val Val Gly
              55              60              65

gca cat tta cca cca gct ttc gca aca act gga acg gtg caa ctg cgc 355
Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly Thr Val Gln Leu Arg
              70              75              80              85

ccc ggt gag ctc ttg ata gcg gaa gat ttc acc ctc acc gtc att gaa 403
Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr Leu Thr Val Ile Glu
              90              95              100

cgg ctt gga cag ttt gca ctt cag gtt ttt gat gca cgc aat ccg aag 451
Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp Ala Arg Asn Pro Lys
              105              110              115

cgt ttt gaa ttc cac tcc atc gca gct ttc cca ccg tcc gag gaa tgg 499
Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro Pro Ser Glu Glu Trp
              120              125              130

cgg att gag gct cgc ttc ttc ccg gaa cct gac act gtt aac acc gct 547
Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp Thr Val Asn Thr Ala
              135              140              145

gca gct gat gga gtt atc gtt gcc acg cct act gcg ggt tgg gtg cac 595
Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr Ala Gly Trp Val His
              150              155              160              165

ttt ttg aag ggc cgt ctg gat tac cgt ctt cgt gta acc gtt cag aaa 643
Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg Val Thr Val Gln Lys
              170              175              180

aat aat cta cgg gca cta ttt agc gac aat tcc tcg acg ttg ggc gtt 691
Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser Ser Thr Leu Gly Val
              185              190              195

tat cag cat cgt ttt gtc gac atc cca cgc cct gat gcc gag gga aac 739
Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro Asp Ala Glu Gly Asn
              200              205              210

acc atc att gat ttc aac cgc gct tat ctt ccc cca aag gca ttg aac 787
Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro Pro Lys Ala Leu Asn

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215	220	225	
cga aag ttc ctg tgc cca tcg ccc agc ctg aac aac cac ctc aat ctc			835
Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn Asn His Leu Asn Leu			
230	235	240	245
acc gtg gag gca ggg gag aag tgg gtg gtt gct gga gga taataacttgc			884
Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala Gly Gly			
	250	255	
taaccgtcct aaa			897

<210> 452
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 452
 Met Thr His Thr Leu Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp
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His Ala Trp His Phe Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly
 20 25 30

Ala Thr Ser Leu Ser Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys
 35 40 45

Asp Ala His Thr Phe Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly
 50 55 60

Gly Gly Val Val Gly Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly
 65 70 75 80

Thr Val Gln Leu Arg Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr
 85 90 95

Leu Thr Val Ile Glu Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp
 100 105 110

Ala Arg Asn Pro Lys Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro
 115 120 125

Pro Ser Glu Glu Trp Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp
 130 135 140

Thr Val Asn Thr Ala Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr
 145 150 155 160

Ala Gly Trp Val His Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg
 165 170 175

Val Thr Val Gln Lys Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser
 180 185 190

Ser Thr Leu Gly Val Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro
 195 200 205

Asp Ala Glu Gly Asn Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro
 210 215 220

Pro Lys Ala Leu Asn Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn
 225 230 235 240

Asn His Leu Asn Leu Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala
 245 250 255

Gly Gly

<210> 453

<211> 789

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (14)..(766)

<223> RXN00953

<400> 453

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 Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser

1

5

10

ttc act caa ggt ctg cag ttc ggc gtt gca gtt gcc gtg att ctc ttt 100
 Phe Thr Gln Gly Leu Gln Phe Gly Val Ala Val Ile Leu Phe
 15 20 25

ggc gtc cgc acc att ctt ggt gaa ctg gtc ccc gca ttc caa ggt att 148
 Gly Val Arg Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile
 30 35 40 45

gct gcg aag gtt gtt ccc gga gct atc ccc gca ttg gat gca ccg atc 196
 Ala Ala Lys Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile
 50 55 60

gtg ttc ccc tac gcg cag aac gcc gtt ctc att ggt ttc ttg tct tcc 244
 Val Phe Pro Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser
 65 70 75

ttc gtc ggt ggc ttg gtt ggc ctg act gtt ctt gca tcg tgg ctg aac 292
 Phe Val Gly Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn
 80 85 90

cca gct ttt ggt gtc gcg ttg att ctg cct ggt ttg gtc ccc cac ttc 340
 Pro Ala Phe Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe
 95 100 105

ttc act ggt ggc gcg gcg ggc gtt tac ggt aat gcc acg ggt ggt cgt 388
 Phe Thr Gly Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg
 110 115 120 125

cga gga gca gta ttt ggc gcc ttt gcc aac ggt ctt ctg att acc ttc 436
 Arg Gly Ala Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe
 130 135 140

ctc cct gct ttc ctg ctt ggt gtg ctt ggt tcc ttc ggg tca gag aac 484
 Leu Pro Ala Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn
 145 150 155

acc act ttc ggt gat gcg gac ttt ggt tgg ttc gga atc gtt gtt ggt 532
 Thr Thr Phe Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly
 160 165 170

tct gca gcc aag gtg gaa ggt gct ggc ggg ctc atc ttg ttg ctc atc 580
 Ser Ala Ala Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile
 175 180 185

atc gca gcg gtt ctt ctg ggt ggc gcg atg gtc ttc cag aag cgc gtc 628
 Ile Ala Ala Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val
 190 195 200 205

gtg aat ggg cac tgg gat cca gct ccc aac cgt gag cgc gtg gag aag 676
 Val Asn Gly His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys
 210 215 220

gcg gaa gct gat gcc act cca acg gct ggg gct cgg acc tac cct aag 724
 Ala Glu Ala Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys
 225 230 235

att gct cct ccg gcg ggc gct cct acc cca ccg gct cga agc 766
 Ile Ala Pro Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
 240 245 250

taagatctcc aaaaccctga gat 789

<210> 454
 <211> 251
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 454
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 20 25 30

Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile Ala Ala Lys
 35 40 45

Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile Val Phe Pro
 50 55 60

Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser Phe Val Gly
 65 70 75 80

Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn Pro Ala Phe
 85 90 95

Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe Phe Thr Gly
 100 105 110

Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg Arg Gly Ala
 115 120 125

Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe Leu Pro Ala
 130 135 140

Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn Thr Thr Phe

145	150	155	160
Gly Asp Ala Asp	Phe Gly Trp Phe Gly	Ile Val Val Gly Ser	Ala Ala
	165	170	175
Lys Val Glu Gly	Ala Gly Gly Leu	Ile Leu Leu Leu	Ile Ala Ala
	180	185	190
Val Leu Leu Gly	Gly Ala Met Val	Phe Gln Lys Arg	Val Val Asn Gly
	195	200	205
His Trp Asp Pro	Ala Pro Asn Arg	Glu Arg Val Glu	Lys Ala Glu Ala
	210	215	220
Asp Ala Thr Pro	Thr Ala Gly Ala	Arg Thr Tyr Pro	Lys Ile Ala Pro
	225	230	235
Pro Ala Gly Ala	Pro Thr Pro Pro	Ala Arg Ser	
	245	250	

<210> 455
 <211> 579
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> RXN00959

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 aattactcgc tggaatattg gtggggatag agttgttgtt atg acg gtg atc gga 115
 Met Thr Val Ile Gly
 1 5
 att att ctt ggc agc ctt ttt ggc gtt ctt gca gtc ctt ctc atc gtg 163
 Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala Val Leu Leu Ile Val
 10 15 20
 gtt ggt gct ttg ggg tgg gcg gct aag ctc cct ggc aac ccg gtt gtg 211
 Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro Gly Asn Pro Val Val
 25 30 35
 ggc att cgt gtc cct gag gtg cgt aaa tcc caa gaa ttg tgg gat atg 259
 Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln Glu Leu Trp Asp Met
 40 45 50
 gcg cac cgt gtc gct ggc ccg ttg tgg gtg ctg tcg gga gtt tcc ttt 307
 Ala His Arg Val Ala Gly Pro Leu Trp Val Leu Ser Gly Val Ser Phe
 55 60 65
 gtt att gca tcg cta gtt gcg ttt gtt gct tct ggt tgg atg tgg ctt 355
 Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser Gly Trp Met Trp Leu
 70 75 80 85
 gtt gtg gcg ttg ggt gtt gag gct gcc atc gcg ttc att ggt atg ggt 403
 Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala Phe Ile Gly Met Gly
 90 95 100

gcg ggt atg gct gca cat act gtt gcg atg gtt gac gcg aag cgc att 451
 Ala Gly Met Ala Ala His Thr Val Ala Met Val Asp Ala Lys Arg Ile
 105 110 115

cgc gaa acc ccg cag gcg cct gtt tcc gct gaa att gaa gag gcc ggt 499
 Arg Glu Thr Pro Gln Ala Pro Val Ser Ala Glu Ile Glu Glu Ala Gly
 120 125 130

ggt gtg act att acc tct gcc gat tat caa caa gac tcc gct gaa tgc 547
 Gly Val Thr Ile Thr Ser Ala Asp Tyr Gln Gln Asp Ser Ala Glu Cys
 135 140 145

ccc caa gat tgacttggat gcagtgcgta gag 579
 Pro Gln Asp
 150

<210> 456

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 456

Met Thr Val Ile Gly Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala
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Val Leu Leu Ile Val Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro
 20 25 30

Gly Asn Pro Val Val Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln
 35 40 45

Glu Leu Trp Asp Met Ala His Arg Val Ala Gly Pro Leu Trp Val Leu
 50 55 60

Ser Gly Val Ser Phe Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser
 65 70 75 80

Gly Trp Met Trp Leu Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala
 85 90 95

Phe Ile Gly Met Gly Ala Gly Met Ala Ala His Thr Val Ala Met Val
 100 105 110

Asp Ala Lys Arg Ile Arg Glu Thr Pro Gln Ala Pro Val Ser Ala Glu
 115 120 125

Ile Glu Glu Ala Gly Gly Val Thr Ile Thr Ser Ala Asp Tyr Gln Gln
 130 135 140

Asp Ser Ala Glu Cys Pro Gln Asp
 145 150

<210> 457

<211> 427

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(427)

<223> FRXA00959

<400> 457

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aattactcgc tggaatattg gtggggatag agttgttggt atg acg gtg atc gga 115
                                         Met Thr Val Ile Gly
                                         1 5
att att ctt ggc agc ctt ttt ggc gtt ctt gca gtc ctt ctc atc gtg 163
Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala Val Leu Leu Ile Val
                        10                        15                        20
gtt ggt gct ttg ggg tgg gcg gct aag ctc cct ggc aac ccg gtt gtg 211
Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro Gly Asn Pro Val Val
                        25                        30                        35
ggc att cgt gtc cct gag gtg cgt aaa tcc caa gaa ttg tgg gat atg 259
Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln Glu Leu Trp Asp Met
                        40                        45                        50
gcg cac cgt gtc gct ggc ccg ttg tgg gtg ctg tcg gga gtt tcc ttt 307
Ala His Arg Val Ala Gly Pro Leu Trp Val Leu Ser Gly Val Ser Phe
                        55                        60                        65
gtt att gca tcg cta gtt gcg ttt gtt gct tct ggt tgg atg tgg ctt 355
Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser Gly Trp Met Trp Leu
                        70                        75                        80                        85
gtt gtg gcg ttg ggt gtt gag gct gcc atc gcg ttc att ggt atg ggt 403
Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala Phe Ile Gly Met Gly
                        90                        95                        100
gcg ggt atg gct gcg cat act ggt 427
Ala Gly Met Ala Ala His Thr Gly
                        105

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<210> 458

<211> 109

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

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  20 25 30
Gly Asn Pro Val Val Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln
  35 40 45
Glu Leu Trp Asp Met Ala His Arg Val Ala Gly Pro Leu Trp Val Leu
  50 55 60
Ser Gly Val Ser Phe Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser
  65 70 75 80

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<400> 459															60
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acctcgcacg tacttttact ccggaaggaa tctagaactt															115
Met Arg Leu Ala Thr															5
1															
atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac															163
Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn															20
10 15															
acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag															211
Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Leu Gln															35
25 30															
gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg															259
Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val															50
40 45															
acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag															307
Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys															65
55 60															
att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc															355
Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly															85
70 75 80															
cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg															403
Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala															100
90 95															
ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag															451
Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys															115
105 110															
gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca															499
Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala															130
120 125															
cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct ggc tac gca															547
Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala Gly Tyr Ala															145
135 140 145															
qtg atg aac gat tac acc acc cgc gat ttc cag tac gca gca cct gca															595

Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln Tyr Ala Ala Pro Ala
 150 155 160 165
 aag act cca cag tgg cac cag ggc aag tct ttg gaa aag tcc gct ggc 643
 Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu Glu Lys Ser Ala Gly
 170 175 180
 ttc ggg cct tgg atg act acc cca gat tct ttt gag ttc ggc ggc gag 691
 Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe Glu Phe Gly Gly Glu
 185 190 195
 ctg gca acc tac ctc gag ggc gag aag gta cag tcc acc cct acc aat 739
 Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln Ser Thr Pro Thr Asn
 200 205 210
 gac ctg gtc ttt agc cca gaa aag ctc atc gaa tac atc acc cac atc 787
 Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu Tyr Ile Thr His Ile
 215 220 225
 tac cca ttg gat gct ggc gac gtc att gtc acc ggt acc cca ggc ggc 835
 Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr Gly Thr Pro Gly Gly
 230 235 240 245
 gtt ggc cac gca cgt aac cca cag cgc tac atc ggt gac ggc gaa acc 883
 Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile Gly Asp Gly Glu Thr
 250 255 260
 gta aag gtt gag att gcg ggc ctc ggc ttc att gaa aac aag acg gtg 931
 Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile Glu Asn Lys Thr Val
 265 270 275
 ttt gaa taaatgacaa ctttccacga tct 960
 Phe Glu

<210> 460

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
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 Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
 20 25 30
 Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
 35 40 45
 Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
 50 55 60
 Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
 65 70 75 80
 Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
 85 90 95
 Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro

100	105	110
Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile 115 120 125		
Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr 130 135 140		
Ile Ala Gly Tyr Ala Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln 145 150 155 160		
Tyr Ala Ala Pro Ala Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu 165 170 175		
Glu Lys Ser Ala Gly Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe 180 185 190		
Glu Phe Gly Gly Glu Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln 195 200 205		
Ser Thr Pro Thr Asn Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu 210 215 220		
Tyr Ile Thr His Ile Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr 225 230 235 240		
Gly Thr Pro Gly Gly Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile 245 250 255		
Gly Asp Gly Glu Thr Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile 260 265 270		
Glu Asn Lys Thr Val Phe Glu 275		

<210> 461
 <211> 538
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(538)
 <223> FRXA00963

<400> 461
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acctcgcacg tacttttact ccggaaggaa tctagaactt atg cgt ctt gca aca 115
 Met Arg Leu Ala Thr
 1 5

atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac 163
 Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn
 10 15 20

acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag 211
 Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Leu Gln
 25 30 35

gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg 259
 Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val
 40 45 50
 acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag 307
 Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys
 55 60 65
 att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc 355
 Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly
 70 75 80 85
 cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg 403
 Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala
 90 95 100
 ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag 451
 Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys
 105 110 115
 gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca 499
 Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala
 120 125 130
 cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct 538
 Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala
 135 140 145

<210> 462

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
 1 5 10 15
 Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
 20 25 30
 Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
 35 40 45
 Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
 50 55 60
 Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
 65 70 75 80
 Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
 85 90 95
 Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro
 100 105 110
 Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
 115 120 125
 Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
 130 135 140

Ile Ala
145

<210> 463
<211> 341
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(318)
<223> RXN00971

<400> 463
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Lys Ala Leu Ser Ile Gly Thr Gln Trp Ala Gln Val Met Gly Ile Asn
1 5 10 15

cac gcc gaa gcc gaa gaa ctc gac gaa gcc ctc tcc ccg ctc att aac 96
His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile Asn
20 25 30

cgc ctc cgc gaa atg ggc ttt gac ccc acc gaa acc gaa gaa gca aac 144
Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala Asn
35 40 45

tcc ctc gct cta cac agc tgc cca ttt gtg gtc aac gac aaa cgc cca 192
Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg Pro
50 55 60

tca gcc ttc gtc tgc gcc atc cac gcc gga ttc atc caa gaa agc ctc 240
Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser Leu
65 70 75 80

ggc gaa aac aac cgc atc cag ctg gaa ctc aaa cca ctc aac gcg ccg 288
Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala Pro
85 90 95

ggc acc tgt aag gtt cac gtg ttc agc gaa taattgctgc actaataagg 338
Gly Thr Cys Lys Val His Val Phe Ser Glu
100 105

ccc 341

<210> 464
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 464
Lys Ala Leu Ser Ile Gly Thr Gln Trp Ala Gln Val Met Gly Ile Asn
1 5 10 15

His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile Asn
20 25 30

Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala Asn
35 40 45

Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg Pro
 50 55 60

Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser Leu
 65 70 75 80

Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala Pro
 85 90 95

Gly Thr Cys Lys Val His Val Phe Ser Glu
 100 105

<210> 465
 <211> 296
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(273)
 <223> FRXA00971

<400> 465
 aac cac gcc gaa gcc gaa gaa ctc gac gaa gcc ctc tcc ccg ctc att 48
 Asn His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile
 1 5 10 15

aac cgc ctc cgc gaa atg ggc ttt gac ccc acc gaa acc gaa gaa gca 96
 Asn Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala
 20 25 30

aac tcc ctc gct cta cac agc tgc cca ttt gtg gtc aac gac aaa cgc 144
 Asn Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg
 35 40 45

cca tca gcc ttc gtc tgc gcc atc cac gcc gga ttc atc caa gaa agc 192
 Pro Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser
 50 55 60

ctc ggt gaa aac aac cgc atc cag ctg gaa ctc aaa cca ctc aac gcg 240
 Leu Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala
 65 70 75 80

ccg ggc acc tgt aag gtt cac gtg ttc agc gaa taattgctgc actaataagg 293
 Pro Gly Thr Cys Lys Val His Val Phe Ser Glu
 85 90

ccc 296

<210> 466
 <211> 91
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 466
 Asn His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile
 1 5 10 15

Asn Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala
 20 25 30
 Asn Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg
 35 40 45
 Pro Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser
 50 55 60
 Leu Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala
 65 70 75 80
 Pro Gly Thr Cys Lys Val His Val Phe Ser Glu
 85 90

<210> 467
 <211> 1503
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1480)
 <223> RXN00991

<400> 467
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 gctttcaccg cttctaaggg caacagctta aaccacgcta atg gac ata ctc ata 115
 Met Asp Ile Leu Ile
 1 5
 agc atc ctc tca ctg cta ggc ttc gtg ctt ctt acc gcg agc acc gga 163
 Ser Ile Leu Ser Leu Leu Gly Phe Val Leu Leu Thr Ala Ser Thr Gly
 10 15 20
 cta ttc gtg gcc att gag ttc gca ctc acc ggc tta gaa aaa tcc act 211
 Leu Phe Val Ala Ile Glu Phe Ala Leu Thr Gly Leu Glu Lys Ser Thr
 25 30 35
 gta gaa aca cat gtg aag caa aaa ggc gac agc agc gcc cgc gca gtg 259
 Val Glu Thr His Val Lys Gln Lys Gly Asp Ser Ser Ala Arg Ala Val
 40 45 50
 cag agg gat cat caa aat ctg tct ttc gtg ctc tct ggt gcc cag ctg 307
 Gln Arg Asp His Gln Asn Leu Ser Phe Val Leu Ser Gly Ala Gln Leu
 55 60 65
 ggc atc acg atc acg aca ctt gcc aca ggc ttc ctc gca gag ccg gtt 355
 Gly Ile Thr Ile Thr Thr Leu Ala Thr Gly Phe Leu Ala Glu Pro Val
 70 75 80 85
 ttg gcc aaa ttc ttc acc cca gca ctt gag ctg gtg gga tta aat gaa 403
 Leu Ala Lys Phe Phe Thr Pro Ala Leu Glu Leu Val Gly Leu Asn Glu
 90 95 100
 tca gca agc tcc gca gta gcc ctc atc atc gca ctg ttg gtg gca act 451
 Ser Ala Ser Ser Ala Val Ala Leu Ile Ile Ala Leu Leu Val Ala Thr
 105 110 115

acc ctc tcc atg gtt ttt ggt gag ttg gtt ccc aaa aac tgg gcg atc	499
Thr Leu Ser Met Val Phe Gly Glu Leu Val Pro Lys Asn Trp Ala Ile	
120 125 130	
acc aac ccg ttg ggc gtg gca cgt ttt gtt gtc cac cct gtc aat tgg	547
Thr Asn Pro Leu Gly Val Ala Arg Phe Val Val His Pro Val Asn Trp	
135 140 145	
ttc aac atg gtt ctc aag ccg ttt att aac ggc atg aac aag tct gca	595
Phe Asn Met Val Leu Lys Pro Phe Ile Asn Gly Met Asn Lys Ser Ala	
150 155 160 165	
aac ttt att gtc cgc aaa ctt ggt att gaa cca gcc gaa gag ctt gcc	643
Asn Phe Ile Val Arg Lys Leu Gly Ile Glu Pro Ala Glu Glu Leu Ala	
170 175 180	
tct gcc cgt tcc tcc caa gag ctc acc gcc ttg gta cgc agc tcc gcg	691
Ser Ala Arg Ser Ser Gln Glu Leu Thr Ala Leu Val Arg Ser Ser Ala	
185 190 195	
gaa agc ggc gga ctg gat caa aac acc gca gcg gtg atc aac cga tcc	739
Glu Ser Gly Gly Leu Asp Gln Asn Thr Ala Ala Val Ile Asn Arg Ser	
200 205 210	
ctg cag ttc ggt gac gcc acc gct gat gaa ttc atg aca cct cgc tcc	787
Leu Gln Phe Gly Asp Ala Thr Ala Asp Glu Phe Met Thr Pro Arg Ser	
215 220 225	
acc att gaa tca ttg cgt gcc aca gac acc gtc aat gat ttg atc gag	835
Thr Ile Glu Ser Leu Arg Ala Thr Asp Thr Val Asn Asp Leu Ile Glu	
230 235 240 245	
ctt gcc ctg gaa acg ggt cac tcc cgc ttc cca gtc acc gaa ggc gac	883
Leu Ala Leu Glu Thr Gly His Ser Arg Phe Pro Val Thr Glu Gly Asp	
250 255 260	
ttg gat gaa acc atc ggc atg gtc cac atc aag gac gca ttc tct gta	931
Leu Asp Glu Thr Ile Gly Met Val His Ile Lys Asp Ala Phe Ser Val	
265 270 275	
gtg cag gca gaa cgc gcc acc acc atg gtg cgc gat cta gcc cgc aaa	979
Val Gln Ala Glu Arg Ala Thr Thr Met Val Arg Asp Leu Ala Arg Lys	
280 285 290	
att cct gtg gta cca gcc agc ctt gac ggc gac tct gtc ctc aac gct	1027
Ile Pro Val Val Pro Ala Ser Leu Asp Gly Asp Ser Val Leu Asn Ala	
295 300 305	
gtc cgc tcc gcc ggc tcc caa gtt att ttg gtt gcc gat gaa tac ggc	1075
Val Arg Ser Ala Gly Ser Gln Val Ile Leu Val Ala Asp Glu Tyr Gly	
310 315 320 325	
gga acc gca ggc atg gtc acc atc gaa gac gtc gtg gag gaa atc ctc	1123
Gly Thr Ala Gly Met Val Thr Ile Glu Asp Val Val Glu Glu Ile Leu	
330 335 340	
ggc gaa atc cac gat gag cac gac gac tcc gac gcc gaa cgc gat ttc	1171
Gly Glu Ile His Asp Glu His Asp Asp Ser Asp Ala Glu Arg Asp Phe	
345 350 355	
caa caa ttc ggc gcc agc tgg gaa gtc tcc ggc ctg gtc cgc atc gat	1219

Gln Gln Phe Gly Ala Ser Trp Glu Val Ser Gly Leu Val Arg Ile Asp
 360 365 370

gaa ctc gaa aaa cgc gtc ggg tac gtc tcc cct gac ggc ccc tac gaa 1267
 Glu Leu Glu Lys Arg Val Gly Tyr Val Ser Pro Asp Gly Pro Tyr Glu
 375 380 385

acc ctc ggc ggc ttg atc atg tac aca gtc ggc gcc att cct cgc gtc 1315
 Thr Leu Gly Gly Leu Ile Met Tyr Thr Val Gly Ala Ile Pro Arg Val
 390 395 400 405

ggc gat gtc gcc cta ctc cca ctg acc gat acc cca acc atg gat gaa 1363
 Gly Asp Val Ala Leu Leu Pro Leu Thr Asp Thr Pro Thr Met Asp Glu
 410 415 420

ttc gaa tcc ggc ttc tcc gga cgc tgg atc gca cga gta acg gtc atg 1411
 Phe Glu Ser Gly Phe Ser Gly Arg Trp Ile Ala Arg Val Thr Val Met
 425 430 435

gaa gat cga cgc atc gac aaa gcc gtt ctc acc ccc atc acc cat gaa 1459
 Glu Asp Arg Arg Ile Asp Lys Ala Val Leu Thr Pro Ile Thr His Glu
 440 445 450

gaa gca aag gag tac gaa aag tgagtatttg ggcaactgtc ctt 1503
 Glu Ala Lys Glu Tyr Glu Lys
 455 460

<210> 468

<211> 460

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

Met Asp Ile Leu Ile Ser Ile Leu Ser Leu Leu Gly Phe Val Leu Leu
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Thr Ala Ser Thr Gly Leu Phe Val Ala Ile Glu Phe Ala Leu Thr Gly
 20 25 30

Leu Glu Lys Ser Thr Val Glu Thr His Val Lys Gln Lys Gly Asp Ser
 35 40 45

Ser Ala Arg Ala Val Gln Arg Asp His Gln Asn Leu Ser Phe Val Leu
 50 55 60

Ser Gly Ala Gln Leu Gly Ile Thr Ile Thr Thr Leu Ala Thr Gly Phe
 65 70 75 80

Leu Ala Glu Pro Val Leu Ala Lys Phe Phe Thr Pro Ala Leu Glu Leu
 85 90 95

Val Gly Leu Asn Glu Ser Ala Ser Ser Ala Val Ala Leu Ile Ile Ala
 100 105 110

Leu Leu Val Ala Thr Thr Leu Ser Met Val Phe Gly Glu Leu Val Pro
 115 120 125

Lys Asn Trp Ala Ile Thr Asn Pro Leu Gly Val Ala Arg Phe Val Val
 130 135 140

His Pro Val Asn Trp Phe Asn Met Val Leu Lys Pro Phe Ile Asn Gly
 145 150 155 160
 Met Asn Lys Ser Ala Asn Phe Ile Val Arg Lys Leu Gly Ile Glu Pro
 165 170 175
 Ala Glu Glu Leu Ala Ser Ala Arg Ser Ser Gln Glu Leu Thr Ala Leu
 180 185 190
 Val Arg Ser Ser Ala Glu Ser Gly Gly Leu Asp Gln Asn Thr Ala Ala
 195 200 205
 Val Ile Asn Arg Ser Leu Gln Phe Gly Asp Ala Thr Ala Asp Glu Phe
 210 215 220
 Met Thr Pro Arg Ser Thr Ile Glu Ser Leu Arg Ala Thr Asp Thr Val
 225 230 235 240
 Asn Asp Leu Ile Glu Leu Ala Leu Glu Thr Gly His Ser Arg Phe Pro
 245 250 255
 Val Thr Glu Gly Asp Leu Asp Glu Thr Ile Gly Met Val His Ile Lys
 260 265 270
 Asp Ala Phe Ser Val Val Gln Ala Glu Arg Ala Thr Thr Met Val Arg
 275 280 285
 Asp Leu Ala Arg Lys Ile Pro Val Val Pro Ala Ser Leu Asp Gly Asp
 290 295 300
 Ser Val Leu Asn Ala Val Arg Ser Ala Gly Ser Gln Val Ile Leu Val
 305 310 315 320
 Ala Asp Glu Tyr Gly Gly Thr Ala Gly Met Val Thr Ile Glu Asp Val
 325 330 335
 Val Glu Glu Ile Leu Gly Glu Ile His Asp Glu His Asp Asp Ser Asp
 340 345 350
 Ala Glu Arg Asp Phe Gln Gln Phe Gly Ala Ser Trp Glu Val Ser Gly
 355 360 365
 Leu Val Arg Ile Asp Glu Leu Glu Lys Arg Val Gly Tyr Val Ser Pro
 370 375 380
 Asp Gly Pro Tyr Glu Thr Leu Gly Gly Leu Ile Met Tyr Thr Val Gly
 385 390 395 400
 Ala Ile Pro Arg Val Gly Asp Val Ala Leu Leu Pro Leu Thr Asp Thr
 405 410 415
 Pro Thr Met Asp Glu Phe Glu Ser Gly Phe Ser Gly Arg Trp Ile Ala
 420 425 430
 Arg Val Thr Val Met Glu Asp Arg Arg Ile Asp Lys Ala Val Leu Thr
 435 440 445
 Pro Ile Thr His Glu Glu Ala Lys Glu Tyr Glu Lys
 450 455 460

<210> 469
 <211> 1185
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1162)
 <223> RXN01004

<400> 469
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 tcacccccat cacccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca 115
 Val Ser Ile Trp Ala
 1 5
 act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
 Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
 10 15 20
 gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc 211
 Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
 25 30 35
 ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
 Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
 40 45 50
 gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
 Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
 55 60 65
 tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc 355
 Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
 70 75 80 85
 att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac 403
 Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
 90 95 100
 cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att 451
 Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
 105 110 115
 ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa 499
 Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
 120 125 130
 acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att 547
 Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
 135 140 145
 acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt 595
 Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
 150 155 160 165
 cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac 643
 Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
 170 175 180

cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc 691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
185 190 195

ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag 739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu
200 205 210

cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg 787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr
215 220 225

ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca 835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala
230 235 240 245

gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga 883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly
250 255 260

tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct 931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala
265 270 275

gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc 979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg
280 285 290

cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat 1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp
295 300 305

ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt 1075
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly
310 315 320 325

gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg 1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val
330 335 340

ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt 1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp
345 350

aactgtgttg gac 1185

<210> 470
<211> 354
<212> PRT
<213> Corynebacterium glutamicum

<400> 470
Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala
1 5 10 15
Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg
20 25 30
Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
35 40 45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
50 55 60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
65 70 75 80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
85 90 95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
100 105 110

Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
115 120 125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
130 135 140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
145 150 155 160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
165 170 175

Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
180 185 190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
195 200 205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
210 215 220

Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
225 230 235 240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
245 250 255

Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
260 265 270

Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
275 280 285

Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
290 295 300

Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
305 310 315 320

Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
325 330 335

Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
340 345 350

Asp Asp

aca gct acg gtg ctc cta gct gcg ggt att ctc att att caa gag cta 643
Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu Ile Ile Gln Glu Leu
170 175 180

ctt tct gct tta tgg ttg cgc cac tac aca cag ggg cca ctt ggg tat 691
 Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln Gly Pro Leu Gly Tyr
 185 190 195

cta tgg cgt tgg gtg act tgg gga agc cgt tcc ccc ttc ctt acc cgt 739
 Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser Pro Phe Leu Thr Arg
 200 205 210

tcc gca tca tgacaggtac ggaagtgtcc tac 771
 Ser Ala Ser
 215

<210> 472
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 472
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Trp Leu Pro Arg Trp Ala Val Ala Val Leu Gly Glu Val Ser Leu Val
 20 25 30

Pro Ala Val Val Phe Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe
 35 40 45

Leu Ile Gly Ser Ala Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu
 50 55 60

Asn Ala Pro Arg Ala Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile
 65 70 75 80

Ala Ile Pro Thr Leu Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly
 85 90 95

Phe Ser Ile Val Ser Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr
 100 105 110

Ile Ser Leu Val Leu Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu
 115 120 125

Ala Ala Val Phe Ala Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile
 130 135 140

Gly Ala Thr Ile Leu Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro
 145 150 155 160

His Ser Thr Ser Trp Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu
 165 170 175

Ile Ile Gln Glu Leu Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln
 180 185 190

Gly Pro Leu Gly Tyr Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser
 195 200 205

Pro Phe Leu Thr Arg Ser Ala Ser
 210 215

170	175	180	
ctt tct gct tta tgg ttg cgc cac tac	aca cag ggg cca ctt ggg tat		691
Leu Ser Ala Leu Trp Leu Arg His Tyr Thr	Gln Gly Pro Leu Gly Tyr		
185	190	195	
cta tgg cgt tgg gtg act tgg gga agc cgt tcc ccc ttc ctt acc cgt			739
Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser Pro Phe Leu Thr Arg			
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tcc gca tca tgacaggtac ggaagtgtcc tac			771
Ser Ala Ser			
215			

<210> 474

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Leu Leu Pro Tyr Ala Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser	
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Trp Leu Pro Arg Trp Ala Val Ala Val Leu Gly Glu Val Ser Leu Val	
20	30

Pro Ala Val Val Phe Gly Gly Gly Phe Leu Leu Ile. Pro Ser Met Phe	
35	45

Leu Ile Gly Ser Ala Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu	
50	60

Asn Ala Pro Arg Ala Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile	
65	80

Ala Ile Pro Thr Leu Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly	
85	95

Phe Ser Ile Val Ser Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr	
100	110

Ile Ser Leu Val Leu Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu	
115	125

Ala Ala Val Phe Ala Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile	
130	140

Gly Ala Thr Ile Leu Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro	
145	160

His Ser Thr Ser Trp Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu	
165	175

Ile Ile Gln Glu Leu Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln	
180	190

Gly Pro Leu Gly Tyr Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser	
195	205

Pro Phe Leu Thr Arg Ser Ala Ser

210

215

<210> 475
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1078)
<223> RXN01023

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atcttttctag tctatcgccc cacaggtagg ctcaggacac atg agt gcc gtg aac 115
Met Ser Ala Val Asn
1 5
agt gct ggt cgc cca gcc aac ggg gga att aac aaa acc ccc atg att 163
Ser Ala Gly Arg Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile
10 15 20
att gcc cta gtg tta tct att gtg ttg gtt ttg gcg gtg ctg ttc ggc 211
Ile Ala Leu Val Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly
25 30 35
gcc cga gtc ctc ctt ggc ccc gcc ggc cag caa cag ata gcc atg agt 259
Ala Arg Val Leu Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser
40 45 50
ggg ctt ccc gcc cca gac gca gaa tct gct gag tgc gcc gca tta ctc 307
Gly Leu Pro Ala Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu
55 60 65
gag gat ctc ccc ggc gag gcc ttc ggg cac acc cgt gca gaa atc atg 355
Glu Asp Leu Pro Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met
70 75 80 85
gat cct gtt cca ccg ggc gct gcc gcc tgg tcc acc tca gac ctc gag 403
Asp Pro Val Pro Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu
90 95 100
cgt gtg acg ctg cgt tgt ggc gtc gat atg cca ttc cag tac acc gcg 451
Arg Val Thr Leu Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala
105 110 115
ctc gcc aac acc gtc gac gtc gac ggc acc acc tgg cta cct gtc tcc 499
Leu Ala Asn Thr Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser
120 125 130
gac atg acc ccc ggc tcc tcc ctg gag acc tgg tac tcc gtc aac cgc 547
Asp Met Thr Pro Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg
135 140 145
ttc ccc gtc gtc gcc atc acc gcc gat gac atc agc acc gac agc gcc 595
Phe Pro Val Val Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala
150 155 160 165
gac aac ccc gtc gcc ccc ttc agc agc gcc gtc gac aag cta gaa aag 643

Asp Asn Pro Val Ala Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys
 170 175 180
 cgc gac ggc cag ccc ttc gac gcc cca ctt acc ggc ttg agc tca gcc 691
 Arg Asp Gly Gln Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala
 185 190 195
 ggc acc aca tgc act tcg ctt ttc gac gcc ctc ccc cgc caa ctc gaa 739
 Gly Thr Thr Cys Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu
 200 205 210
 gtc ggc ggc gac gac ggc aca acg tac gaa cgc atc gag gag gac cgc 787
 Val Gly Gly Asp Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg
 215 220 225
 atg cag gcc gcc gga tac tcc gac gac gca gtc gcg tgg gac acg ccg 835
 Met Gln Ala Ala Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro
 230 235 240 245
 gga tta gaa ccc att gtg atc cgt tgc ggc gtg gag cct tct gag aac 883
 Gly Leu Glu Pro Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn
 250 255 260
 tac gca gcc ggt gcc atg ttg cag cag atc gat gac atc ccg tgg ttc 931
 Tyr Ala Ala Gly Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe
 265 270 275
 gag gac acc att ttg gcc tcc ggt acc acc tcg tct acc tgg tat gcc 979
 Glu Asp Thr Ile Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala
 280 285 290
 ctt gga cgc gag atc gac atc gcc gtg tct ctg cct cag gct gct tcc 1027
 Leu Gly Arg Glu Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser
 295 300 305
 tct tcc ctg att act atc tcc ggt ttc att gaa gac acg gtt cct gcg 1075
 Ser Ser Leu Ile Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala
 310 315 320 325
 gaa taagacataa aaaatcgccc cac 1101
 Glu

<210> 476

<211> 326

<212> PRT

<213> Corynebacterium glutamicum .

<400> 476

Met Ser Ala Val Asn Ser Ala Gly Arg Pro Ala Asn Gly Gly Ile Asn
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Lys Thr Pro Met Ile Ile Ala Leu Val Leu Ser Ile Val Leu Val Leu
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Ala Val Leu Phe Gly Ala Arg Val Leu Leu Gly Pro Ala Gly Gln Gln
 35 40 45

Gln Ile Ala Met Ser Gly Leu Pro Ala Pro Asp Ala Glu Ser Ala Glu
 50 55 60

Cys Ala Ala Leu Leu Glu Asp Leu Pro Gly Glu Ala Phe Gly His Thr
 65 70 75 80
 Arg Ala Glu Ile Met Asp Pro Val Pro Pro Gly Ala Ala Ala Trp Ser
 85 90 95
 Thr Ser Asp Leu Glu Arg Val Thr Leu Arg Cys Gly Val Asp Met Pro
 100 105 110
 Phe Gln Tyr Thr Ala Leu Ala Asn Thr Val Asp Val Asp Gly Thr Thr
 115 120 125
 Trp Leu Pro Val Ser Asp Met Thr Pro Gly Ser Ser Leu Glu Thr Trp
 130 135 140
 Tyr Ser Val Asn Arg Phe Pro Val Val Ala Ile Thr Ala Asp Asp Ile
 145 150 155 160
 Ser Thr Asp Ser Ala Asp Asn Pro Val Ala Pro Phe Ser Ser Ala Val
 165 170 175
 Asp Lys Leu Glu Lys Arg Asp Gly Gln Pro Phe Asp Ala Pro Leu Thr
 180 185 190
 Gly Leu Ser Ser Ala Gly Thr Thr Cys Thr Ser Leu Phe Asp Ala Leu
 195 200 205
 Pro Arg Gln Leu Glu Val Gly Gly Asp Asp Gly Thr Thr Tyr Glu Arg
 210 215 220
 Ile Glu Glu Asp Arg Met Gln Ala Ala Gly Tyr Ser Asp Asp Ala Val
 225 230 235 240
 Ala Trp Asp Thr Pro Gly Leu Glu Pro Ile Val Ile Arg Cys Gly Val
 245 250 255
 Glu Pro Ser Glu Asn Tyr Ala Ala Gly Ala Met Leu Gln Gln Ile Asp
 260 265 270
 Asp Ile Pro Trp Phe Glu Asp Thr Ile Leu Ala Ser Gly Thr Thr Ser
 275 280 285
 Ser Thr Trp Tyr Ala Leu Gly Arg Glu Ile Asp Ile Ala Val Ser Leu
 290 295 300
 Pro Gln Ala Ala Ser Ser Ser Leu Ile Thr Ile Ser Gly Phe Ile Glu
 305 310 315 320
 Asp Thr Val Pro Ala Glu
 325

<210> 477

<211> 974

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(951)

<223> FRXA01023

<400> 477

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Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly Ala Arg Val Leu	
20 25 30	
ctt ggc ccc gcc ggc cag caa cag ata gcc atg agt ggg ctt ccc gcc	144
Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser Gly Leu Pro Ala	
35 40 45	
cca gac gca gaa tct gct gag tgc gcc gca tta ctc gag gat ctc ccc	192
Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu Glu Asp Leu Pro	
50 55 60	
ggc gag gcc ttc ggg cac acc cgt gca gaa atc atg gat cct gtt cca	240
Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met Asp Pro Val Pro	
65 70 75 80	
ccg ggc gct gcc gcc tgg tcc acc tca gac ctc gag cgt gtg acg ctg	288
Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu Arg Val Thr Leu	
85 90 95	
cgt tgt ggc gtc gat atg cca ttc cag tac acc gcg ctc gcc aac acc	336
Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala Leu Ala Asn Thr	
100 105 110	
gtc gac gtc gac ggc acc acc tgg cta cct gtc tcc gac atg acc ccc	384
Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser Asp Met Thr Pro	
115 120 125	
ggc tcc tcc ctg gag acc tgg tac tcc gtc aac cgc ttc ccc gtc gtc	432
Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg Phe Pro Val Val	
130 135 140	
gcc atc acc gcc gat gac atc agc acc gac agc gcc gac aac ccc gtc	480
Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala Asp Asn Pro Val	
145 150 155 160	
gac ccc ttc agc agc gcc gtc gac aag cta gaa aag cgc gac ggc cag	528
Asp Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys Arg Asp Gly Gln	
165 170 175	
ccc ttc gac gcc cca ctt acc ggc ttg agc tca gcc ggc acc aca tgc	576
Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala Gly Thr Thr Cys	
180 185 190	
act tcg ctt ttc gac gcc ctc ccc cgc caa ctc gaa gtc ggc ggc gac	624
Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu Val Gly Gly Asp	
195 200 205	
gac ggc aca acg tac gaa cgc atc gag gag gac cgc atg cag gcc gcc	672
Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg Met Gln Ala Ala	
210 215 220	
gga tac tcc gac gac gca gtc gcg tgg gac acg ccg gga tta gaa ccc	720
Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro Gly Leu Glu Pro	

225 230 235 240
 att gtg atc cgt tgc ggc gtg gag cct tct gag aac tac gca gcc ggt 768
 Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn Tyr Ala Ala Gly
 245 250 255

 gcc atg ttg cag cag atc gat gac atc ccg tgg ttc gag gac acc att 816
 Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe Glu Asp Thr Ile
 260 265 270

 ttg gcc tcc ggt acc acc tcg tct acc tgg tat gcc ctt gga cgc gag 864
 Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala Leu Gly Arg Glu
 275 280 285

 atc gac atc gcc gtg tct ctg cct cag gct gct tcc tct tcc ctg att 912
 Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser Ser Ser Leu Ile
 290 295 300

 act atc tcc ggt ttc att gaa gac acg gtt cct gcg gaa taagacataa 961
 Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala Glu
 305 310 315

 aaaatcgccc cac 974

<210> 478
 <211> 317
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 478
 Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile Ile Ala Leu Val
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 Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly Ala Arg Val Leu
 20 25 30

 Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser Gly Leu Pro Ala
 35 40 45

 Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu Glu Asp Leu Pro
 50 55 60

 Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met Asp Pro Val Pro
 65 70 75 80

 Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu Arg Val Thr Leu
 85 90 95

 Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala Leu Ala Asn Thr
 100 105 110

 Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser Asp Met Thr Pro
 115 120 125

 Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg Phe Pro Val Val
 130 135 140

 Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala Asp Asn Pro Val
 145 150 155 160

Asp	Pro	Phe	Ser	Ser	Ala	Val	Asp	Lys	Leu	Glu	Lys	Arg	Asp	Gly	Gln	
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Pro	Phe	Asp	Ala	Pro	Leu	Thr	Gly	Leu	Ser	Ser	Ala	Gly	Thr	Thr	Cys	
			180					185					190			
Thr	Ser	Leu	Phe	Asp	Ala	Leu	Pro	Arg	Gln	Leu	Glu	Val	Gly	Gly	Asp	
			195					200					205			
Asp	Gly	Thr	Thr	Tyr	Glu	Arg	Ile	Glu	Glu	Asp	Arg	Met	Gln	Ala	Ala	
			210					215					220			
Gly	Tyr	Ser	Asp	Asp	Ala	Val	Ala	Trp	Asp	Thr	Pro	Gly	Leu	Glu	Pro	
			225					230					235		240	
Ile	Val	Ile	Arg	Cys	Gly	Val	Glu	Pro	Ser	Glu	Asn	Tyr	Ala	Ala	Gly	
			245					250					255			
Ala	Met	Leu	Gln	Gln	Ile	Asp	Asp	Ile	Pro	Trp	Phe	Glu	Asp	Thr	Ile	
			260					265					270			
Leu	Ala	Ser	Gly	Thr	Thr	Ser	Ser	Thr	Trp	Tyr	Ala	Leu	Gly	Arg	Glu	
			275					280					285			
Ile	Asp	Ile	Ala	Val	Ser	Leu	Pro	Gln	Ala	Ala	Ser	Ser	Ser	Leu	Ile	
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Thr	Ile	Ser	Gly	Phe	Ile	Glu	Asp	Thr	Val	Pro	Ala	Glu				
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<210> 479
<211> 2172
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(2149)  
<223> RXN01028
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                                         Val Ile Tyr Pro Pro
                                         1                               5

ctc acc cct gca tcc gaa gag aaa ttc aac aag atc acc tca gtc gct 163
Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile Thr Ser Val Ala
                        10                        15                        20

gct gtg agc aag cgc cca acc acc ctg ccg tat ttc cgt gca gat ggt 211
Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe Arg Ala Asp Gly
                        25                        30                        35

tca cct act cgt ggc ttt gct aac ttc tcc aca gga ggt att cac ggt 259
Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly Gly Ile His Gly
                        40                        45                        50

gcg gaa tac aac gaa gat cgt ttt gac cat gat caa gat cta cac aca 307

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gtg	gca	acc	cgt	gaa	ttc	ttc	gcc	att	ctt	gat	gcg	aca	tta	gcg	gct	355	
Val	Ala	Thr	Arg	Glu	Phe	Phe	Ala	Ile	Leu	Asp	Ala	Thr	Leu	Ala	Ala		
70					75					80					85		
ctc	tac	gca	gcc	cac	caa	gcc	gaa	cct	gaa	tcg	gcg	gac	tac	cag	att	403	
Leu	Tyr	Ala	Ala	His	Gln	Ala	Glu	Pro	Glu	Ser	Ala	Asp	Tyr	Gln	Ile		
				90					95					100			
gca	caa	gac	gca	ctc	gcc	tgg	gca	aag	aat	gta	ctt	agc	gat	caa	aaa	451	
Ala	Gln	Asp	Ala	Leu	Ala	Trp	Ala	Lys	Asn	Val	Leu	Ser	Asp	Gln	Lys		
			105					110					115				
ctc	atc	gct	aag	tcg	cct	cag	tta	tac	aac	ccc	gaa	acc	ggg	gtc	acc	499	
Leu	Ile	Ala	Lys	Ser	Pro	Gln	Leu	Tyr	Asn	Pro	Glu	Thr	Gly	Val	Thr		
		120					125					130					
tat	gag	tgg	gag	ttt	gtc	gct	caa	gca	gca	tgg	tgg	att	cgc	aac	aaa	547	
Tyr	Glu	Trp	Glu	Phe	Val	Ala	Gln	Ala	Ala	Trp	Trp	Ile	Arg	Asn	Lys		
	135					140					145						
ccg	gtt	gag	gtt	att	tta	cca	aca	ggt	gaa	tca	atg	acc	gta	aaa	cac	595	
Pro	Val	Glu	Val	Ile	Leu	Pro	Thr	Gly	Glu	Ser	Met	Thr	Val	Lys	His		
150					155					160					165		
aaa	tct	gta	ttg	gca	tct	gcg	tcc	tac	cca	ctc	cga	gac	aac	gtg	gcg	643	
Lys	Ser	Val	Leu	Ala	Ser	Ala	Ser	Tyr	Pro	Leu	Arg	Asp	Asn	Val	Ala		
				170					175					180			
tac	tgg	cgt	agc	gaa	ccc	aaa	aca	cca	cag	ctg	ttt	ccc	gta	gca	aaa	691	
Tyr	Trp	Arg	Ser	Glu	Pro	Lys	Thr	Pro	Gln	Leu	Phe	Pro	Val	Ala	Lys		
			185					190					195				
tct	ggt	ggt	tcc	tcg	ctt	gag	aag	aag	tac	aac	tac	acc	tct	gtg	ggt	739	
Ser	Gly	Gly	Ser	Ser	Leu	Glu	Lys	Lys	Tyr	Asn	Tyr	Thr	Ser	Val	Gly		
		200					205					210					
act	gct	att	cac	gag	gac	ttt	agc	agt	tac	tat	ccg	ctc	ttg	ctc	acc	787	
Thr	Ala	Ile	His	Glu	Asp	Phe	Ser	Ser	Tyr	Tyr	Pro	Leu	Leu	Leu	Thr		
	215					220					225						
aat	atg	gct	gca	ttt	acc	aat	gct	gac	tta	ggt	att	gat	gag	aaa	acc	835	
Asn	Met	Ala	Ala	Phe	Thr	Asn	Ala	Asp	Leu	Gly	Ile	Asp	Glu	Lys	Thr		
230					235					240					245		
ggg	cgc	cct	cgt	gac	cgc	tac	cgt	gaa	atc	tac	gaa	caa	aaa	gag	atc	883	
Gly	Arg	Pro	Arg	Asp	Arg	Tyr	Arg	Glu	Ile	Tyr	Glu	Gln	Lys	Glu	Ile		
				250					255					260			
tat	ggc	gca	cag	cgc	aaa	gac	ccc	tcc	att	gat	gaa	gaa	aca	aag	caa	931	
Tyr	Gly	Ala	Gln	Arg	Lys	Asp	Pro	Ser	Ile	Asp	Glu	Glu	Thr	Lys	Gln		
			265					270					275				
cgt	cta	ggg	att	ttg	cgc	gaa	ggt	acc	aag	ttg	att	ctt	aac	tcg	gcc	979	
Arg	Leu	Gly	Ile	Leu	Arg	Glu	Gly	Thr	Lys	Leu	Ile	Leu	Asn	Ser	Ala		
		280					285					290					
acc	ggt	gct	gct	gat	gct	ggt	cac	gac	acc	ccg	atc	ctc	atg	aac	aat	1027	
Thr	Gly	Ala	Ala	Asp	Ala	Gly	His	Asp	Thr	Pro	Ile	Leu	Met	Asn	Asn		

295	300	305	
cgc gtt att gcc atg agg att att ggg cag cta ttt tct tgg aga att Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe Ser Trp Arg Ile 310 315 320 325			1075
ggg caa gct caa tca ctg gct ggt gca acg att att tcc act aac act Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile Ser Thr Asn Thr 330 335 340			1123
gat ggc ctg tat tcc gta ctc gat atg ggg act aac cag cgc gtt ctt Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn Gln Arg Val Leu 345 350 355			1171
gat gaa cac gct aca gcc atc ggt gtg caa att gag cct gaa gaa ctg Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu Pro Glu Glu Leu 360 365 370			1219
gat att gtc tcc aag gat tcc aac tca cgt gcc gaa ttt ctc ggc aat Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu Phe Leu Gly Asn 375 380 385			1267
ggc tac atc aat gcg gcc ggt gac ttg gcg tgt tgg gat gga ccc aac Gly Tyr Ile Asn Ala Ala Gly Asp Leu Ala Cys Trp Asp Gly Pro Asn 390 395 400 405			1315
tct cgg aac tca cta gat cac ccg gcc ttt gtt gac cat gtg ctg gtg Ser Arg Asn Ser Leu Asp His Pro Ala Phe Val Asp His Val Leu Val 410 415 420			1363
aag tat ttc cag ctc gtc gtc aac aac act gtg cca gag att cca gaa Lys Tyr Phe Gln Leu Val Val Asn Asn Thr Val Pro Glu Ile Pro Glu 425 430 435			1411
aca cct gag ctt gag ggt gta ccg ctg gct ctt gat caa ccc atg aac Thr Pro Glu Leu Glu Gly Val Pro Leu Ala Leu Asp Gln Pro Met Asn 440 445 450			1459
cgc cac gaa gtc tcg aag att gtc gcc act atg cac aag gaa ttc gag Arg His Glu Val Ser Lys Ile Val Ala Thr Met His Lys Glu Phe Glu 455 460 465			1507
ccg aaa aag ctg ctg tcg ttt tac caa aac att ttg gcc tct tca cgc Pro Lys Lys Leu Leu Ser Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg 470 475 480 485			1555
ggt tct aat acc ttc cta ttc tct gtc ccc tat atc cct gca aca gaa Gly Ser Asn Thr Phe Leu Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu 490 495 500			1603
gga gaa gaa acc cac cct gca aca gat acc agc act att gcg aca cca Gly Glu Glu Thr His Pro Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro 505 510 515			1651
acc ttg agc ttt gat gct tat ggt aat aag gcc gag gtc atg ccg act Thr Leu Ser Phe Asp Ala Tyr Gly Asn Lys Ala Glu Val Met Pro Thr 520 525 530			1699
caa tcc act gtg gat aag cgc gtg ccc tct ttg ctg cag tat tac acg Gln Ser Thr Val Asp Lys Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr 535 540 545			1747

cgt aca ttc cat gtg cga caa gat acg cag cag gct gtc ttt gat gtt 1795
 Arg Thr Phe His Val Arg Gln Asp Thr Gln Gln Ala Val Phe Asp Val
 550 555 560 565

att ggc gcc aac ccc gtg ctc atc gcc gca gca aaa gct gca tcc ata 1843
 Ile Gly Ala Asn Pro Val Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile
 570 575 580

tca ccg gct tct gct gat tca cgt aga aag aag ggc ctg gcc tcc acc 1891
 Ser Pro Ala Ser Ala Asp Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr
 585 590 595

aac gct gac cca gta gcc aag cat gta cta gaa att gca gga gct gat 1939
 Asn Ala Asp Pro Val Ala Lys His Val Leu Glu Ile Ala Gly Ala Asp
 600 605 610

gtg gaa tcg ctg cgc cat gaa aag gat ctc aag gtc acc aag cac act 1987
 Val Glu Ser Leu Arg His Glu Lys Asp Leu Lys Val Thr Lys His Thr
 615 620 625

ggc caa gac cca gca ctg cct gtc gtg gtc ttt aac caa acc att tgg 2035
 Gly Gln Asp Pro Ala Leu Pro Val Val Val Phe Asn Gln Thr Ile Trp
 630 635 640 645

cat aac ccc aac gac gat gtg att aat gca tta ctg ggc gct att gac 2083
 His Asn Pro Asn Asp Asp Val Ile Asn Ala Leu Leu Gly Ala Ile Asp
 650 655 660

cag gat gcc tac att gac atg gcg atc tcg tcc tac aac aag tcc tgg 2131
 Gln Asp Ala Tyr Ile Asp Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp
 665 670 675

cac aac att atc ccg gct taactaccgc tgggtagacc cct 2172
 His Asn Ile Ile Pro Ala
 680

<210> 480

<211> 683

<212> PRT

<213> Corynebacterium glutamicum

<400> 480

Val Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys
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 20 25 30

Phe Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr
 35 40 45

Gly Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp
 50 55 60

Gln Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp
 65 70 75 80

Ala Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser
 85 90 95

Ala Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val
 100 105 110
 Leu Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro
 115 120 125
 Glu Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp
 130 135 140
 Trp Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser
 145 150 155 160
 Met Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu
 165 170 175
 Arg Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu
 180 185 190
 Phe Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn
 195 200 205
 Tyr Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr
 210 215 220
 Pro Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly
 225 230 235 240
 Ile Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr
 245 250 255
 Glu Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp
 260 265 270
 Glu Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu
 275 280 285
 Ile Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro
 290 295 300
 Ile Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu
 305 310 315 320
 Phe Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile
 325 330 335
 Ile Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr
 340 345 350
 Asn Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile
 355 360 365
 Glu Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala
 370 375 380
 Glu Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala Gly Asp Leu Ala Cys
 385 390 395 400
 Trp Asp Gly Pro Asn Ser Arg Asn Ser Leu Asp His Pro Ala Phe Val
 405 410 415

Asp His Val Leu Val Lys Tyr Phe Gln Leu Val Val Asn Asn Thr Val
420 425 430

Pro Glu Ile Pro Glu Thr Pro Glu Leu Glu Gly Val Pro Leu Ala Leu
435 440 445

Asp Gln Pro Met Asn Arg His Glu Val Ser Lys Ile Val Ala Thr Met
450 455 460

His Lys Glu Phe Glu Pro Lys Lys Leu Leu Ser Phe Tyr Gln Asn Ile
465 470 475 480

Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu Phe Ser Val Pro Tyr
485 490 495

Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro Ala Thr Asp Thr Ser
500 505 510

Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala Tyr Gly Asn Lys Ala
515 520 525

Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys Arg Val Pro Ser Leu
530 535 540

Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg Gln Asp Thr Gln Gln
545 550 555 560

Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val Leu Ile Ala Ala Ala
565 570 575

Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp Ser Arg Arg Lys Lys
580 585 590

Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala Lys His Val Leu Glu
595 600 605

Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His Glu Lys Asp Leu Lys
610 615 620

Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu Pro Val Val Val Phe
625 630 635 640

Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp Val Ile Asn Ala Leu
645 650 655

Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp Met Ala Ile Ser Ser
660 665 670

Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
675 680

<210> 481

<211> 647

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(624)

<223> FRXA01028

<400> 481

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ttc tct gtc ccc tat atc cct gca aca gaa gga gaa gaa acc cac cct	96
Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro	
20 25 30	
gca aca gat acc agc act att gcg aca cca acc ttg agc ttt gat gct	144
Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala	
35 40 45	
tat ggt aat aag gcc gag gtc atg ccg act caa tcc act gtg gat aag	192
Tyr Gly Asn Lys Ala Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys	
50 55 60	
cgc gtg ccc tct ttg ctg cag tat tac acg cgt aca ttc cat gtg cga	240
Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg	
65 70 75 80	
caa gat acg cag cag gct gtc ttt gat gtt att ggc gcc aac ccc gtg	288
Gln Asp Thr Gln Gln Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val	
85 90 95	
ctc atc gcc gca gca aaa gct gca tcc ata tca ccg gct tct gct gat	336
Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp	
100 105 110	
tca cgt aga aag aag ggc ctg gcc tcc acc aac gct gac cca gta gcc	384
Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala	
115 120 125	
aag cat gta cta gaa att gca gga gct gat gtg gaa tcg ctg cgc cat	432
Lys His Val Leu Glu Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His	
130 135 140	
gaa aag gat ctc aag gtc acc aag cac act ggc caa gac cca gca ctg	480
Glu Lys Asp Leu Lys Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu	
145 150 155 160	
cct gtc gtg gtc ttt aac caa acc att tgg cat aac ccc aac gac gat	528
Pro Val Val Val Phe Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp	
165 170 175	
gtg att aat gca tta ctg ggc gct att gac cag gat gcc tac att gac	576
Val Ile Asn Ala Leu Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp	
180 185 190	
atg gcg atc tcg tcc tac aac aag tcc tgg cac aac att atc ccg gct	624
Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala	
195 200 205	
taactaccgc tgggtagacc cct	647

<210> 482

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 482

Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu
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 Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro
 20 25 30
 Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala
 35 40 45
 Tyr Gly Asn Lys Ala Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys
 50 55 60
 Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg
 65 70 75 80
 Gln Asp Thr Gln Gln Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val
 85 90 95
 Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp
 100 105 110
 Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala
 115 120 125
 Lys His Val Leu Glu Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His
 130 135 140
 Glu Lys Asp Leu Lys Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu
 145 150 155 160
 Pro Val Val Val Phe Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp
 165 170 175
 Val Ile Asn Ala Leu Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp
 180 185 190
 Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
 195 200 205

<210> 483

<211> 1230

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1230)

<223> FRXA01812

<400> 483

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 Ser Phe Asn Asp Val Asp Pro Ala Val Thr His Pro His Leu Thr Val
 1 5 10 15
 atc tac cca ccg ctc acc cct gca tcc gaa gag aaa ttc aac aag atc 96
 Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile
 20 25 30

acc tca gtc gct gct gtg agc aag cgc cca acc acc ctg ccg tat ttc	144
Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe	
35 40 45	
cgt gca gat ggt tca cct act cgt ggc ttt gct aac ttc tcc aca gga	192
Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly	
50 55 60	
ggt att cac ggt gcg gaa tac aac gaa gat cgt ttt gac cat gat caa	240
Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln	
65 70 75 80	
gat cta cac aca gtg gca acc cgt gaa ttc ttc gcc att ctt gat gcg	288
Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala	
85 90 95	
aca tta gcg gct ctc tac gca gcc cac caa gcc gaa cct gaa tcg gcg	336
Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala	
100 105 110	
gac tac cag att gca caa gac gca ctc gcc tgg gca aag aat gta ctt	384
Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu	
115 120 125	
agc gat caa aaa ctc atc gct aag tcg cct cag tta tac aac ccc gaa	432
Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu	
130 135 140	
acc ggg gtc acc tat gag tgg gag ttt gtc gct caa gca gca tgg tgg	480
Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp	
145 150 155 160	
att cgc aac aaa ccg gtt gag gtt att tta cca aca ggt gaa tca atg	528
Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met	
165 170 175	
acc gta aaa cac aaa tct gta ttg gca tct gcg tcc tac cca ctc cga	576
Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg	
180 185 190	
gac aac gtg gcg tac tgg cgt agc gaa ccc aaa aca cca cag ctg ttt	624
Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe	
195 200 205	
ccc gta gca aaa tct ggt ggt tcc tcg ctt gag aag aag tac aac tac	672
Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr	
210 215 220	
acc tct gtg ggt act gct att cac gag gac ttt agc agt tac tat ccg	720
Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro	
225 230 235 240	
ctc ttg ctc acc aat atg gct gca ttt acc aat gct gac tta ggt att	768
Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile	
245 250 255	
gat gag aaa acc ggg cgc cct cgt gac cgc tac cgt gaa atc tac gaa	816
Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu	
260 265 270	
caa aaa gag atc tat ggc gca cag cgc aaa gac ccc tcc att gat gaa	864

Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu
 275 280 285
 gaa aca aag caa cgt cta ggg att ttg cgc gaa ggt acc aag ttg att 912
 Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile
 290 295 300
 ctt aac tcg gcc acc ggt gct gct gat gct ggt cac gac acc ccg atc 960
 Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile
 305 310 315 320
 ctc atg aac aat cgc gtt att gcc atg agg att att ggg cag cta ttt 1008
 Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe
 325 330 335
 tct tgg aga att ggg caa gct caa tca ctg gct ggt gca acg att att 1056
 Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile
 340 345 350
 tcc act aac act gat ggc ctg tat tcc gta ctc gat atg ggg act aac 1104
 Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn
 355 360 365
 cag cgc gtt ctt gat gaa cac gct aca gcc atc ggt gtg caa att gag 1152
 Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu
 370 375 380
 cct gaa gaa ctg gat att gtc tcc aag gat tcc aac tca cgt gcc gaa 1200
 Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu
 385 390 395 400
 ttt ctc ggc aat ggc tac atc aat gcg gcc 1230
 Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala
 405 410

<210> 484

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

Ser Phe Asn Asp Val Asp Pro Ala Val Thr His Pro His Leu Thr Val
 1 5 10 15

Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile
 20 25 30

Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe
 35 40 45

Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly
 50 55 60

Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln
 65 70 75 80

Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala
 85 90 95

Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala

100					105					110						
Asp	Tyr	Gln	Ile	Ala	Gln	Asp	Ala	Leu	Ala	Trp	Ala	Lys	Asn	Val	Leu	
115					120					125						
Ser	Asp	Gln	Lys	Leu	Ile	Ala	Lys	Ser	Pro	Gln	Leu	Tyr	Asn	Pro	Glu	
130					135					140						
Thr	Gly	Val	Thr	Tyr	Glu	Trp	Glu	Phe	Val	Ala	Gln	Ala	Ala	Trp	Trp	
145					150					155					160	
Ile	Arg	Asn	Lys	Pro	Val	Glu	Val	Ile	Leu	Pro	Thr	Gly	Glu	Ser	Met	
165					170					175						
Thr	Val	Lys	His	Lys	Ser	Val	Leu	Ala	Ser	Ala	Ser	Tyr	Pro	Leu	Arg	
180					185					190						
Asp	Asn	Val	Ala	Tyr	Trp	Arg	Ser	Glu	Pro	Lys	Thr	Pro	Gln	Leu	Phe	
195					200					205						
Pro	Val	Ala	Lys	Ser	Gly	Gly	Ser	Ser	Leu	Glu	Lys	Lys	Tyr	Asn	Tyr	
210					215					220						
Thr	Ser	Val	Gly	Thr	Ala	Ile	His	Glu	Asp	Phe	Ser	Ser	Tyr	Tyr	Pro	
225					230					235					240	
Leu	Leu	Leu	Thr	Asn	Met	Ala	Ala	Phe	Thr	Asn	Ala	Asp	Leu	Gly	Ile	
245					250					255						
Asp	Glu	Lys	Thr	Gly	Arg	Pro	Arg	Asp	Arg	Tyr	Arg	Glu	Ile	Tyr	Glu	
260					265					270						
Gln	Lys	Glu	Ile	Tyr	Gly	Ala	Gln	Arg	Lys	Asp	Pro	Ser	Ile	Asp	Glu	
275					280					285						
Glu	Thr	Lys	Gln	Arg	Leu	Gly	Ile	Leu	Arg	Glu	Gly	Thr	Lys	Leu	Ile	
290					295					300						
Leu	Asn	Ser	Ala	Thr	Gly	Ala	Ala	Asp	Ala	Gly	His	Asp	Thr	Pro	Ile	
305					310					315					320	
Leu	Met	Asn	Asn	Arg	Val	Ile	Ala	Met	Arg	Ile	Ile	Gly	Gln	Leu	Phe	
325					330					335						
Ser	Trp	Arg	Ile	Gly	Gln	Ala	Gln	Ser	Leu	Ala	Gly	Ala	Thr	Ile	Ile	
340					345					350						
Ser	Thr	Asn	Thr	Asp	Gly	Leu	Tyr	Ser	Val	Leu	Asp	Met	Gly	Thr	Asn	
355					360					365						
Gln	Arg	Val	Leu	Asp	Glu	His	Ala	Thr	Ala	Ile	Gly	Val	Gln	Ile	Glu	
370					375					380						
Pro	Glu	Glu	Leu	Asp	Ile	Val	Ser	Lys	Asp	Ser	Asn	Ser	Arg	Ala	Glu	
385					390					395					400	
Phe	Leu	Gly	Asn	Gly	Tyr	Ile	Asn	Ala	Ala							
405					410											

<210> 485

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<220>  
<221> CDS  
<222> (101)..(814)  
<223> RXN01069
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atc tta gtg gac acc ggg atg ggg atg aat tac acg ttt aac att gcc 739
 Ile Leu Val Asp Thr Gly Met Gly Met Asn Tyr Thr Phe Asn Ile Ala
 200 205 210

cat acg tgg ggc aag atc ttc gcg gtt ttg atc ttc gcg gtg cca gta 787
 His Thr Trp Gly Lys Ile Phe Ala Val Leu Ile Phe Ala Val Pro Val
 215 220 225

ctc atc gtt tta tta acc gtt ctc ctt taacctcgat ccaccgatgt 834
 Leu Ile Val Leu Leu Thr Val Leu Leu
 230 235

gcc 837

<210> 486

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 486

Val Asn Asp Leu Pro Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp
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Val Leu Ala Thr Val Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu
 20 25 30

Tyr Val Tyr Tyr Pro Ser Leu Pro Asp Pro Met Pro Val His Trp Asn
 35 40 45

Gly Ser Gly Glu Ala Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe
 50 55 60

Leu Ser Leu Ile Leu Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser
 65 70 75 80

Gly Met Gln Ala Leu Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg
 85 90 95

Gly Gly Ala Lys Ser Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr
 100 105 110

Lys Ala Thr Ser Met His Met Gly Trp Tyr Met Phe Val Leu Asn Ala
 115 120 125

Leu Ile Leu Val Met Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro
 130 135 140

Gly Gly Phe Ile Ile Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val
 145 150 155 160

Leu Leu Val Leu Ile Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr
 165 170 175

Pro Met Pro Asp Gln Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp
 180 185 190

Pro Asp Asp Asn Arg Ile Leu Val Asp Thr Gly Met Gly Met Asn Tyr

195	200	205
Thr Phe Asn Ile Ala His	Thr Trp Gly Lys Ile	Phe Ala Val Leu Ile
210	215	220
Phe Ala Val Pro Val Leu	Ile Val Leu Leu Thr	Val Leu Leu
225	230	235

<210> 487
 <211> 703
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(703)
 <223> FRXA01069

<400> 487
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 Val Asn Asp Leu Pro 5
 1
 aac cta cca aag ctg ccc ttc aac tgg aca tgg gtg ctg gca act gtt 163
 Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp Val Leu Ala Thr Val 20
 10 15
 gcc acg aca gtg gtg ttg gcg ggt att ggt ttg tat gtg tat tac ccg 211
 Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu Tyr Val Tyr Tyr Pro 35
 25 30
 tcg ttg cca gat cct atg ccg gtg cat tgg aat gga tcc ggg gag gcg 259
 Ser Leu Pro Asp Pro Met Pro Val His Trp Asn Gly Ser Gly Glu Ala 50
 40 45
 gat aat tgg acg cct aaa tcg gtg ggt tcg ttt ctt tca ctg att ttg 307
 Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe Leu Ser Leu Ile Leu 65
 55 60
 ata ggg cca ggc att att ttg ctg acc ctg tcg ggt atg cag gcg ttg 355
 Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser Gly Met Gln Ala Leu 85
 70 75 80
 ctg acc atg cag tct gga gtg atc acg caa cgc ggt ggg gcg aaa tcg 403
 Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg Gly Gly Ala Lys Ser 100
 90 95
 gcg aat gaa gcg cac cgg cag tgg gaa acc tac aag gca aca agc atg 451
 Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr Lys Ala Thr Ser Met 115
 105 110
 cac atg ggt tgg tac atg ttt gtg ctc aac gct ttg att ttg gtg atg 499
 His Met Gly Trp Tyr Met Phe Val Leu Asn Ala Leu Ile Leu Val Met 130
 120 125
 atc ctc aat gag ttc cgc cca aac cct ctg cct ggt gga ttt atc atc 547
 Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro Gly Gly Phe Ile Ile 145
 135 140 145

ggg ctt att gga att att gct gcc acg att gtc ctg ttg gtt ctg att 595
 Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val Leu Leu Val Leu Ile
 150 155 160 165
 gga aaa aca acc acg agt ttg gca aag aaa tac ccc atg cct gac caa 643
 Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr Pro Met Pro Asp Gln
 170 175 180
 gat gga aag acg tgg ggg att ttc tac aac gat ccg gac gat aat cgg 691
 Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp Pro Asp Asp Asn Arg
 185 190 195
 atc tta gtg gac 703
 Ile Leu Val Asp
 200

<210> 488

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Val Asn Asp Leu Pro Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp
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 Val Leu Ala Thr Val Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu
 20 25 30
 Tyr Val Tyr Tyr Pro Ser Leu Pro Asp Pro Met Pro Val His Trp Asn
 35 40 45
 Gly Ser Gly Glu Ala Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe
 50 55 60
 Leu Ser Leu Ile Leu Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser
 65 70 75 80
 Gly Met Gln Ala Leu Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg
 85 90 95
 Gly Gly Ala Lys Ser Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr
 100 105 110
 Lys Ala Thr Ser Met His Met Gly Trp Tyr Met Phe Val Leu Asn Ala
 115 120 125
 Leu Ile Leu Val Met Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro
 130 135 140
 Gly Gly Phe Ile Ile Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val
 145 150 155 160
 Leu Leu Val Leu Ile Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr
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 Pro Asp Asp Asn Arg Ile Leu Val Asp

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Leu Val Val Asp Ser 1 5																
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Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu Thr Thr Thr Glu Thr 10 15 20																
gat tcg gcc acc gcg ctg aac ctg cag atg tcg gaa gct ggc tac ctg 211																
Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser Glu Ala Gly Tyr Leu 25 30 35																
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Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser Val Met Leu Ser Ala 40 45 50																
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Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp Ala Leu Ala Ala Glu 55 60 65																
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Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu Ala Leu Val Glu Gln 70 75 80 85																
gct aca gga atg atc acg cag gcc ttg agc ttc gtg cag tac ttc ctc 403																
Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe Val Gln Tyr Phe Leu 90 95 100																
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aat acc ttc tcc atg att gtg gct cag cgc atg cgt gag ttc gct ctc 499																
Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met Arg Glu Phe Ala Leu 120 125 130																
ctg cga gcc ctg ggt gcg gcg cca gga cag atc act cgc tct gtg gtg 547																
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ggc	atg	ccg	atg	gga	tcc	agc	gtt	ggc	ttg	act	cct	tct	gca	gtg	gtt	691
Gly	Met	Pro	Met	Gly	Ser	Ser	Val	Gly	Leu	Thr	Pro	Ser	Ala	Val	Val	
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Thr	Ala	Leu	Val	Leu	Gly	Thr	Val	Val	Thr	Ile	Val	Ser	Ala	Trp	Ala	
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Pro	Ala	Arg	Arg	Ala	Gly	Glu	Val	Lys	Pro	Val	Glu	Ala	Met	Arg	Asn	
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Met	Glu	Thr	Thr	Thr	Met	Arg	Ser	Met	Met	Gly	Arg	Thr	Ile	Thr	Gly	
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Gly	Ile	Val	Leu	Ala	Leu	Gly	Ile	Ile	Phe	Ala	Ile	Ala	Gly	Ala	Met	
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Met	Thr	Asp	Ser	Ser	Thr	Ala	Thr	Arg	Ser	Ile	Leu	Val	Gly	Ile	Gly	
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gca	ctg	ttt	gtc	atc	gtg	ggg	acg	ttc	ctc	ttc	tca	cca	gcg	ctc	tcc	979
Ala	Leu	Phe	Val	Ile	Val	Gly	Thr	Phe	Leu	Phe	Ser	Pro	Ala	Leu	Ser	
		280					285					290				
atg	cct	gtg	gtg	ggg	ggc	ctg	ggc	aag	gtt	atc	ggg	gca	ccg	ttt	ggc	1027
Met	Pro	Val	Val	Gly	Gly	Leu	Gly	Lys	Val	Ile	Gly	Ala	Pro	Phe	Gly	
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agc	gtt	gga	agc	ctt	gct	gcg	acc	aac	tcc	aag	cga	aac	cct	cgc	cgt	1075
Ser	Val	Gly	Ser	Leu	Ala	Ala	Thr	Asn	Ser	Lys	Arg	Asn	Pro	Arg	Arg	
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Thr	Ala	Thr	Thr	Ala	Phe	Ala	Leu	Thr	Leu	Gly	Ile	Ala	Leu	Val	Thr	
			330						335					340		
gca	att	ggc	atg	ctt	tct	gca	acc	atg	aag	gac	gca	gtc	tcc	gac	atg	1171
Ala	Ile	Gly	Met	Leu	Ser	Ala	Thr	Met	Lys	Asp	Ala	Val	Ser	Asp	Met	
			345					350					355			
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Met	Ala	Glu	Gln	Tyr	Thr	Ala	Asp	Tyr	Ile	Leu	Gln	Gly	Pro	Thr	Asn	
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Gly	Ser	Ile	Thr	Met	Pro	Lys	Glu	Ser	Val	Asn	Asp	Val	Arg	Asp	Ala	
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Glu	Gly	Val	Ala	Asp	Val	Val	Leu	Val	Ser	Met	Asn	Ser	Ala	Ser	Val	
390					395				400						405	
aac	ggg	cag	gct	tca	tac	agc	cag	ctg	ggc	cag	tct	gta	acc	ttt	gtc	1363
Asn	Gly	Gln	Ala	Ser	Tyr	Ser	Gln	Leu	Gly	Gln	Ser	Val	Thr	Phe	Val	

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tcc ctc gac ttg agc aac cca ggt gtt gtg act aac cag acg ttt gct Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr Asn Gln Thr Phe Ala 440 445 450			1459
gat gaa aac ggc tgg gca gta ggc gat act ctg cag ctt gaa tca atg Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu Gln Leu Glu Ser Met 455 460 465			1507
ggg cag acc atc ggc gat atc gag ttg atc ggt acc ttc acc gga aac Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly Thr Phe Thr Gly Asn 470 475 480 485			1555
gac gcc atc gga aat atg atc atc tcc gaa agt tcc ttg gct gat aca Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser Ser Leu Ala Asp Thr 490 495 500			1603
cca gcg gca gac act gct gtt cct cag atg atg ctg gtg gta ggc gaa Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met Leu Val Val Gly Glu 505 510 515			1651
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gaa acg gtt gcg atg atc gac acc atg atg aac att ctg tac gcg ctg Glu Thr Val Ala Met Ile Asp Thr Met Met Asn Ile Leu Tyr Ala Leu 550 555 560 565			1795
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tcc gct gta gtc ggt gtt atc gcc gcg ctg tgg ccg gca gtc aag gca 2131
Ser Ala Val Val Gly Val Ile Ala Ala Leu Trp Pro Ala Val Lys Ala
665 670 675

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tca 2187

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<212> PRT

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35 40 45

Val Met Leu Ser Ala Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp
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Ala Leu Ala Ala Glu Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu
65 70 75 80

Ala Leu Val Glu Gln Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe
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Val Gln Tyr Phe Leu Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly
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Thr Phe Ile Ile Ala Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met
115 120 125

Arg Glu Phe Ala Leu Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile
130 135 140

Thr Arg Ser Val Val Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser
145 150 155 160

Ala Leu Gly Val Leu Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala
165 170 175

Val Leu Asn Asn Leu Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr
180 185 190

Pro Ser Ala Val Val Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile
195 200 205

Val Ser Ala Trp Ala Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val
210 215 220

Glu Ala Met Arg Asn Met Glu Thr Thr Thr Met Arg Ser Met Met Gly

225 230 235 240
 Arg Thr Ile Thr Gly Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala
 245 250 255
 Ile Ala Gly Ala Met Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile
 260 265 270
 Leu Val Gly Ile Gly Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe
 275 280 285
 Ser Pro Ala Leu Ser Met Pro Val Val Gly Gly Leu Gly Lys Val Ile
 290 295 300
 Gly Ala Pro Phe Gly Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys
 305 310 315 320
 Arg Asn Pro Arg Arg Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly
 325 330 335
 Ile Ala Leu Val Thr Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp
 340 345 350
 Ala Val Ser Asp Met Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu
 355 360 365
 Gln Gly Pro Thr Asn Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn
 370 375 380
 Asp Val Arg Asp Ala Glu Gly Val Ala Asp Val Val Leu Val Ser Met
 385 390 395 400
 Asn Ser Ala Ser Val Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln
 405 410 415
 Ser Val Thr Phe Val Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr
 420 425 430
 Glu Ser Ile Asp Gly Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr
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 Asn Gln Thr Phe Ala Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu
 450 455 460
 Gln Leu Glu Ser Met Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly
 465 470 475 480
 Thr Phe Thr Gly Asn Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser
 485 490 495
 Ser Leu Ala Asp Thr Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met
 500 505 510
 Leu Val Val Gly Glu Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn
 515 520 525
 Leu Glu Asp Ala Val Ala Asp Tyr Ile Val Ile Ser Val Lys Ser Ala
 530 535 540
 Thr Glu Phe Ala Gly Glu Thr Val Ala Met Ile Asp Thr Met Met Asn
 545 550 555 560

Ile Leu Tyr Ala Leu Leu Ala Leu Ser Val Ile Val Ala Ile Ile Gly
565 570 575

Ile Ile Asn Thr Leu Ala Leu Asn Val Ile Glu Arg Arg Gln Glu Ile
580 585 590

Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr Met
595 600 605

Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile Gly
610 615 620

Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met Ser
625 630 635 640

Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val Gly
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Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu Trp
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<211> 1726

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<223> FRXA02898

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Leu Val Val Asp Ser
1 5

agt ggc cgc tac aac gtc acc atc aca ggc ctg acc acc act gag acg 163
Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu Thr Thr Thr Glu Thr
10 15 20

gat tcg gcc acc gcg ctg aac ctg cag atg tcg gaa gct ggc tac ctg 211
Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser Glu Ala Gly Tyr Leu
25 30 35

gag cgt tac acc gac ggg gct acc gtc ccc agc gtc atg ctg tcg gct 259
Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser Val Met Leu Ser Ala
40 45 50

gca gat ggc acc acg cct caa gag ctt gtc gac gcc ctc gct gcc gaa 307
Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp Ala Leu Ala Ala Glu
55 60 65

ctt gga tcg aac ttt gat gta gaa acc ggc gaa gcg cta gtc gag cag 355
Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu Ala Leu Val Glu Gln

70	75	80	85	
gct aca gga atg atc acg cag gcc ttg agc ttc gtg cag tac ttc ctc				403
Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe Val Gln Tyr Phe Leu	90	95	100	
ggt gcc ttc ggt ctc att gca ctg ctg gtt ggt acc ttc atc atc gcg				451
Val Ala Phe Gly Leu Ile Ala Leu Val Gly Thr Phe Ile Ile Ala	105	110	115	
aat acc ttc tcc atg att gtg gct cag cgc atg cgt gag ttc gct ctc				499
Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met Arg Glu Phe Ala Leu	120	125	130	
ctg cga gcc ctg ggt gcg gcg cca gga cag atc act cgc tct gtg gtg				547
Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile Thr Arg Ser Val Val	135	140	145	
ctg gaa gca acc atc gtt ggc ctc ttc ggc tct gct ctt ggt gtg ctg				595
Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser Ala Leu Gly Val Leu	150	155	160	165
ggt ggt atg ggc ctc gta gcg atc att tca gct gtc ctc aat aac ctg				643
Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala Val Leu Asn Asn Leu	170	175	180	
ggc atg ccg atg gga tcc agc gtt ggc ttg act cct tct gca gtg gtt				691
Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr Pro Ser Ala Val Val	185	190	195	
acc gcg ctc gta ttg ggc acc gtt gtc acc att gtg agc gcg tgg gct				739
Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile Val Ser Ala Trp Ala	200	205	210	
ccg gct cgt cgt gca ggt gag gtt aag cct gtt gaa gcg atg cgc aac				787
Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val Glu Ala Met Arg Asn	215	220	225	
atg gaa acc acc act atg cgt tcc atg atg ggg cgc acg atc acc ggt				835
Met Glu Thr Thr Thr Met Arg Ser Met Met Gly Arg Thr Ile Thr Gly	230	235	240	245
ggc atc gtt cta gca ctc ggc atc atc ttt gcg att gcc ggt gcg atg				883
Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala Ile Ala Gly Ala Met	250	255	260	
atg act gat tct tcc acc gct act cgt tcc atc ctg gtg ggc att ggt				931
Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile Leu Val Gly Ile Gly	265	270	275	
gca ctg ttt gtc atc gtg ggt acg ttc ctc ttc tca cca gcg ctc tcc				979
Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe Ser Pro Ala Leu Ser	280	285	290	
atg cct gtg gtg ggt ggc ctg ggc aag gtt atc ggt gca ccg ttt ggc				1027
Met Pro Val Val Gly Gly Leu Gly Lys Val Ile Gly Ala Pro Phe Gly	295	300	305	
agc gtt gga agc ctt gct gcg acc aac tcc aag cga aac cct cgc cgt				1075
Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys Arg Asn Pro Arg Arg	310	315	320	325

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 Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly Ile Ala Leu Val Thr
 330 335 340

gca att ggc atg ctt tct gca acc atg aag gac gca gtc tcc gac atg 1171
 Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp Ala Val Ser Asp Met
 345 350 355

atg gcg gag cag tac acc gca gat tac atc ctg cag gga cca acc aac 1219
 Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu Gln Gly Pro Thr Asn
 360 365 370

ggt tcc atc acc atg ccg aag gaa tct gtc aat gat gtt cgc gat gct 1267
 Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn Asp Val Arg Asp Ala
 375 380 385

gag ggc gtt gcc gat gtc gtg ctc gtt tcc atg aac tct gcc tcg gtg 1315
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 390 395 400 405

aac ggt cag gct tca tac agc cag ctg ggc cag tct gta acc ttt gtc 1363
 Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln Ser Val Thr Phe Val
 410 415 420

gct gac ggc gac ctg agc aag gtc atc agc aca gaa agc att gat ggc 1411
 Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr Glu Ser Ile Asp Gly
 425 430 435

tcc ctc gac ttg agc aac cca ggt gtt gtg act aac cag acg ttt gct 1459
 Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr Asn Gln Thr Phe Ala
 440 445 450

gat gaa aac ggc tgg gca gta ggc gat act ctg cag ctt gaa tca atg 1507
 Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu Gln Leu Glu Ser Met
 455 460 465

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 Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly Thr Phe Thr Gly Asn
 470 475 480 485

gac gcc atc gga aat atg atc atc tcc gaa agt tcc ttg gct gat aca 1603
 Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser Ser Leu Ala Asp Thr
 490 495 500

cca gcg gca gac act gct gtt cct cag atg atg ctg gtg gta ggc gaa 1651
 Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met Leu Val Val Gly Glu
 505 510 515

gaa ggc ttt gat aag gaa caa ctg cgc acc aac ttg gaa gac gca gtc 1699
 Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn Leu Glu Asp Ala Val
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gct gat tac att gtc atc tct gtg aaa 1726
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<211> 542

<212> PRT

<213> Corynebacterium glutamicum

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Glu Ala Gly Tyr Leu Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser
35 40 45
Val Met Leu Ser Ala Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp
50 55 60
Ala Leu Ala Ala Glu Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu
65 70 75 80
Ala Leu Val Glu Gln Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe
85 90 95
Val Gln Tyr Phe Leu Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly
100 105 110
Thr Phe Ile Ile Ala Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met
115 120 125
Arg Glu Phe Ala Leu Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile
130 135 140
Thr Arg Ser Val Val Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser
145 150 155 160
Ala Leu Gly Val Leu Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala
165 170 175
Val Leu Asn Asn Leu Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr
180 185 190
Pro Ser Ala Val Val Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile
195 200 205
Val Ser Ala Trp Ala Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val
210 215 220
Glu Ala Met Arg Asn Met Glu Thr Thr Thr Met Arg Ser Met Met Gly
225 230 235 240
Arg Thr Ile Thr Gly Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala
245 250 255
Ile Ala Gly Ala Met Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile
260 265 270
Leu Val Gly Ile Gly Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe
275 280 285
Ser Pro Ala Leu Ser Met Pro Val Val Gly Gly Leu Gly Lys Val Ile
290 295 300
Gly Ala Pro Phe Gly Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys

305 310 315 320
 Arg Asn Pro Arg Arg Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly
 325 330 335
 Ile Ala Leu Val Thr Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp
 340 345 350
 Ala Val Ser Asp Met Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu
 355 360 365
 Gln Gly Pro Thr Asn Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn
 370 375 380
 Asp Val Arg Asp Ala Glu Gly Val Ala Asp Val Val Leu Val Ser Met
 385 390 395 400
 Asn Ser Ala Ser Val Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln
 405 410 415
 Ser Val Thr Phe Val Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr
 420 425 430
 Glu Ser Ile Asp Gly Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr
 435 440 445
 Asn Gln Thr Phe Ala Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu
 450 455 460
 Gln Leu Glu Ser Met Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly
 465 470 475 480
 Thr Phe Thr Gly Asn Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser
 485 490 495
 Ser Leu Ala Asp Thr Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met
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 <222> (1)..(387)
 <223> FRXA01071

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 ggc atc atc aac acc ctg gca ctg aat gtg atc gag cgt cgc cag gag 96

Gly Ile Ile Asn Thr Leu Ala Leu Asn Val Ile Glu Arg Arg Gln Glu
 20 25 30

atc ggt atg ctc cgc gca gtt ggc gtg aag cgc gga cag gtc cgc acc 144
 Ile Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr
 35 40 45

atg atc acc tta gaa tct gtt cag atc gcc atc tac ggt gct gtg att 192
 Met Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile
 50 55 60

ggt atc gcg att ggt ctt ggt ctg ggc tgg gcc ttt gtg aca gtg atg 240
 Gly Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met
 65 70 75 80

tca ggc gaa gga cta gac gct gcg gtt agt atc ccg tgg ggt cag gtc 288
 Ser Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val
 85 90 95

gga ctg atg ctt gtt ggt tcc gct gta gtc ggt gtt atc gcc gcg ctg 336
 Gly Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu
 100 105 110

tgg ccg gca gtc aag gca tct agg aca cca cct ttg gat gcg att acc 384
 Trp Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr
 115 120 125

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<210> 494

<211> 129

<212> PRT

<213> Corynebacterium glutamicum

<400> 494

Asn Ile Leu Tyr Ala Leu Leu Ala Leu Ser Val Ile Val Ala Ile Ile
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Ile Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr
 35 40 45

Met Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile
 50 55 60

Gly Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met
 65 70 75 80

Ser Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val
 85 90 95

Gly Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu
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Trp Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr
 115 120 125

Asp

<210> 495

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(511)

<223> RXN01075

<400> 495

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                                         Met Asp Asn Pro Val
                                         1                               5

aac atc ctc aat gag cag gaa gct ttg gag cgc ctg cag tcg gtg tct 163
Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg Leu Gln Ser Val Ser
                        10                        15                        20

ctt ggt cgc gtg gtg gtt cgt cgc agc gat gag atg gac att ttc ccg 211
Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu Met Asp Ile Phe Pro
                        25                        30                        35

gtg aac ttc att gtg gat aag ggc gca att tac att cgt aca gct gag 259
Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr Ile Arg Thr Ala Glu
                        40                        45                        50

ggc aac aag ttg ttc agc atg aat ctc aac cac gat gtg ctc ttt gaa 307
Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His Asp Val Leu Phe Glu
                        55                        60                        65

gcc gat gag gtc aag gac gga aag gcc tgg tcc gtg gtg gtt cgt gcg 355
Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser Val Val Val Arg Ala
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acc gca gag att gtg cgc aag ctg gat gag atc gct act gcc gac act 403
Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile Ala Thr Ala Asp Thr
                        90                        95                        100

ttg gag ttg aag cct tgg att cca acc ctg aag tcc aac ttt gcc cgt 451
Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys Ser Asn Phe Ala Arg
                        105                        110                        115

att gtt ccg aat gaa atc act ggg cgg gag ttc acc ctc ggc gag gag 499
Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe Thr Leu Gly Glu Glu
                        120                        125                        130

cct gag cgc tac tagctttgcc acatttcact aaa 534
Pro Glu Arg Tyr
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<213> Corynebacterium glutamicum

<400> 496

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 20 25 30

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 35 40 45

Ile Arg Thr Ala Glu Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His
 50 55 60

Asp Val Leu Phe Glu Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser
 65 70 75 80

Val Val Val Arg Ala Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile
 85 90 95

Ala Thr Ala Asp Thr Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys
 100 105 110

Ser Asn Phe Ala Arg Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe
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Thr Leu Gly Glu Glu Pro Glu Arg Tyr
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<212> DNA

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<223> FRXA01075

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 Met Asp Asn Pro Val
 1 5

aac atc ctc aat gag cag gaa gct ttg gag cgc ctg cag tcg gtg tct 163
 Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg Leu Gln Ser Val Ser
 10 15 20

ctt ggt cgc gtg gtg gtt cgt cgc agc gat gag atg gac att ttc ccg 211
 Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu Met Asp Ile Phe Pro
 25 30 35

gtg aac ttc att gtg gat aag ggc gca att tac att cgt aca gct gag 259
 Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr Ile Arg Thr Ala Glu
 40 45 50

ggc aac aag ttg ttc agc atg aat ctc aac cac gat gtg ctc ttt gaa 307
 Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His Asp Val Leu Phe Glu
 55 60 65

gcc gat gag gtc aag gac gga aag gcc tgg tcc gtg gtg gtt cgt gcg 355
 Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser Val Val Val Arg Ala
 70 75 80 85

acc gca gag att gtg cgc aag ctg gat gag atc gct act gcc gac act 403
 Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile Ala Thr Ala Asp Thr
 90 95 100

ttg gag ttg aag cct tgg att cca acc ctg aag tcc aac ttt gcc cgt 451
 Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys Ser Asn Phe Ala Arg
 105 110 115

att gtt ccg aat gaa atc act ggg cgg gag ttc acc ctc ggc gag gag 499
 Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe Thr Leu Gly Glu Glu
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cct gag cgc tac tagctttgcc acatttcact aaa 534
 Pro Glu Arg Tyr
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<210> 498

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 498

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Leu Gln Ser Val Ser Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu
 20 25 30

Met Asp Ile Phe Pro Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr
 35 40 45

Ile Arg Thr Ala Glu Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His
 50 55 60

Asp Val Leu Phe Glu Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser
 65 70 75 80

Val Val Val Arg Ala Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile
 85 90 95

Ala Thr Ala Asp Thr Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys
 100 105 110

Ser Asn Phe Ala Arg Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe
 115 120 125

Thr Leu Gly Glu Glu Pro Glu Arg Tyr
 130 135

<210> 499

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<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(1114)

<223> RXN01128

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				Met	Ser	Phe	Thr	Phe	
				1				5	

att	cgt	act	ttt	ttc	gta	ctt	ttt	ggc	atc	acg	ttg	tta	gtg	tca	tgc	163
Ile	Arg	Thr	Phe	Phe	Val	Leu	Phe	Gly	Ile	Thr	Leu	Leu	Val	Ser	Cys	
			10					15					20			

gtt	cca	gag	cct	cct	gac	tcc	tac	act	aaa	gaa	tcc	act	gtg	ctg	cgg	211
Val	Pro	Glu	Pro	Pro	Asp	Ser	Tyr	Thr	Lys	Glu	Ser	Thr	Val	Leu	Arg	
		25						30					35			

tat	cag	gtc	tct	gat	ttc	aat	cta	aac	ttc	gtg	gaa	tta	gca	ggt	gcg	259
Tyr	Gln	Val	Ser	Asp	Phe	Asn	Leu	Asn	Phe	Val	Glu	Leu	Ala	Val	Ala	
		40					45					50				

ctt	ggg	tat	ttg	aac	aac	att	gag	ctc	caa	gta	gtc	gga	tct	gta	caa	307
Leu	Gly	Tyr	Leu	Asn	Asn	Ile	Glu	Leu	Gln	Val	Val	Gly	Ser	Val	Gln	
	55					60					65					

ggc	ggc	gtt	gag	tcc	att	gaa	tcg	ctc	aaa	aag	gat	gac	att	gac	ttc	355
Gly	Gly	Val	Glu	Ser	Ile	Glu	Ser	Leu	Lys	Lys	Asp	Asp	Ile	Asp	Phe	
	70				75					80				85		

gcg	gca	gtc	ccc	ttc	att	ggc	ctt	gtt	gca	gga	gag	ata	gcc	acc	ggt	403
Ala	Ala	Val	Pro	Phe	Ile	Gly	Leu	Val	Ala	Gly	Glu	Ile	Ala	Thr	Gly	
			90						95				100			

gcg	ccc	atc	aaa	gca	gtg	gcc	gca	agt	tac	gga	att	tcc	cac	gat	tct	451
Ala	Pro	Ile	Lys	Ala	Val	Ala	Ala	Ser	Tyr	Gly	Ile	Ser	His	Asp	Ser	
			105					110					115			

tct	tct	gca	ctt	cta	gtc	ctt	aaa	gac	agt	gag	ata	cac	gaa	gtg	cac	499
Ser	Ser	Ala	Leu	Leu	Val	Leu	Lys	Asp	Ser	Glu	Ile	His	Glu	Val	His	
		120					125					130				

gat	ctc	att	ggc	aaa	aca	gtt	ggc	ata	aac	acc	ctc	ggt	gct	ctg	gga	547
Asp	Leu	Ile	Gly	Lys	Thr	Val	Gly	Ile	Asn	Thr	Leu	Gly	Ala	Leu	Gly	
	135					140					145					

tct	gcg	atg	gtt	gag	cgt	cat	cta	ttc	gac	gcc	ggt	ctc	acc	gaa	cct	595
Ser	Ala	Met	Val	Glu	Arg	His	Leu	Phe	Asp	Ala	Gly	Leu	Thr	Glu	Pro	
	150				155					160				165		

gag	atc	gtg	agc	gtc	act	caa	cgt	gca	tta	ccc	ggt	gag	tac	tta	gaa	643
Glu	Ile	Val	Ser	Val	Thr	Gln	Arg	Ala	Leu	Pro	Gly	Glu	Tyr	Leu	Glu	
				170				175						180		

caa	cgc	ctc	tac	cag	ggg	caa	gtt	gat	gca	att	tgg	gtc	acc	gat	agc	691
Gln	Arg	Leu	Tyr	Gln	Gly	Gln	Val	Asp	Ala	Ile	Trp	Val	Thr	Asp	Ser	

185	190	195	
gct aaa cac caa gcg ctt gaa act	gga gat ttt cgg atc ttg gca gag	739	
Ala Lys His Gln Ala Leu Glu Thr	Gly Asp Phe Arg Ile Leu Ala Glu		
200	205	210	
gat tca gac ctt gtg cag gaa ctc aac act	ggc tgc atg gtg gtg tcg	787	
Asp Ser Asp Leu Val Gln Glu Leu Asn Thr	Gly Cys Met Val Val Ser		
215	220	225	
caa aaa ctc atc gac gag cac ccc gca gtg gtt	gga gaa tta gtg gat	835	
Gln Lys Leu Ile Asp Glu His Pro Ala Val Val	Gly Glu Leu Val Asp		
230	235	240	
gga gta gct cag gca atc gag ttt gaa cga tcc	cac tcc cct gaa gaa	883	
Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser	His Ser Pro Glu Glu		
250	255	260	
gtg cgc gaa gtt tat ttc aac tac ctc gaa gcc	cat ggt cag agt gat	931	
Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala	His Gly Gln Ser Asp		
265	270	275	
aga ata tcc agc ttt aga tat tgg gag cat tcg	ggc atc gca acc cga	979	
Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser	Gly Ile Ala Thr Arg		
280	285	290	
ggt gga gtg ctc agt gat agg gag ttc agc atg	tgg tcc cac tgg att	1027	
Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met	Trp Ser His Trp Ile		
295	300	305	
gac cgc caa tac gac gtc ccc gat atc aat cca	gca agt att tac acc	1075	
Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro	Ala Ser Ile Tyr Thr		
310	315	320	
aac caa ttc aac cca tac cga aaa gta aac ccc	tcg cca taaaaggcaa	1124	
Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro	Ser Pro		
330	335		
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20	25	30	
Ser Thr Val Leu Arg Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val			
35	40	45	
Glu Leu Ala Val Ala Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val			
50	55	60	
Val Gly Ser Val Gln Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys			
65	70	75	
80			

Asp Asp Ile Asp Phe Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly
85 90 95
Glu Ile Ala Thr Gly Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly
100 105 110
Ile Ser His Asp Ser Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu
115 120 125
Ile His Glu Val His Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr
130 135 140
Leu Gly Ala Leu Gly Ser Ala Met Val Glu Arg His Leu Phe Asp Ala
145 150 155 160
Gly Leu Thr Glu Pro Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro
165 170 175
Gly Glu Tyr Leu Glu Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile
180 185 190
Trp Val Thr Asp Ser Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe
195 200 205
Arg Ile Leu Ala Glu Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly
210 215 220
Cys Met Val Val Ser Gln Lys Leu Ile Asp Glu His Pro Ala Val Val
225 230 235 240
Gly Glu Leu Val Asp Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser
245 250 255
His Ser Pro Glu Glu Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala
260 265 270
His Gly Gln Ser Asp Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser
275 280 285
Gly Ile Ala Thr Arg Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met
290 295 300
Trp Ser His Trp Ile Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro
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Ala Ser Ile Tyr Thr Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro
325 330 335

Ser Pro

<210> 501
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1114)

<223> FRXA01128

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Met Ser Phe Thr Phe
1 5

att cgt act ttt ttc gta ctt ttt ggc atc acg ttg tta gtg tca tgc 163
Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr Leu Leu Val Ser Cys
10 15 20

gtt cca gag cct cct gac tcc tac act aaa gaa tcc act gtg ctg cgg 211
Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu Ser Thr Val Leu Arg
25 30 35

tat cag gtc tct gat ttc aat cta aac ttc gtg gaa tta gca gtt gcg 259
Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val Glu Leu Ala Val Ala
40 45 50

ctt ggg tat ttg aac aac att gag ctc caa gta gtc gga tct gta caa 307
Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val Val Gly Ser Val Gln
55 60 65

ggc ggc gtt gag tcc att gaa tcg ctc aaa aag gat gac att gac ttc 355
Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys Asp Asp Ile Asp Phe
70 75 80 85

gcg gca gtc ccc ttc att ggc ctt gtt gca gga gag ata gcc acc ggt 403
Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly Glu Ile Ala Thr Gly
90 95 100

gcg ccc atc aaa gca gtg gcc gca agt tac gga att tcc cac gat tct 451
Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly Ile Ser His Asp Ser
105 110 115

tct tct gca ctt cta gtc ctt aaa gac agt gag ata cac gaa gtg cac 499
Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu Ile His Glu Val His
120 125 130

gat ctc att ggc aaa aca gtt ggc ata aac acc ctc ggt gct ctg gga 547
Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr Leu Gly Ala Leu Gly
135 140 145

tct gcg atg gtt gag cgt cat cta ttc gac gcc ggt ctc acc gaa cct 595
Ser Ala Met Val Glu Arg His Leu Phe Asp Ala Gly Leu Thr Glu Pro
150 155 160 165

gag atc gtg agc gtc act caa cgt gca tta ccc ggt gag tac tta gaa 643
Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro Gly Glu Tyr Leu Glu
170 175 180

caa cgc ctc tac cag ggg caa gtt gat gca att tgg gtc acc gat agc 691
Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile Trp Val Thr Asp Ser
185 190 195

gct aaa cac caa gcg ctt gaa act gga gat ttt cgg atc ttg gca gag 739
Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe Arg Ile Leu Ala Glu
200 205 210

gat tca gac ctt gtg cag gaa ctc aac act ggc tgc atg gtg gtg tcg 787
Asp Ser Asp Leu Val Gln Glu, Leu Asn Thr Gly Cys Met Val Val Ser
215 220 225

caa aaa ctc atc gac gag cac ccc gca gtg gtt gga gaa tta gtg gat 835
Gln Lys Leu Ile Asp Glu His Pro Ala Val Val Gly Glu Leu Val Asp
230 235 240 245

gga gta gct cag gca atc gag ttt gaa cga tcc cac tcc cct gaa gaa 883
Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser His Ser Pro Glu Glu
250 255 260

gtg cgc gaa gtt tat ttc aac tac ctc gaa gcc cat ggt cag agt gat 931
Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala His Gly Gln Ser Asp
265 270 275

aga ata tcc agc ttt aga tat tgg gag cat tcg ggc atc gca acc cga 979
Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser Gly Ile Ala Thr Arg
280 285 290

ggt gga gtg ctc agt gat agg gag ttc agc atg tgg tcc cac tgg att 1027
Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met Trp Ser His Trp Ile
295 300 305

gac cgc caa tac gac gtc ccc gat atc aat cca gca agt att tac acc 1075
Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro Ala Ser Ile Tyr Thr
310 315 320 325

aac caa ttc aac cca tac cga aaa gta aac ccc tcg cca taaaaggcaa 1124
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<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

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Ser Thr Val Leu Arg Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val
35 40 45

Glu Leu Ala Val Ala Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val
50 55 60

Val Gly Ser Val Gln Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys
65 70 75 80

Asp Asp Ile Asp Phe Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly
85 90 95

Glu Ile Ala Thr Gly Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly
100 105 110

Ile Ser His Asp Ser Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu
 115 120 125
 Ile His Glu Val His Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr
 130 135 140
 Leu Gly Ala Leu Gly Ser Ala Met Val Glu Arg His Leu Phe Asp Ala
 145 150 155 160
 Gly Leu Thr Glu Pro Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro
 165 170 175
 Gly Glu Tyr Leu Glu Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile
 180 185 190
 Trp Val Thr Asp Ser Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe
 195 200 205
 Arg Ile Leu Ala Glu Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly
 210 215 220
 Cys Met Val Val Ser Gln Lys Leu Ile Asp Glu His Pro Ala Val Val
 225 230 235 240
 Gly Glu Leu Val Asp Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser
 245 250 255
 His Ser Pro Glu Glu Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala
 260 265 270
 His Gly Gln Ser Asp Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser
 275 280 285
 Gly Ile Ala Thr Arg Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met
 290 295 300
 Trp Ser His Trp Ile Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro
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 Ser Pro

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 <212> DNA
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 <222> (101)..(871)
 <223> RXN01134

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Val	Pro	Tyr	Thr	Ala	Gln	Ile	Val	Pro	Leu	Ala	Val	Ile	Leu	Thr	Leu	
				10					15					20		
ctt	gat	gca	gaa	gaa	atg	gcc	acc	gca	cgt	tca	tgg	gat	cgt	ttg	aat	211
Leu	Asp	Ala	Glu	Glu	Met	Ala	Thr	Ala	Arg	Ser	Trp	Asp	Arg	Leu	Asn	
			25					30					35			
cag	tgg	ttc	tgg	agc	ggc	gtc	ttg	ggc	gag	ctt	tat	ggc	tcg	cct	gct	259
Gln	Trp	Phe	Trp	Ser	Gly	Val	Leu	Gly	Glu	Leu	Tyr	Gly	Ser	Pro	Ala	
		40				45						50				
gtg	atc	gca	cgt	tcc	ggc	cgc	gat	acc	gat	caa	gtt	gct	gcg	tgg	att	307
Val	Ile	Ala	Arg	Ser	Gly	Arg	Asp	Thr	Asp	Gln	Val	Ala	Ala	Trp	Ile	
	55					60					65					
cgt	gaa	ggc	gcc	ggc	gaa	act	gcg	gtt	gtg	cca	aag	act	att	cgc	gat	355
Arg	Glu	Gly	Ala	Gly	Glu	Thr	Ala	Val	Val	Pro	Lys	Thr	Ile	Arg	Asp	
	70				75					80					85	
acc	gtt	ttc	cac	gaa	tca	cgt	ctt	ctc	agt	gca	acc	caa	gac	acc	gga	403
Thr	Val	Phe	His	Glu	Ser	Arg	Leu	Leu	Ser	Ala	Thr	Gln	Asp	Thr	Gly	
				90					95					100		
gtg	tgg	aag	ggc	atc	ttc	gca	ctg	ctc	atg	ggc	agg	gga	gca	cgc	gac	451
Val	Trp	Lys	Gly	Ile	Phe	Ala	Leu	Leu	Met	Gly	Arg	Gly	Ala	Arg	Asp	
			105					110					115			
tgg	cgc	acc	gga	cag	cag	ttt	gat	cgc	tgg	act	ttt	gat	gag	ctg	ggc	499
Trp	Arg	Thr	Gly	Gln	Gln	Phe	Asp	Arg	Trp	Thr	Phe	Asp	Glu	Leu	Gly	
		120					125					130				
tgc	aat	ttc	cac	cag	att	ttc	ccc	acc	aaa	tgg	tgc	aag	gaa	cgc	ggc	547
Cys	Asn	Phe	His	Gln	Ile	Phe	Pro	Thr	Lys	Trp	Cys	Lys	Glu	Arg	Gly	
	135					140					145					
atc	gat	cct	gtc	ctt	acg	gaa	tca	gta	ctg	aac	cgc	acc	ccg	atg	ggc	595
Ile	Asp	Pro	Val	Leu	Thr	Glu	Ser	Val	Leu	Asn	Arg	Thr	Pro	Met	Gly	
	150				155					160				165		
cgc	cgt	acc	gaa	gta	gtc	atc	ggc	gat	acc	cct	cca	tcc	cgc	tac	ctg	643
Arg	Arg	Thr	Glu	Val	Val	Ile	Gly	Asp	Thr	Pro	Pro	Ser	Arg	Tyr	Leu	
			170					175						180		
tct	cgt	gtt	caa	tcc	aag	tcg	ctc	atg	ggc	gat	gag	gaa	ttc	gat	cag	691
Ser	Arg	Val	Gln	Ser	Lys	Ser	Leu	Met	Gly	Asp	Glu	Glu	Phe	Asp	Gln	
			185					190					195			
atg	ctg	gat	acc	cac	ctg	ctc	agc	gcg	gaa	gac	ctg	cac	agt	tcc	aac	739
Met	Leu	Asp	Thr	His	Leu	Leu	Ser	Ala	Glu	Asp	Leu	His	Ser	Ser	Asn	
		200					205					210				
acc	acg	cac	ttc	ttt	gct	tct	cga	cgc	acc	aac	ttc	atc	gac	atg	gtc	787
Thr	Thr	His	Phe	Phe	Ala	Ser	Arg	Arg	Thr	Asn	Phe	Ile	Asp	Met	Val	
	215					220					225					
gag	gat	gcc	atc	ggc	aaa	gcg	gtg	atc	agg	gac	gtc	aac	gag	tca	gat	835
Glu	Asp	Ala	Ile	Gly	Lys	Ala	Val	Ile	Arg	Asp	Val	Asn	Glu	Ser	Asp	

230

235

240

245

ctc acc ggt gga cac gat ggt ccc tcg gta cac ggg
 Leu Thr Gly Gly His Asp Gly Pro Ser Val His Gly
 250 255

871

<210> 504

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 504

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Val Ile Leu Thr Leu Leu Asp Ala Glu Glu Met Ala Thr Ala Arg Ser
 20 25 30

Trp Asp Arg Leu Asn Gln Trp Phe Trp Ser Gly Val Leu Gly Glu Leu
 35 40 45

Tyr Gly Ser Pro Ala Val Ile Ala Arg Ser Gly Arg Asp Thr Asp Gln
 50 55 60

Val Ala Ala Trp Ile Arg Glu Gly Ala Gly Glu Thr Ala Val Val Pro
 65 70 75 80

Lys Thr Ile Arg Asp Thr Val Phe His Glu Ser Arg Leu Leu Ser Ala
 85 90 95

Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu Met Gly
 100 105 110

Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg Trp Thr
 115 120 125

Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr Lys Trp
 130 135 140

Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val Leu Asn
 145 150 155 160

Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp Thr Pro
 165 170 175

Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met Gly Asp
 180 185 190

Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala Glu Asp
 195 200 205

Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg Thr Asn
 210 215 220

Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile Arg Asp
 225 230 235 240

Val Asn Glu Ser Asp Leu Thr Gly Gly His Asp Gly Pro Ser Val His
 245 250 255

Gly

<210> 505
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 Ser Ala Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu
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 atg ggc agg gga gca cgc gac tgg cgc acc gga cag cag ttt gat cgc 96
 Met Gly Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg
 20 25 30

 tgg act ttt gat gag ctg ggt tgc aat ttc cac cag att ttc ccc acc 144
 Trp Thr Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr
 35 40 45

 aaa tgg tgc aag gaa cgc ggc atc gat cct gtc ctt acg gaa tca gta 192
 Lys Trp Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val
 50 55 60

 ctg aac cgc acc ccg atg ggt cgc cgt acc gaa gta gtc atc ggc gat 240
 Leu Asn Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp
 65 70 75 80

 acc cct cca tcc cgc tac ctg tct cgt gtt caa tcc aag tcg ctc atg 288
 Thr Pro Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met
 85 90 95

 ggt gat gag gaa ttc gat cag atg ctg gat acc cac ctg ctc agc gcg 336
 Gly Asp Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala
 100 105 110

 gaa gac ctg cac agt tcc aac acc acg cac ttc ttt gct tct cga cgc 384
 Glu Asp Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg
 115 120 125

 acc aac ttc atc gac atg gtc gag gat gcc atc ggt aaa gcg gtg atc 432
 Thr Asn Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile
 130 135 140

 agg gac gtc aac gag tca gat ctc acc 459
 Arg Asp Val Asn Glu Ser Asp Leu Thr
 145 150

<210> 506
 <211> 153
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 506

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 Met Gly Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg
 20 25 30
 Trp Thr Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr
 35 40 45
 Lys Trp Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val
 50 55 60
 Leu Asn Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp
 65 70 75 80
 Thr Pro Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met
 85 90 95
 Gly Asp Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala
 100 105 110
 Glu Asp Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg
 115 120 125
 Thr Asn Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile
 130 135 140
 Arg Asp Val Asn Glu Ser Asp Leu Thr
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<210> 507

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1033)

<223> RXN01140

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 tataaccact gttcttcgtg gttttccagt aggtgtgctg atg gca cta gac acc 115
 Met Ala Leu Asp Thr
 1 5
 cgc ggc gag gaa atg cgt ttc cgg cca cgc gcg ctg tcc ggc gcc cca 163
 Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala Leu Ser Gly Ala Pro
 10 15 20
 gat acg ggc aag gat cca ggt ctt ttg ctt ctc gac gga caa cag cgc 211
 Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu Asp Gly Gln Gln Arg
 25 30 35
 ctc acc acc ctt tat cat tgc ttc agt ggc gat ggc tat gta aat acg 259
 Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp Gly Tyr Val Asn Thr
 40 45 50

gtg gac ttc cga tca aag aaa gtg acc cgg aag ttt tat att gat gtt Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys Phe Tyr Ile Asp Val 55 60 65	307
gct aag gct gtt gaa tct ccg gtc atg tcc gat gag gct att ttt tca Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp Glu Ala Ile Phe Ser 70 75 80 85	355
gtc gac gaa acc ggc aaa atc atc tcc cac ttc ggt cca gtg atc gac Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe Gly Pro Val Ile Asp 90 95 100	403
ggc ggc atc acc gat tta gaa aca gca ctt gct cat ggt tgc ctt cca Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala His Gly Cys Leu Pro 105 110 115	451
gtt tct gtg ctg ctg gat gat aac ggc act gat ttc ctc ttt gac ctc Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp Phe Leu Phe Asp Leu 120 125 130	499
gcc gat atg gca gga gaa ggc gct cgc gaa cac gcg aag cgc ttc caa Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His Ala Lys Arg Phe Gln 135 140 145	547
tca caa atc gtt aag acc tta gtt agt tac gac atc cca atg atc cga Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp Ile Pro Met Ile Arg 150 155 160 165	595
ctg gat cgt gaa acc gcc aag ggt gga att ggt tcc atc ttt gct cag Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly Ser Ile Phe Ala Gln 170 175 180	643
gcc aat agc tct ggc ttg cag atg gat gtc ttt gat ttg ctc acc gcg Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe Asp Leu Leu Thr Ala 185 190 195	691
gtg ttc gca gcc gat gaa tcg gtg gag acc gaa ttc tca ctg cgt gat Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu Phe Ser Leu Arg Asp 200 205 210	739
gac tgg gtg cgg gtt gaa cga aac ctt cgc caa cac tcc gca ctt gat Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln His Ser Ala Leu Asp 215 220 225	787
ggc atc ggc agc acg gag ttc ctc acc gca gta gcc ctg ttg gtc agt Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val Ala Leu Leu Val Ser 230 235 240 245	835
gcc cgc aag gga cat gcg tct ggt tac cgt gaa gat atc ttg aac ttg Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu Asp Ile Leu Asn Leu 250 255 260	883
acg ctg gct gaa tac att cct gct gcc gat gaa atg atc aag ggc ttc Thr Leu Ala Glu Tyr Ile Pro Ala Ala Asp Glu Met Ile Lys Gly Phe 265 270 275	931
gac gag gcg gct gaa ttc ctg cgt cag cga tgc att ttt gag tct cga Asp Glu Ala Ala Glu Phe Leu Arg Gln Arg Cys Ile Phe Glu Ser Arg 280 285 290	979
cca ggt tcc ata cac cgc gca gat tgt tcc act ggc cgt gat cct cac	1027

Pro Gly Ser Ile His Arg Ala Asp Cys Ser Thr Gly Arg Asp Pro His
 295 300 305

cct gct tgatgcagaa gaaatggcca ccg

1056

Pro Ala

310

<210> 508

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Met Ala Leu Asp Thr Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala
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 20 25 30

Asp Gly Gln Gln Arg Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp
 35 40 45

Gly Tyr Val Asn Thr Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys
 50 55 60

Phe Tyr Ile Asp Val Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp
 65 70 75 80

Glu Ala Ile Phe Ser Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe
 85 90 95

Gly Pro Val Ile Asp Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala
 100 105 110

His Gly Cys Leu Pro Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp
 115 120 125

Phe Leu Phe Asp Leu Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His
 130 135 140

Ala Lys Arg Phe Gln Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp
 145 150 155 160

Ile Pro Met Ile Arg Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly
 165 170 175

Ser Ile Phe Ala Gln Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe
 180 185 190

Asp Leu Leu Thr Ala Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu
 195 200 205

Phe Ser Leu Arg Asp Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln
 210 215 220

His Ser Ala Leu Asp Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val
 225 230 235 240

Ala Leu Leu Val Ser Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu
 245 250 255

Asp Ile Leu Asn Leu Thr Leu Ala Glu Tyr Ile Pro Ala Ala Asp Glu
 260 265 270

Met Ile Lys Gly Phe Asp Glu Ala Ala Glu Phe Leu Arg Gln Arg Cys
 275 280 285

Ile Phe Glu Ser Arg Pro Gly Ser Ile His Arg Ala Asp Cys Ser Thr
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Gly Arg Asp Pro His Pro Ala
 305 310

<210> 509
 <211> 886
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(886)
 <223> FRXA01140

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 Met Ala Leu Asp Thr
 1 5

cgc ggc gag gaa atg cgt ttc cgg cca cgc gcg ctg tcc ggc gcc cca 163
 Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala Leu Ser Gly Ala Pro
 10 15 20

gat acg ggc aag gat cca ggt ctt ttg ctt ctc gac gga caa cag cgc 211
 Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu Asp Gly Gln Gln Arg
 25 30 35

ctc acc acc ctt tat cat tgc ttc agt ggc gat ggc tat gta aat acg 259
 Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp Gly Tyr Val Asn Thr
 40 45 50

gtg gac ttc cga tca aag aaa gtg acc cgg aag ttt tat att gat gtt 307
 Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys Phe Tyr Ile Asp Val
 55 60 65

gct aag gct gtt gaa tct ccg gtc atg tcc gat gag gct att ttt tca 355
 Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp Glu Ala Ile Phe Ser
 70 75 80 85

gtc gac gaa acc ggc aaa atc atc tcc cac ttc ggt cca gtg atc gac 403
 Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe Gly Pro Val Ile Asp
 90 95 100

ggc ggc atc acc gat tta gaa aca gca ctt gct cat ggt tgc ctt cca 451
 Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala His Gly Cys Leu Pro
 105 110 115

gtt tct gtg ctg ctg gat gat aac ggc act gat ttc ctc ttt gac ctc 499
 Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp Phe Leu Phe Asp Leu

120	125	130	
gcc gat atg gca gga gaa ggc gct cgc gaa cac gcg aag cgc ttc caa			547
Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His Ala Lys Arg Phe Gln			
135	140	145	
tca caa atc gtt aag acc tta gtt agt tac gac atc cca atg atc cga			595
Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp Ile Pro Met Ile Arg			
150	155	160	165
ctg gat cgt gaa acc gcc aag ggt gga att ggt tcc atc ttt gct cag			643
Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly Ser Ile Phe Ala Gln			
	170	175	180
gcc aat agc tct ggc ttg cag atg gat gtc ttt gat ttg ctc acc gcg			691
Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe Asp Leu Leu Thr Ala			
	185	190	195
gtg ttc gca gcc gat gaa tcg gtg gag acc gaa ttc tca ctg cgt gat			739
Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu Phe Ser Leu Arg Asp			
	200	205	210
gac tgg gtg cgg gtt gaa cga aac ctt cgc caa cac tcc gca ctt gat			787
Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln His Ser Ala Leu Asp			
	215	220	225
ggc atc ggc agc acg gag ttc ctc acc gca gta gcc ctg ttg gtc agt			835
Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val Ala Leu Leu Val Ser			
230	235	240	245
gcc cgc aag gga cat gcg tct ggt tac cgt gaa gat atc ttg aac ttg			883
Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu Asp Ile Leu Asn Leu			
	250	255	260
acg			886
Thr			

<210> 510

<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 510

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Leu	Ser	Gly	Ala	Pro	Asp	Thr	Gly	Lys	Asp	Pro	Gly	Leu	Leu	Leu	Leu
		20						25				30			

Asp	Gly	Gln	Gln	Arg	Leu	Thr	Thr	Leu	Tyr	His	Cys	Phe	Ser	Gly	Asp
		35					40					45			

Gly	Tyr	Val	Asn	Thr	Val	Asp	Phe	Arg	Ser	Lys	Lys	Val	Thr	Arg	Lys
	50					55					60				

Phe	Tyr	Ile	Asp	Val	Ala	Lys	Ala	Val	Glu	Ser	Pro	Val	Met	Ser	Asp
65					70					75					80

Glu	Ala	Ile	Phe	Ser	Val	Asp	Glu	Thr	Gly	Lys	Ile	Ile	Ser	His	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85	90	95
Gly Pro Val Ile Asp Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala 100 105 110		
His Gly Cys Leu Pro Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp 115 120 125		
Phe Leu Phe Asp Leu Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His 130 135 140		
Ala Lys Arg Phe Gln Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp 145 150 155 160		
Ile Pro Met Ile Arg Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly 165 170 175		
Ser Ile Phe Ala Gln Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe 180 185 190		
Asp Leu Leu Thr Ala Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu 195 200 205		
Phe Ser Leu Arg Asp Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln 210 215 220		
His Ser Ala Leu Asp Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val 225 230 235 240		
Ala Leu Leu Val Ser Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu 245 250 255		
Asp Ile Leu Asn Leu Thr 260		

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 <212> DNA
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<220>
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 <222> (101)..(700)
 <223> RXN01148

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 Met Thr Ser Pro Val
 1 5
 gaa aac gtt aag aaa aag cca cgc cca ttg gcg ctg tca ccg tcg cgc 163
 Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala Leu Ser Pro Ser Arg
 10 15 20
 gcc ggg gat tac cag cag tgt ccc ctg ttg tat cgc ttc cgc gcg att 211
 Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr Arg Phe Arg Ala Ile
 25 30 35

gat cgc ctg cca gag cct aag acc gtc gcc cag gtc aaa ggc acg ttg 259
Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln Val Lys Gly Thr Leu
40 45 50

gtg cac gct gtg ttg gaa tat atg cac aag ttg ccg cgt gaa gaa cgc 307
Val His Ala Val Leu Glu Tyr Met His Lys Leu Pro Arg Glu Glu Arg
55 60 65

gaa tat cca gcc atg gtg aag caa ctc aag ccc acc tgg gcg cag atg 355
Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro Thr Trp Ala Gln Met
70 75 80 85

tgt gaa gaa gac gca gag ctc aaa gag ctt gtt cca gaa gat gag ctt 403
Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val Pro Glu Asp Glu Leu
90 95 100

tat gat ttc ctc gtg gat tcc cgc acc ctg ctg cgt ggc tac ttt gaa 451
Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu Arg Gly Tyr Phe Glu
105 110 115

atg gaa aat cct caa ggt ttc gac gcc acc gaa tgc gaa atg tac gtg 499
Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu Cys Glu Met Tyr Val
120 125 130

gac act gtg ctg ccc aac ggc gtt cct gtt cgt ggt ttt atc gac cgt 547
Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg Gly Phe Ile Asp Arg
135 140 145

gtg gat acc gcc cca ccg gcc aag tcc gag tta tcg act aca aga ctg 595
Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu Ser Thr Thr Arg Leu
150 155 160 165

gca aga aac caa agc cgc agt gga gcc agc aag cgc agt tcc aga tgc 643
Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys Arg Ser Ser Arg Cys
170 175 180

tgt tct atg cac tgg tct act ggc gca tgt tca atg aaa tcc cag ctc 691
Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser Met Lys Ser Gln Leu
185 190 195

agc ttc gtt taatgtacct caaagtcaac gat 723
Ser Phe Val
200

<210> 512

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 512

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Leu Ser Pro Ser Arg Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr
20 25 30

Arg Phe Arg Ala Ile Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln
35 40 45

Val Lys Gly Thr Leu Val His Ala Val Leu Glu Tyr Met His Lys Leu

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<div style="display: flex; justify-content: space-between;"> <div> Met Thr Ser Pro Val 1 5 </div> </div>																		
gaa aac gtt aag aaa aag cca cgc cca ttg gcg ctg tca ccg tcg cgc																		163
<div style="display: flex; justify-content: space-between;"> <div>Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala Leu Ser Pro Ser Arg</div> <div>10 15 20</div> </div>																		
gcc ggg gat tac cag cag tgt ccc ctg ttg tat cgc ttc cgc gcg att																		211
<div style="display: flex; justify-content: space-between;"> <div>Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr Arg Phe Arg Ala Ile</div> <div>25 30 35</div> </div>																		
gat cgc ctg cca gag cct aag acc gtc gcc cag gtc aaa ggc acg ttg																		259
<div style="display: flex; justify-content: space-between;"> <div>Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln Val Lys Gly Thr Leu</div> <div>40 45 50</div> </div>																		
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Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro Thr Trp Ala Gln Met			
70	75	80	85
tgt gaa gaa gac gca gag ctc aaa gag ctt gtt cca gaa gat gag ctt			403
Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val Pro Glu Asp Glu Leu			
	90	95	100
tat gat ttc ctc gtg gat tcc cgc acc ctg ctg cgt ggc tac ttt gaa			451
Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu Arg Gly Tyr Phe Glu			
	105	110	115
atg gaa aat cct caa ggt ttc gac gcc acc gaa tgc gaa atg tac gtg			499
Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu Cys Glu Met Tyr Val			
	120	125	130
gac act gtg ctg ccc aac ggc gtt cct gtt cgt ggt ttt atc gac cgt			547
Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg Gly Phe Ile Asp Arg			
	135	140	145
gtg gat acc gcc cca ccg gcc aag tcc gag tta tcg act aca aga ctg			595
Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu Ser Thr Thr Arg Leu			
	150	155	160
gca aga aac caa agc cgc agt gga gcc agc aag cgc agt tcc aga tgc			643
Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys Arg Ser Ser Arg Cys			
	170	175	180
tgt tct atg cac tgg tct act ggc gca tgt tca atg aaa tcc cag ctc			691
Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser Met Lys Ser Gln Leu			
	185	190	195
agc ttc gtt taatgtacct caaagtcaac gat			723
Ser Phe Val			
200			

<210> 514

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

Met Thr Ser Pro Val Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala	
1	15

Leu Ser Pro Ser Arg Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr	
20	30

Arg Phe Arg Ala Ile Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln	
35	45

Val Lys Gly Thr Leu Val His Ala Val Leu Glu Tyr Met His Lys Leu	
50	60

Pro Arg Glu Glu Arg Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro	
65	75

Thr Trp Ala Gln Met Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val	
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<400> 515																
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Pro	Phe	Leu	Ser	Pro	Ile	Val	Thr	Ser	Thr	His	Ala	Val	Val	Ala	Tyr	
1				5		10						15				
tcc	acc	gcg	cgt	gga	ttt	ggg	gag	cac	cgg	gtg	cgt	tgg	gac	tat	gcg	96
Ser	Thr	Ala	Arg	Gly	Phe	Gly	Glu	His	Arg	Val	Arg	Trp	Asp	Tyr	Ala	
20				25						30						
caa	gag	tcc	cca	ctg	cgc	gat	act	cgt	ggc	ttt	gat	ctg	cgc	cga	tac	144
Gln	Glu	Ser	Pro	Leu	Arg	Asp	Thr	Arg	Gly	Phe	Asp	Leu	Arg	Arg	Tyr	
35				40						45						
cac	cag	gcc	cct	gtg	gtg	gat	ccg	cac	gcc	att	ggg	gtg	gcc	aac	gtg	192
His	Gln	Ala	Pro	Val	Val	Asp	Pro	His	Ala	Ile	Gly	Val	Ala	Asn	Val	
50				55						60						
ttt	gtg	ccc	aat	ggg	gcc	agg	ttt	tat	gtc	gat	cac	gcg	cac	ccg	gaa	240
Phe	Val	Pro	Asn	Gly	Ala	Arg	Phe	Tyr	Val	Asp	His	Ala	His	Pro	Glu	
65				70						75				80		
tac	tcc	tcc	cca	gag	gtc	acc	aat	gcg	tgg	gat	gcc	atg	gtt	tac	gac	288
Tyr	Ser	Ser	Pro	Glu	Val	Thr	Asn	Ala	Trp	Asp	Ala	Met	Val	Tyr	Asp	
85				90						95						
gcc	gct	ggg	gac	cac	atc	ctt	atg	cag	gcc	gtc	tct	gat	gtt	gcg	agt	336
Ala	Ala	Gly	Asp	His	Ile	Leu	Met	Gln	Ala	Val	Ser	Asp	Val	Ala	Ser	

100	105	110	
ttc acc agc cag aat agg tct gtg ttg gac ggc cat gat ccg tgt cca			384
Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro			
115	120	125	
gct ttg aaa atc tac aaa aac aat gtc gac ggt aag ggt gct agc tac			432
Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr			
130	135	140	
ggg ttc cac gag aat tac ctc tac tca cgt gag acg gat ttt gat gtg			480
Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val			
145	150	155	160
ctg gct cag gca ttg atc cca ttt ttt gtg tgc cgg cag gtc atc atc			528
Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile			
165	170	175	
ggt gcc gga cgt gtg			543
Gly Ala Gly Arg Val			
180			

<210> 516

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 516

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Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala			
20	25	30	
Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr			
35	40	45	
His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val			
50	55	60	
Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu			
65	70	75	80
Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp			
85	90	95	
Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser			
100	105	110	
Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro			
115	120	125	
Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr			
130	135	140	
Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val			
145	150	155	160
Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile			
165	170	175	

<400> 517																	
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Pro	Phe	Leu	Ser	Pro	Ile	Val	Thr	Ser	Thr	His	Ala	Val	Val	Ala	Tyr		
1				5				10				15					
tcc	acc	gcg	cgt	gga	ttt	ggg	gag	cac	cgg	gtg	cgt	tgg	gac	tat	gcg	96	
Ser	Thr	Ala	Arg	Gly	Phe	Gly	Glu	His	Arg	Val	Arg	Trp	Asp	Tyr	Ala		
20				25				30									
caa	gag	tcc	cca	ctg	cgc	gat	act	cgt	ggc	ttt	gat	ctg	cgc	cga	tac	144	
Gln	Glu	Ser	Pro	Leu	Arg	Asp	Thr	Arg	Gly	Phe	Asp	Leu	Arg	Arg	Tyr		
35				40				45									
cac	cag	gcc	cct	gtg	gtg	gat	ccg	cac	gcc	att	ggg	gtg	gcc	aac	gtg	192	
His	Gln	Ala	Pro	Val	Val	Asp	Pro	His	Ala	Ile	Gly	Val	Ala	Asn	Val		
50				55				60									
ttt	gtg	ccc	aat	ggg	gcc	agg	ttt	tat	gtc	gat	cac	gcg	cac	ccg	gaa	240	
Phe	Val	Pro	Asn	Gly	Ala	Arg	Phe	Tyr	Val	Asp	His	Ala	His	Pro	Glu		
65				70				75				80					
tac	tcc	tcc	cca	gag	gtc	acc	aat	gcg	tgg	gat	gcc	atg	gtt	tac	gac	288	
Tyr	Ser	Ser	Pro	Glu	Val	Thr	Asn	Ala	Trp	Asp	Ala	Met	Val	Tyr	Asp		
85				90				95									
gcc	gct	ggg	gac	cac	atc	ctt	atg	cag	gcc	gtc	tct	gat	gtt	gcg	agt	336	
Ala	Ala	Gly	Asp	His	Ile	Leu	Met	Gln	Ala	Val	Ser	Asp	Val	Ala	Ser		
100				105				110									
ttc	acc	agc	cag	aat	agg	tct	gtg	ttg	gac	ggc	cat	gat	ccg	tgt	cca	384	
Phe	Thr	Ser	Gln	Asn	Arg	Ser	Val	Leu	Asp	Gly	His	Asp	Pro	Cys	Pro		
115				120				125									
gct	ttg	aaa	atc	tac	aaa	aac	aat	gtc	gac	ggg	aag	ggg	gct	agc	tac	432	
Ala	Leu	Lys	Ile	Tyr	Lys	Asn	Asn	Val	Asp	Gly	Lys	Gly	Ala	Ser	Tyr		
130				135				140									
ggg	ttc	cac	gag	aat	tac	ctc	tac	tca	cgt	gag	acg	gat	ttt	gat	gtg	480	
Gly	Phe	His	Glu	Asn	Tyr	Leu	Tyr	Ser	Arg	Glu	Thr	Asp	Phe	Asp	Val		
145				150				155				160					
ctg	gct	cag	gca	ttg	atc	cca	ttt	ttt	gtg	tgc	cgg	cag	gtc	atc	atc	528	
Leu	Ala	Gln	Ala	Leu	Ile	Pro	Phe	Phe	Val	Cys	Arg	Gln	Val	Ile	Ile		
165				170				175									
ggt	gcc	gga	cgt	gtg												543	

Gly Ala Gly Arg Val
180

<210> 518
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 518
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Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
20 25 30
Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
35 40 45
His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
50 55 60
Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
65 70 75 80
Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
85 90 95
Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
100 105 110
Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
115 120 125
Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
130 135 140
Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145 150 155 160
Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
165 170 175
Gly Ala Gly Arg Val
180

<210> 519
<211> 677
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (39)..(677)
<223> RXN01154

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Leu Ser Lys Lys Ile Ser
1 5

ctg gaa acc aca ctc aac cgc ggc att atc aac acc cgc gat gaa cca 104
 Leu Glu Thr Thr Leu Asn Arg Gly Ile Ile Asn Thr Arg Asp Glu Pro
 10 15 20

cac acc gac gct gat cac tgg ggt cgc ctg cac gtg atc atc ggc gat 152
 His Thr Asp Ala Asp His Trp Gly Arg Leu His Val Ile Ile Gly Asp
 25 30 35

gcc aac atg tcg cag act gcg aat ttc ctc aaa ttc ggc atg acc tcc 200
 Ala Asn Met Ser Gln Thr Ala Asn Phe Leu Lys Phe Gly Met Thr Ser
 40 45 50

cta gtg ctg gat gcc att gag gct ggg gtg gat ttc tct gaa ctc aag 248
 Leu Val Leu Asp Ala Ile Glu Ala Gly Val Asp Phe Ser Glu Leu Lys
 55 60 65 70

ctg aag aac gca gtg agt gaa gta gca aag gtc tcc cat gat ctt tcc 296
 Leu Lys Asn Ala Val Ser Glu Val Ala Lys Val Ser His Asp Leu Ser
 75 80 85

ctt acc cac cag ctg cga ttg gcg gat ggt tca gag ctc acc gct att 344
 Leu Thr His Gln Leu Arg Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile
 90 95 100

gat att ctg cgc cgc tat ttg gac aag gtg cag ccg ttt gca gaa acc 392
 Asp Ile Leu Arg Arg Tyr Leu Asp Lys Val Gln Pro Phe Ala Glu Thr
 105 110 115

cca gtg gaa cag cgt gtc act gcg ctg tgg ggt gaa gtg ctg ggg ctc 440
 Pro Val Glu Gln Arg Val Thr Ala Leu Trp Gly Glu Val Leu Gly Leu
 120 125 130

ctg gag aat gat ctg ctc tcc acc agc cat ctc ctt gat tgg act gca 488
 Leu Glu Asn Asp Leu Leu Ser Thr Ser His Leu Leu Asp Trp Thr Ala
 135 140 145 150

aaa ctt gcc ctg atc aag tct ttt gag gcg cgt ggg ctg tcc att aac 536
 Lys Leu Ala Leu Ile Lys Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn
 155 160 165

gat ccc aag atg tac ctc att gac ctg cag tac agc gat att gat cca 584
 Asp Pro Lys Met Tyr Leu Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro
 170 175 180

cag aag agt ctg tat cac gca ctg gta tcc aag ggg cgg atg aaa aca 632
 Gln Lys Ser Leu Tyr His Ala Leu Val Ser Lys Gly Arg Met Lys Thr
 185 190 195

ctg tgc agt gcg cag gac att gca gat gca gcg gcc act tca ccg 677
 Leu Cys Ser Ala Gln Asp Ile Ala Asp Ala Ala Ala Thr Ser Pro
 200 205 210

<210> 520

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 520

Leu Ser Lys Lys Ile Ser Leu Glu Thr Thr Leu Asn Arg Gly Ile Ile

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 Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His Trp Gly Arg Leu
 20 25 30
 His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr Ala Asn Phe Leu
 35 40 45
 Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile Glu Ala Gly Val
 50 55 60
 Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser Glu Val Ala Lys
 65 70 75 80
 Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg Leu Ala Asp Gly
 85 90 95
 Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr Leu Asp Lys Val
 100 105 110
 Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val Thr Ala Leu Trp
 115 120 125
 Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu Ser Thr Ser His
 130 135 140
 Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys Ser Phe Glu Ala
 145 150 155 160
 Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu Ile Asp Leu Gln
 165 170 175
 Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His Ala Leu Val Ser
 180 185 190
 Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp Ile Ala Asp Ala
 195 200 205
 Ala Ala Thr Ser Pro
 210

<210> 521
 <211> 603
 <212> DNA
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<220>
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 <222> (1)..(603)
 <223> FRXA01154

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 Glu Gly Ile Ile Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His
 1 5 10 15
 tgg ggt cgc ctg cac gtg atc atc ggc gat gcc aac atg tcg cag act 96
 Trp Gly Arg Leu His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr
 20 25 30

gcg aat ttc ctc aaa ttc ggc atg acc tcc cta gtg ctg gat gcc att 144
Ala Asn Phe Leu Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile
35 40 45

gag gct ggg gtg gat ttc tct gaa ctc aag ctg aag aac gca gtg agt 192
Glu Ala Gly Val Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser
50 55 60

gaa gta gca aag gtc tcc cat gat ctt tcc ctt acc cac cag ctg cga 240
Glu Val Ala Lys Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg
65 70 75 80

ttg gcg gat ggt tca gag ctc acc gct att gat att ctg cgc cgc tat 288
Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr
85 90 95

ttg gac aag gtg cag ccg ttt gca gaa acc cca gtg gaa cag cgt gtc 336
Leu Asp Lys Val Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val
100 105 110

act gcg ctg tgg ggt gaa gtg ctg ggg ctc ctg gag aat gat ctg ctc 384
Thr Ala Leu Trp Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu
115 120 125

tcc acc agc cat ctc ctt gat tgg act gca aaa ctt gcc ctg atc aag 432
Ser Thr Ser His Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys
130 135 140

tct ttt gag gcg cgt ggg ctg tcc att aac gat ccc aag atg tac ctc 480
Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu
145 150 155 160

att gac ctg cag tac agc gat att gat cca cag aag agt ctg tat cac 528
Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His
165 170 175

gca ctg gta tcc aag ggg cgg atg aaa aca ctg tgc agt gcg cag gac 576
Ala Leu Val Ser Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp
180 185 190

att gca gat gca gcg gcc act tca ccg 603
Ile Ala Asp Ala Ala Ala Thr Ser Pro
195 200

<210> 522

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 522

Glu Gly Ile Ile Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His
1 5 10 15

Trp Gly Arg Leu His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr
20 25 30

Ala Asn Phe Leu Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile
35 40 45

Glu Ala Gly Val Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser

50		55		60
Glu Val Ala Lys Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg				
65		70	75	80
Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr				
	85		90	95
Leu Asp Lys Val Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val				
	100		105	110
Thr Ala Leu Trp Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu				
	115		120	125
Ser Thr Ser His Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys				
	130		135	140
Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu				
	145		150	155
Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His				
	165		170	175
Ala Leu Val Ser Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp				
	180		185	190
Ile Ala Asp Ala Ala Ala Thr Ser Pro				
	195		200	

<210> 523

<211> 1570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1570)

<223> RXN01155

<400> 523

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	Val Glu Ser Ala Leu	
	1	5

acc cgc agg atc atg ggc att gaa acg gag tat ggc ctc acc ttt gtt	163
Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr Gly Leu Thr Phe Val	
	10 15 20

gat ggt gat tcc aaa aag ctt cgc cca gat gag ata gct cga agg atg	211
Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu Ile Ala Arg Arg Met	
	25 30 35

ttt cgt ccc atc gtg gag aaa tat tcc agc tct aat atc ttc ata ccc	259
Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser Asn Ile Phe Ile Pro	
	40 45 50

aat ggt tcc cgg ttg tat ctt gat gtg ggt tcc cac ccg gag tac gcc	307
Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser His Pro Glu Tyr Ala	

55	60	65	
acc gcc gag tgt gat aat ttg acc cag ctg atc aat ttt gaa aaa gct Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile Asn Phe Glu Lys Ala 70 75 80 85			355
ggc gat gtt att gca gat cgc atg gct gta gat gcc gaa gag tcg ctg Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp Ala Glu Glu Ser Leu 90 95 100			403
gcg aaa gaa gac att gct ggg cag gtg tac ctg ttt aaa aac aat gtc Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu Phe Lys Asn Asn Val 105 110 115			451
gat tcc gtg ggc aat tct tat ggc tgc cac gaa aac tac ctt gtg ggt Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu Asn Tyr Leu Val Gly 120 125 130			499
cgc tcc atg ccg ttg aag gcg ttg ggt aaa agg ctg atg ccg ttt ctg Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg Leu Met Pro Phe Leu 135 140 145			547
att acc cgc cag ctc atc tgc ggc gcc ggc agg atc cat cac ccc aat Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg Ile His His Pro Asn 150 155 160 165			595
cct ttg gat aaa ggc gaa tcc ttc ccc ttg ggc tac tgc ata tcc cag Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly Tyr Cys Ile Ser Gln 170 175 180			643
cgc tct gac cac gtg tgg gag ggc gta tca agt gcc acc act aga tca Arg Ser Asp His Val Trp Glu Gly Val Ser Ser Ala Thr Thr Arg Ser 185 190 195			691
cgc ccc att atc aac acc cgt gat gag cca cat gcg gat tcc cat tct Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His Ala Asp Ser His Ser 200 205 210			739
tac cgc agg ctg cac gtg att gtg ggt gat gcc aac atg gca gag ccc Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala Asn Met Ala Glu Pro 215 220 225			787
agc atc gcg ttg aag gtc ggc tcc acg ttg ctg gtt ctg gaa atg att Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu Val Leu Glu Met Ile 230 235 240 245			835
gag gca gat ttc ggt ttg ccc agc tta gag ctt gcc aat gat att gcc Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu Ala Asn Asp Ile Ala 250 255 260			883
tca att agg gaa atc tcc cgc gat gca aca gga tcc aca ctg ttg tcc Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly Ser Thr Leu Leu Ser 265 270 275			931
ctg aaa gat ggc acc acc atg act gcc ttg cag atc cag cag gtg gtc Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln Ile Gln Gln Val Val 280 285 290			979
ttt gag cat gcc tcg aag tgg ttg gag cag cgc ccc gaa cca gaa ttt Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg Pro Glu Pro Glu Phe 295 300 305			1027

tct ggc acc tcc aac aca gag atg gcc cgc gtg ctg gat ctg tgg ggt 1075
 Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val Leu Asp Leu Trp Gly
 310 315 320 325
 cgc atg ttg aaa gcg att gag tcc ggt gat ttc agc gaa gtg gat aca 1123
 Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe Ser Glu Val Asp Thr
 330 335 340
 gaa att gac tgg gtg atc aaa aag aag ctc att gat cgt ttc att cag 1171
 Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile Asp Arg Phe Ile Gln
 345 350 355
 cgc ggc aac ctt ggg ttg gat gat cca aaa ctt gcc caa gtg gac ttg 1219
 Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu Ala Gln Val Asp Leu
 360 365 370
 act tat cac gat att agg cca ggt aga ggc cta ttt agc gtg ctg caa 1267
 Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu Phe Ser Val Leu Gln
 375 380 385
 agc cgc ggc atg atc aaa cgg tgg act act gat gag gcg att tta gct 1315
 Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp Glu Ala Ile Leu Ala
 390 395 400 405
 gcg gtg gat acc gct cct gat aca aca cgt gct cat ttg cgc ggg cga 1363
 Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala His Leu Arg Gly Arg
 410 415 420
 atc ctt aaa gcg gcg gat act ctg gga gta cct gtg act gtc gat tgg 1411
 Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro Val Thr Val Asp Trp
 425 430 435
 atg cgt cac aag gtc aac cga ccg gag cca caa tcg gtg gaa ttg ggg 1459
 Met Arg His Lys Val Asn Arg Pro Glu Pro Gln Ser Val Glu Leu Gly
 440 445 450
 gat cct ttt tcc ctt tta aat cct caa caa cca gcc caa gaa act gct 1507
 Asp Pro Phe Ser Leu Leu Asn Pro Gln Gln Pro Ala Gln Glu Thr Ala
 455 460 465
 ttg agc att ctt ctc cta ggc gga acc tct tac att gcc ggt gag att 1555
 Leu Ser Ile Leu Leu Leu Gly Gly Thr Ser Tyr Ile Ala Gly Glu Ile
 470 475 480 485
 gcc acg ttg acg ttt 1570
 Ala Thr Leu Thr Phe
 490

<210> 524

<211> 490

<212> PRT

<213> Corynebacterium glutamicum

<400> 524

Val Glu Ser Ala Leu Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr
 1 5 10 15

Gly Leu Thr Phe Val Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu
 20 25 30

Ile Ala Arg Arg Met Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser
 35 40 45
 Asn Ile Phe Ile Pro Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser
 50 55 60
 His Pro Glu Tyr Ala Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile
 65 70 75 80
 Asn Phe Glu Lys Ala Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp
 85 90 95
 Ala Glu Glu Ser Leu Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu
 100 105 110
 Phe Lys Asn Asn Val Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu
 115 120 125
 Asn Tyr Leu Val Gly Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg
 130 135 140
 Leu Met Pro Phe Leu Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg
 145 150 155 160
 Ile His His Pro Asn Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly
 165 170 175
 Tyr Cys Ile Ser Gln Arg Ser Asp His Val Trp Glu Gly Val Ser Ser
 180 185 190
 Ala Thr Thr Arg Ser Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His
 195 200 205
 Ala Asp Ser His Ser Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala
 210 215 220
 Asn Met Ala Glu Pro Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu
 225 230 235 240
 Val Leu Glu Met Ile Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu
 245 250 255
 Ala Asn Asp Ile Ala Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly
 260 265 270
 Ser Thr Leu Leu Ser Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln
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 290 295 300
 Pro Glu Pro Glu Phe Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val
 305 310 315 320
 Leu Asp Leu Trp Gly Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe
 325 330 335
 Ser Glu Val Asp Thr Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile
 340 345 350

Asp Arg Phe Ile Gln Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu
 355 360 365
 Ala Gln Val Asp Leu Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu
 370 375 380
 Phe Ser Val Leu Gln Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp
 385 390 395 400
 Glu Ala Ile Leu Ala Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala
 405 410 415
 His Leu Arg Gly Arg Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro
 420 425 430
 Val Thr Val Asp Trp Met Arg His Lys Val Asn Arg Pro Glu Pro Gln
 435 440 445
 Ser Val Glu Leu Gly Asp Pro Phe Ser Leu Leu Asn Pro Gln Gln Pro
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 Val Glu Ser Ala Leu 5
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 acc cgc agg atc atg ggc att gaa acg gag tat ggc ctc acc ttt gtt 163
 Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr Gly Leu Thr Phe Val 20
 10 15
 gat ggt gat tcc aaa aag ctt cgc cca gat gag ata gct cga agg atg 211
 Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu Ile Ala Arg Arg Met 35
 25 30
 ttt cgt ccc atc gtg gag aaa tat tcc agc tct aat atc ttc ata ccc 259
 Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser Asn Ile Phe Ile Pro 50
 40 45
 aat ggt tcc cgg ttg tat ctt gat gtg ggt tcc cac ccg gag tac gcc 307
 Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser His Pro Glu Tyr Ala 65
 55 60

acc gcc gag tgt gat aat ttg acc cag ctg atc aat ttt gaa aaa gct	355
Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile Asn Phe Glu Lys Ala	
70 75 80 85	
ggc gat gtt att gca gat cgc atg gct gta gat gcc gaa gag tcg ctg	403
Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp Ala Glu Glu Ser Leu	
90 95 100	
gcg aaa gaa gac att gct ggg cag gtg tac ctg ttt aaa aac aat gtc	451
Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu Phe Lys Asn Asn Val	
105 110 115	
gat tcc gtg ggc aat tct tat ggc tgc cac gaa aac tac ctt gtg ggt	499
Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu Asn Tyr Leu Val Gly	
120 125 130	
cgc tcc atg ccg ttg aag gcg ttg ggt aaa agg ctg atg ccg ttt ctg	547
Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg Leu Met Pro Phe Leu	
135 140 145	
att acc cgc cag ctc atc tgc ggc gcc ggc agg atc cat cac ccc aat	595
Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg Ile His His Pro Asn	
150 155 160 165	
cct ttg gat aaa ggc gaa tcc ttc ccc ttg ggc tac tgc ata tcc cag	643
Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly Tyr Cys Ile Ser Gln	
170 175 180	
cgc tct gac cac gtg tgg gag ggc gta tca agt gcc acc act aga tca	691
Arg Ser Asp His Val Trp Glu Gly Val Ser Ser Ala Thr Thr Arg Ser	
185 190 195	
cgc ccc att atc aac acc cgt gat gag cca cat gcg gat tcc cat tct	739
Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His Ala Asp Ser His Ser	
200 205 210	
tac cgc agg ctg cac gtg att gtg ggt gat gcc aac atg gca gag ccc	787
Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala Asn Met Ala Glu Pro	
215 220 225	
agc atc gcg ttg aag gtc ggc tcc acg ttg ctg gtt ctg gaa atg att	835
Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu Val Leu Glu Met Ile	
230 235 240 245	
gag gca gat ttc ggt ttg ccc agc tta gag ctt gcc aat gat att gcc	883
Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu Ala Asn Asp Ile Ala	
250 255 260	
tca att agg gaa atc tcc cgc gat gca aca gga tcc aca ctg ttg tcc	931
Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly Ser Thr Leu Leu Ser	
265 270 275	
ctg aaa gat ggc acc acc atg act gcc ttg cag atc cag cag gtg gtc	979
Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln Ile Gln Gln Val Val	
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ttt gag cat gcc tcg aag tgg ttg gag cag cgc ccc gaa cca gaa ttt	1027
Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg Pro Glu Pro Glu Phe	
295 300 305	
tct ggc acc tcc aac aca gag atg gcc cgc gtg ctg gat ctg tgg ggt	1075

Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val Leu Asp Leu Trp Gly
 310 315 320 325
 cgc atg ttg aaa gcg att gag tcc ggt gat ttc agc gaa gtg gat aca 1123
 Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe Ser Glu Val Asp Thr
 330 335 340
 gaa att gac tgg gtg atc aaa aag aag ctc att gat cgt ttc att cag 1171
 Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile Asp Arg Phe Ile Gln
 345 350 355
 cgc ggc aac ctt ggg ttg gat gat cca aaa ctt gcc caa gtg gac ttg 1219
 Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu Ala Gln Val Asp Leu
 360 365 370
 act tat cac gat att agg cca ggt aga ggc cta ttt agc gtg ctg caa 1267
 Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu Phe Ser Val Leu Gln
 375 380 385
 agc cgc ggc atg atc aaa cgg tgg act act gat gag gcg att tta gct 1315
 Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp Glu Ala Ile Leu Ala
 390 395 400 405
 gcg gtg gat acc gct cct gat aca aca cgt gct cat ttg cgc ggg cga 1363
 Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala His Leu Arg Gly Arg
 410 415 420
 atc ctt aaa gcg gcg gat act ctg gga gta cct gtg act gtc gat tgg 1411
 Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro Val Thr Val Asp Trp
 425 430 435
 atg cgt cac aag gtc aac cga ccg gag cca caa tcg gtg gaa ttg ggg 1459
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 Asp Pro
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 35 40 45
 Asn Ile Phe Ile Pro Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser
 50 55 60
 His Pro Glu Tyr Ala Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile
 65 70 75 80

Asn Phe Glu Lys Ala Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp
85 90 95

Ala Glu Glu Ser Leu Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu
100 105 110

Phe Lys Asn Asn Val Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu
115 120 125

Asn Tyr Leu Val Gly Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg
130 135 140

Leu Met Pro Phe Leu Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg
145 150 155 160

Ile His His Pro Asn Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly
165 170 175

Tyr Cys Ile Ser Gln Arg Ser Asp His Val Trp Glu Gly Val Ser Ser
180 185 190

Ala Thr Thr Arg Ser Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His
195 200 205

Ala Asp Ser His Ser Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala
210 215 220

Asn Met Ala Glu Pro Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu
225 230 235 240

Val Leu Glu Met Ile Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu
245 250 255

Ala Asn Asp Ile Ala Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly
260 265 270

Ser Thr Leu Leu Ser Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln
275 280 285

Ile Gln Gln Val Val Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg
290 295 300

Pro Glu Pro Glu Phe Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val
305 310 315 320

Leu Asp Leu Trp Gly Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe
325 330 335

Ser Glu Val Asp Thr Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile
340 345 350

Asp Arg Phe Ile Gln Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu
355 360 365

Ala Gln Val Asp Leu Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu
370 375 380

Phe Ser Val Leu Gln Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp
385 390 395 400

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519

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<211> 132

<212> PRT

<213> Corynebacterium glutamicum

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Lys Thr Ala Asp Gly Glu Ile Tyr Glu Val Pro Phe Ala Asp Asp Ala
35 40 45

Glu Ile Pro Glu Glu Trp Met Cys Lys Asn Gly Lys Leu Gly Ile Leu
50 55 60

Met Glu Gly Glu Gly Val Glu Ser Lys Pro Val Lys Pro Pro Arg Thr
65 70 75 80

His Trp Asp Met Leu Arg Glu Arg Arg Ser Ile Glu Glu Leu Asp Val
85 90 95

Leu Leu Glu Glu Arg Ile Glu Ala Leu Arg Lys Arg Arg Arg Asn Ala
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Ala Lys Leu Leu Lys Ala Gln Gln Glu Ala Glu Glu Ala Glu Lys Ala
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<212> DNA

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<223> FRXA01167

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Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu Trp Met Cys Lys
20 25 30

aac ggt aag cta ggc atc ctc atg gaa ggt gag gga gtc gag tcc aag 144
Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly Val Glu Ser Lys
35 40 45

ccg gtc aag cct cca cgt act cac tgg gat atg ttg cgt gag cgt cgc 192

Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu Arg Glu Arg Arg
 50 55 60

tca att gaa gag ctg gat gtg ctg ctg gaa gag cgc atc gag gca ctt 240
 Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg Ile Glu Ala Leu
 65 70 75 80

cgt aag cgt cgt cgc aat gca gcg aaa ctg ctg aag gct cag caa gag 288
 Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys Ala Gln Gln Glu
 85 90 95

gct gaa gaa gca gaa aag gca gct gaa gag gtt taatcttcct gcctaagtta 341
 Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
 100 105

gaa 344

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Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu Trp Met Cys Lys
 20 25 30

Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly Val Glu Ser Lys
 35 40 45

Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu Arg Glu Arg Arg
 50 55 60

Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg Ile Glu Ala Leu
 65 70 75 80

Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys Ala Gln Gln Glu
 85 90 95

Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
 100 105

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 <223> RXN01169

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attatcctca gacagctttt agcgcaaaca aggagcatca ttg aaa cgg gtc gtt 115
 Leu Lys Arg Val Val

	1	5	
gaa gcg tgg gat aga ttt caa atc cca ctg tat atc acg gct ctt atc Glu Ala Trp Asp Arg Phe Gln Ile Pro Leu Tyr Ile Thr Ala Leu Ile	10	20	163
gcc gga gca ctg gtg ggt ttg cag tgg cca ggc tct aca ggg ggt ttc Ala Gly Ala Leu Val Gly Leu Gln Trp Pro Gly Ser Thr Gly Gly Phe	25	30	211
gaa agc gcc att aac cca gcg tta atg gcg ctg ctt tat gcc act ttt Glu Ser Ala Ile Asn Pro Ala Leu Met Ala Leu Leu Tyr Ala Thr Phe	40	50	259
ctc ggt att ccg atc act cgg att ggt gca gcg ctg aaa gat ctg aga Leu Gly Ile Pro Ile Thr Arg Ile Gly Ala Ala Leu Lys Asp Leu Arg	55	60	307
ttt ctc ata gtg ctc atg tcc gtc aat ttt gtt gca gtg cct ctg gtg Phe Leu Ile Val Leu Met Ser Val Asn Phe Val Ala Val Pro Leu Val	70	80	355
gct ttt gcg ttg agc aga ttc att gcg ggt gat gag gcg ctt cta atc Ala Phe Ala Leu Ser Arg Phe Ile Ala Gly Asp Glu Ala Leu Leu Ile	90	95	403
gga ttt tta ctg gtg att ctc gcg ccg tgc att gat tac gtc att gtc Gly Phe Leu Leu Val Ile Leu Ala Pro Cys Ile Asp Tyr Val Ile Val	105	110	451
ttt gct ggt ttg gcc agg gcc gcc caa gac aag ctc ctt gcc gcc acg Phe Ala Gly Leu Ala Arg Ala Ala Gln Asp Lys Leu Leu Ala Ala Thr	120	125	499
cca ata tta atg ctt gtc caa atc ctg ctg atc ccc gtc ttc ctg gct Pro Ile Leu Met Leu Val Gln Ile Leu Leu Ile Pro Val Phe Leu Ala	135	140	547
gtt ttt gtg ggt tca gat gcc ctt ggc tca atc tct ttc ggc cca ttt Val Phe Val Gly Ser Asp Ala Leu Gly Ser Ile Ser Phe Gly Pro Phe	150	155	595
gta gaa gca ttt ttc ctc ctg att ctc att cca ctt gtt gct gct gcg Val Glu Ala Phe Phe Leu Leu Ile Leu Ile Pro Leu Val Ala Ala Ala	170	175	643
gga act cag caa gtg gca aga aag tgg cag gta gga cgt aca att atg Gly Thr Gln Gln Val Ala Arg Lys Trp Gln Val Gly Arg Thr Ile Met	185	190	691
gct gct gca gaa gca atc atg gtg cct tta atg atg ctg acg ttg ttc Ala Ala Ala Glu Ala Ile Met Val Pro Leu Met Met Leu Thr Leu Phe	200	205	739
gct gtc atc gca tcg caa gtg gaa gct gtg agt ggt caa ttc acc gat Ala Val Ile Ala Ser Gln Val Glu Ala Val Ser Gly Gln Phe Thr Asp	215	220	787
atc gcc aca gta gtg cca cta tat gtc gcc ttt ttg atg gtg atg att Ile Ala Thr Val Val Pro Leu Tyr Val Ala Phe Leu Met Val Met Ile	230	235	835

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cca att ggt ggc ggg ata tcc aaa ctc ggt ggc tta ggt ttc aaa gag      883
Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly Gly Leu Gly Phe Lys Glu
                250                255                260

caa cga gcc atc gtt ttt agc gga gca acc cgt aac tct ttg gtc gtt      931
Gln Arg Ala Ile Val Phe Ser Gly Ala Thr Arg Asn Ser Leu Val Val
                265                270                275

tta cct tta gcg tta gca ctt ccc gca ggc ctg gaa ata gcg gcc gtc      979
Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly Leu Glu Ile Ala Ala Val
                280                285                290

gta gtt gtc act caa acc ctc gtg gaa ctg att ggc atg gtt gtc tac      1027
Val Val Val Thr Gln Thr Leu Val Glu Leu Ile Gly Met Val Val Tyr
                295                300                305

gtg cgc atc atc cct tta att ttc cat gaa aag cag aca tac agg aaa      1075
Val Arg Ile Ile Pro Leu Ile Phe His Glu Lys Gln Thr Tyr Arg Lys
310                315                320                325

ctt tca ggc ata ggg gag tca tgaaacagaa cggcaagcta agg      1119
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20                25                30

Ser Thr Gly Gly Phe Glu Ser Ala Ile Asn Pro Ala Leu Met Ala Leu
35                40                45

Leu Tyr Ala Thr Phe Leu Gly Ile Pro Ile Thr Arg Ile Gly Ala Ala
50                55                60

Leu Lys Asp Leu Arg Phe Leu Ile Val Leu Met Ser Val Asn Phe Val
65                70                75                80

Ala Val Pro Leu Val Ala Phe Ala Leu Ser Arg Phe Ile Ala Gly Asp
85                90                95

Glu Ala Leu Leu Ile Gly Phe Leu Leu Val Ile Leu Ala Pro Cys Ile
100               105               110

Asp Tyr Val Ile Val Phe Ala Gly Leu Ala Arg Ala Ala Gln Asp Lys
115               120               125

Leu Leu Ala Ala Thr Pro Ile Leu Met Leu Val Gln Ile Leu Leu Ile
130               135               140

Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser Ile
145               150               155               160

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Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile Pro
 165 170 175
 Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln Val
 180 185 190
 Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu Met
 195 200 205
 Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val Ser
 210 215 220
 Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala Phe
 225 230 235 240
 Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly Gly
 245 250 255
 Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr Arg
 260 265 270
 Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly Leu
 275 280 285
 Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu Ile
 290 295 300
 Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu Lys
 305 310 315 320
 Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
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 atc tct ttc ggc cca ttt gta gaa gca ttt ttc ctc ctg att ctc att 96
 Ile Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile
 20 25 30
 cca ctt gtt gct gct gcg gga act cag caa gtg gca aga aag tgg cag 144
 Pro Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln
 35 40 45
 gta gga cgt aca att atg gct gct gca gaa gca atc atg gtg cct tta 192
 Val Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu
 50 55 60

atg atg ctg acg ttg ttc gct gtc atc gca tgc caa gtg gaa gct gtg 240
 Met Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val
 65 70 75 80
 agt ggt caa ttc acc gat atc gcc aca gta gtg cca cta tat gtc gcc 288
 Ser Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala
 85 90 95
 ttt ttg atg gtg atg att cca att ggt ggc ggg ata tcc aaa ctc ggt 336
 Phe Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly
 100 105 110
 ggc tta ggt ttc aaa gag caa cga gcc atc gtt ttt agc gga gca acc 384
 Gly Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr
 115 120 125
 cgt aac tct ttg gtc gtt tta cct tta gcg tta gca ctt ccc gca ggc 432
 Arg Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly
 130 135 140
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 Leu Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu
 145 150 155 160
 att ggc atg gtt gtc tac gtg cgc atc atc cct tta att ttc cat gaa 528
 Ile Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu
 165 170 175
 aag cag aca tac agg aaa ctt tca ggc ata ggg gag tca tgaaacagaa 577
 Lys Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
 180 185
 cggcaagcta agg 590

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 534
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 Pro Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln
 35 40 45
 Val Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu
 50 55 60
 Met Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val
 65 70 75 80
 Ser Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala
 85 90 95
 Phe Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly

100	105	110
Gly Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr		
115	120	125
Arg Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly		
130	135	140
Leu Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu		
145	150	155
Ile Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu		
165	170	175
Lys Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser		
180	185	

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<212> DNA

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<223> RXN01173

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                                   Met His Val Ser Thr
                                   1           5

ctt cca aac aag aaa ctg cgt act cgc att ttc gca ggc acc gct gcc 163
Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe Ala Gly Thr Ala Ala
                                   10           15           20

gtc gca ctg tca ctt ggt gtt gcg tct tgc tca aac gca gaa gat gct 211
Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser Asn Ala Glu Asp Ala
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gtg gat agc gca aca gat gct gcc aac tct gca acc tcc gcc gcg gga 259
Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala Thr Ser Ala Ala Gly
                                   40           45           50

tct gca att aac gat gcc acc ggc act tcc agc gca tcc acc aca gag 307
Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser Ala Ser Thr Thr Glu
                                   55           60           65

cct tcc gga acc tct gga tcc gac tcc ggg tct gac tct gct gga gga 355
Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser Asp Ser Ala Gly Gly
                                   70           75           80           85

gac acc act gaa gta gaa agc gcc gat ggg tcc acc atc agc atc cca 403
Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser Thr Ile Ser Ile Pro
                                   90           95           100

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Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly Phe Ser Thr Pro Glu

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Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu Val Thr Phe Pro Glu			
120	125	130	
ggc tac att gtt aac tct gca gaa ggt ggt gca caa gca ctg gtc ggc			547
Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala Gln Ala Leu Val Gly			
135	140	145	
atg atc ggt gaa acc tgg atc ggc gaa ggc gga cta tcc gcg gca gtg			595
Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly Leu Ser Ala Ala Val			
150	155	160	165
ggc ctc cca act ggg cct gaa gaa gca aca aca aat ggt tgg act caa			643
Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr Asn Gly Trp Thr Gln			
170	175	180	
cag ttc aca tct gga gta att agc tgg ctt gat gat gga tca gga cag			691
Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp Asp Gly Ser Gly Gln			
185	190	195	
ttc gca gct tct gtt gaa cct gct taagggaatc tcacctggcc tcc			738
Phe Ala Ala Ser Val Glu Pro Ala			
200	205		

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 <213> Corynebacterium glutamicum

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 Met His Val Ser Thr Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe
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 Ala Gly Thr Ala Ala Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser
 20 25 30
 Asn Ala Glu Asp Ala Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala
 35 40 45
 Thr Ser Ala Ala Gly Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser
 50 55 60
 Ala Ser Thr Thr Glu Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser
 65 70 75 80
 Asp Ser Ala Gly Gly Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser
 85 90 95
 Thr Ile Ser Ile Pro Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly
 100 105 110
 Phe Ser Thr Pro Glu Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu
 115 120 125
 Val Thr Phe Pro Glu Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala
 130 135 140
 Gln Ala Leu Val Gly Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly

ggc tac att gtt aac tct gca gaa ggt ggt gca caa gca ctg gtc ggc 547
 Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala Gln Ala Leu Val Gly
 135 140 145
 atg atc ggt gaa acc tgg atc ggc gaa ggc gga cta tcc gcg gca gtg 595
 Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly Leu Ser Ala Ala Val
 150 155 160 165
 ggt ctc cca act ggg cct gaa gaa gca aca aca aat ggt tgg act caa 643
 Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr Asn Gly Trp Thr Gln
 170 175 180
 cag ttc aca tct gga gta att agc tgg ctt gat gat gga tca gga cag 691
 Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp Asp Gly Ser Gly Gln
 185 190 195
 ttc gca gct tct gtt gaa cct gct taagggaatc tcacctggcc tcc 738
 Phe Ala Ala Ser Val Glu Pro Ala
 200 205

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Met His Val Ser Thr Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe
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 Ala Gly Thr Ala Ala Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser
 20 25 30
 Asn Ala Glu Asp Ala Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala
 35 40 45
 Thr Ser Ala Ala Gly Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser
 50 55 60
 Ala Ser Thr Thr Glu Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser
 65 70 75 80
 Asp Ser Ala Gly Gly Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser
 85 90 95
 Thr Ile Ser Ile Pro Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly
 100 105 110
 Phe Ser Thr Pro Glu Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu
 115 120 125
 Val Thr Phe Pro Glu Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala
 130 135 140
 Gln Ala Leu Val Gly Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly
 145 150 155 160
 Leu Ser Ala Ala Val Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr
 165 170 175
 Asn Gly Trp Thr Gln Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp

180	185	190	
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			Met Ser Asn Met Gln
			1 5
gga aac gat tcc aag aaa tct agc ggc gcg agt cgt gcg gag agc cca 163			
Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser Arg Ala Glu Ser Pro			
10	15	20	
ctg atc aag ttc cgg aca ttg att atc gtc atc ttt gtc atc ttg atc 211			
Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile Phe Val Ile Leu Ile			
25	30	35	
gtt ggt ttg gca tct att gca gtg gga cct gtc gtg tac cag ctc atc 259			
Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val Val Tyr Gln Leu Ile			
40	45	50	
atg gga cct ggt gtg aaa acc gaa gga atc cag gct gat ggc gca gca 307			
Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln Ala Asp Gly Ala Ala			
55	60	65	
cct gcg tcc acc gac atg aac ggc acc tgg gat gtt gcc cca ggg agt 355			
Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp Val Ala Pro Gly Ser			
70	75	80	85
att cca aac acc acc tca gct gga ttc acc ttc gct gag atc ctg cca 403			
Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe Ala Glu Ile Leu Pro			
90	95	100	
ggc gaa gaa aag atc acc tcc ggc tca acc act ggt gtc act ggc gaa 451			
Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr Gly Val Thr Gly Glu			
105	110	115	
gtg gtc atc gag gat aac tcc ctg atc tct ggt ctg att acc gtc aac 499			
Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly Leu Ile Thr Val Asn			
120	125	130	
atg act cac atc acc acc gat cag gaa aag cgc gac atc aac gtg cgc 547			
Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg Asp Ile Asn Val Arg			
135	140	145	
act aag ctc ttc cac acc gat cag tac cca gaa gca acc ttt gag gtt 595			
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Phe Val Ile Leu Ile Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val
  35          40          45
Val Tyr Gln Leu Ile Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln
  50          55          60
Ala Asp Gly Ala Ala Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp
  65          70          75          80
Val Ala Pro Gly Ser Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe
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Ala Glu Ile Leu Pro Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr
  100          105          110
Gly Val Thr Gly Glu Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly
  115          120          125
Leu Ile Thr Val Asn Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg
  130          135          140
Asp Ile Asn Val Arg Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu

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 Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr Gly Val Thr Gly Glu
 105 110 115
 gtg gtc atc gag gat aac tcc ctg atc tct ggt ctg att acc gtc aac 499
 Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly Leu Ile Thr Val Asn
 120 125 130
 atg act cac atc acc acc gat cag gaa aag cgc gac atc aac gtg cgc 547
 Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg Asp Ile Asn Val Arg
 135 140 145
 act aag ctc ttc cac acc gat cag tac cca gaa gca acc ttt gag gtt 595
 Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu Ala Thr Phe Glu Val
 150 155 160 165
 acc gat tcc gtt gat ctt tct gcg ctc cca gac acc gga tcc att gct 643
 Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp Thr Gly Ser Ile Ala
 170 175 180
 cag gtt gtc atc cca ggc gag ttg acc atc cac ggt gaa acc aag gct 691
 Gln Val Val Ile Pro Gly Glu Leu Thr Ile His Gly Glu Thr Lys Ala
 185 190 195
 gtg gag cct acc ttt gat gta ctt cgt act ggt gac caa gtt atc gtg 739
 Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly Asp Gln Val Ile Val
 200 205 210
 gct tcc gat atc gaa atc aac cgc ctc gac ttc ggt gta gaa acc cca 787
 Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe Gly Val Glu Thr Pro
 215 220 225
 gag ttc atc gcc gca aag atc aat gag acc ggc gag atc aac gtc cga 835
 Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly Glu Ile Asn Val Arg
 230 235 240 245
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 Ile Val Leu Glu Lys
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<213> Corynebacterium glutamicum

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 Phe Val Ile Leu Ile Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val
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 Val Tyr Gln Leu Ile Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln
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 Ala Asp Gly Ala Ala Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp

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gsg tgc sgg sgc ttk gkg rtc ggk ggt kcc ctc sgs cyg gcc ctg acc Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu Xaa Xaa Ala Leu Thr 215 220 225	787
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rra mar arr rgg rrk rmk gsk kkt ktk gtg gyk gsk sgk ykt tkt cgw Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa 250 255 260	883
cgm cks sws ram gwr rts rkc gsc gmc swc cty syw gmm say cmk ssg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa 265 270 275	931
ssk scw kgr wss rcy gcy scm ssm ggs ksk csm swk wtr kks yss sks Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa 280 285 290	979
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acc atc ctc cac cgc cat ccg cag tgc gac cag ggc gtc ggg cag ctc Thr Ile Leu His Arg His Pro Gln Cys Asp Gln Gly Val Gly Gln Leu 390 395 400 405	1315
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Ala Leu Arg Arg Val
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<223> Xaa = Arg or Leu

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<221> VARIANT

<222> 264, 289

<223> Xaa = Glu, Val, Asp, Gln, Leu,

<223> or His

<220>

<221> VARIANT

<222> 267

<223> Xaa = Val, Met, or Ile

<220>

<221> VARIANT

<222> 268

<223> Xaa = Gly, Val, Ser, or Ile

<220>

<221> VARIANT

<222> 270

<223> Xaa = Asp or Ala

<220>

<221> VARIANT

<222> 271

<223> Xaa = Asp, Val, His, or Leu

<220>

<221> VARIANT

<222> 272

<223> Xaa = Leu

<220>

<221> VARIANT

<222> 273, 307

<223> Xaa = Val, Ala, Leu, or Pro

<220>

<221> VARIANT

<222> 274

<223> Xaa = Asp, Ala, or Glu

<220>

<221> VARIANT

<222> 275

<223> Xaa = Thr or His

<220>

<221> VARIANT

<222> 276

<223> Xaa = Gln, His, or Pro

<220>

<221> VARIANT

<222> 277, 278, 285

<223> Xaa = Gly, Pro, Arg, or Ala

<220>

<221> VARIANT

<222> 279, 284

<223> Xaa = Ala or Pro

<220>

<221> VARIANT

<222> 280

<223> Xaa = Gly, Trp, or STOP codon

<220>

<221> VARIANT

<222> 281

<223> Xaa = Arg, Trp, Thr, Ser, or Cys

<220>

<221> VARIANT

<222> 287

<223> Xaa = Gly, Ala, Trp, Cys, or Ser

<220>

<221> VARIANT

<222> 288, 300, 317

<223> Xaa = Arg or Pro

<220>

<221> VARIANT

<222> 290

<223> Xaa = Met, Ile, or Leu

<220>

<221> VARIANT

<222> 292

<223> Xaa = Trp, Ser, Cys, Arg, or Pro

<220>

<221> VARIANT

<222> 293

<223> Xaa = Gly, Val, Arg, or Leu

<220>

<221> VARIANT

<222> 294

<223> Xaa = Arg, Ser, Thr, Cys, or STOP codon

<220>

<221> VARIANT

<222> 297

<223> Xaa = Val or Phe

<220>

<221> VARIANT

<222> 304

<223> Xaa = Lys, Asn, Thr, Gln, His, or Pro

<220>

<221> VARIANT

<222> 305

<223> Xaa = Met, Ile, Thr, Leu, or Pro

<220>

<221> VARIANT

<222> 308

<223> Xaa = Arg, Met, Ile, Trp, Leu,

<223> or STOP codon

<220>

<221> VARIANT

<222> 309

<223> Xaa = Gly, Glu, Asp, Cys, Tyr,

<223> or STOP codon

<220>

<221> VARIANT

<222> 311

<223> Xaa = Phe

<220>

<221> VARIANT

<222> 312

<223> Xaa = Trp, Leu, Arg, or STOP codon

<220>

<221> VARIANT

<222> 313

<223> Xaa = Gly, Glu, Arg, or Lys

<220>

<221> VARIANT

<222> 314

<223> Xaa = Gly, Glu, Cys, Tyr,

<223> or STOP codon

<220>

<221> VARIANT

<222> 315

<223> Xaa = Gly, Glu, Asp, Arg, Gln, or His

<220>

<221> VARIANT

<222> 316

<223> Xaa = Tyr, Leu, Phe, Gln, His, Leu,

<223> or STOP codon

<220>

<221> VARIANT

<222> 318

<223> Xaa = Gly, Val, Arg, Ser, or Ile

<400> 544

Met	Ile	Ile	Ser	Thr	Asn	Thr	Ala	His	Pro	Leu	His	Glu	Pro	His	Val
1				5					10					15	

Pro	Ser	His	His	Asn	Arg	Met	Asn	Thr	Leu	Arg	Ala	Gly	Val	Leu	Gly
			20					25					30		

Ala	Asn	Asp	Gly	Ile	Val	Ser	Ile	Ala	Ala	Leu	Leu	Leu	Gly	Val	Ile
		35					40					45			

Ala	Thr	Gly	Ala	Ser	Asp	Thr	Val	Val	Phe	Gly	Ala	Gly	Leu	Ala	Ser
	50					55					60				

Thr	Ile	Ala	Gly	Ala	Val	Ser	Met	Ala	Leu	Gly	Glu	Tyr	Val	Ser	Val
65					70					75					80

Ser	Ser	Gln	Arg	Asp	Thr	Glu	Arg	Val	Leu	Ile	Ala	Lys	Glu	Ala	Lys
				85					90					95	

Glu	Leu	Ala	Glu	Asp	Pro	Thr	Ala	Glu	His	Val	Glu	Leu	Ser	Glu	Ile
			100					105					110		

Leu	His	Ser	Tyr	Gly	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			115				120						125		

Xaa	Xaa	Gly	Xaa	Gly	Asp	Ala	Leu	Gly	Ala	His	Leu	Gln	Leu	Glu	Leu
			130			135					140				

Gly Ile Asp Asn Glu Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser
 145 150 155 160
 Ser Ala Val Ala Phe Leu Leu Gly Ala Leu Leu Pro Met Val Xaa Val
 165 170 175
 Phe Xaa Ala Xaa Xaa Gly Trp Asp Ala Gly Xaa Xaa Phe Val Val Thr
 180 185 190
 Xaa Leu Val Leu Ala Xaa Thr Gly Phe Ile Ser Xaa Xaa Xaa Xaa Gly
 195 200 205
 Thr Xaa Xaa Met Arg Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu
 210 215 220
 Xaa Xaa Ala Leu Thr Xaa Pro Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 225 230 235 240
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa
 245 250 255
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 260 265 270
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 275 280 285
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 290 295 300
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
 305 310 315 320
 Pro Leu Ser Gly Glu Ile Leu Leu Ala Gly Leu Gly Gly Glu Ile Gly
 325 330 335
 Met Gly Glu Pro Arg Ile Pro Val Thr Thr Gly Asp Leu Glu Thr Arg
 340 345 350
 Gly Leu Gln Cys Leu Gly Lys Leu Gly Gln Trp Pro Pro Val Gly Gly
 355 360 365
 Gly His Gly Met Ile His Arg Phe Gln Arg Arg Pro Gly Glu Lys Gly
 370 375 380
 His Gln Gln Ala Thr Thr Ile Leu His Arg His Pro Gln Cys Asp Gln
 385 390 395 400
 Gly Val Gly Gln Leu Ala Arg Ala His Val Asp Gln Gly Val Pro Gly
 405 410 415
 Gln Gln Ala Cys Pro Ala Leu Arg Arg Val
 420 425

<210> 545

<211> 793

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(793)

<223> FRXA01229

<400> 545

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tagccccgaa agacggcgag ggttggtctt gcttcgttgt gggaaaaacta ggcccttaat 60

aagctgtgct tataggggtct cctgcaccga taaaggactg atg atc atc tcc act 115
Met Ile Ile Ser Thr
1 5

aac acc gct cac ccc ctg cac gaa ccg cac gta ccc agc cac cac aat 163
Asn Thr Ala His Pro Leu His Glu Pro His Val Pro Ser His His Asn
10 15 20

cgt atg aat act ctg cgt gcc ggt gtg ctg ggt gct aat gac ggt atc 211
Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly Ala Asn Asp Gly Ile
25 30 35

gtc tcc att gct gcg cta ctg ctc ggt gtg atc gcc acc ggc gcc agt 259
Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile Ala Thr Gly Ala Ser
40 45 50

gac acc gtc gtg ttc ggc gct ggt ttg gcc tca acg atc gcg ggg gcg 307
Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser Thr Ile Ala Gly Ala
55 60 65

gta tct atg gct ctc ggt gag tac gtc tct gtc tcc tca cag cgt gat 355
Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val Ser Ser Gln Arg Asp
70 75 80 85

acc gaa cgg gtg ctc atc gca aaa gaa gcg aag gag ctg gcc gaa gac 403
Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys Glu Leu Ala Glu Asp
90 95 100

ccg acg gcc gag cac gtc gag ctg tcg gag atc cta cac tcc tac ggc 451
Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile Leu His Ser Tyr Gly
105 110 115

atc tcc cct gag act gcg aac cag gcg gcc acc gag atc ggg cag ggc 499
Ile Ser Pro Glu Thr Ala Asn Gln Ala Ala Thr Glu Ile Gly Gln Gly
120 125 130

gac gcc ttg ggc gcc cac ctt cag ctc gag ctc ggt att gat aat gag 547
Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu Gly Ile Asp Asn Glu
135 140 145

caa ctg acc agc ccc ttg gcc gcc gcc ttc tcc tcg gcc gtg gct ttc 595
Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser Ser Ala Val Ala Phe
150 155 160 165

ctg ctc gga gca ctg ctg ccg atg gtg tcg gta ttc atc gcc cct gca 643
Leu Leu Gly Ala Leu Leu Pro Met Val Ser Val Phe Ile Ala Pro Ala
170 175 180

ggc tgg gac gcc ggc gtg gtc ttc gta gtc acg ctg ctg gtc ctg gcg 691
Gly Trp Asp Ala Gly Val Val Phe Val Val Thr Leu Leu Val Leu Ala
185 190 195

gtg acc ggg ttc atc tca gcc cag atc tcg ggt acc tcc cca atg cgc 739

```

Val Thr Gly Phe Ile Ser Ala Gln Ile Ser Gly Thr Ser Pro Met Arg
 200 205 210

gcg tgc ggg cgc ttg gtg atc ggt ggt gcc ctc ggc ctg gcc cta acc 787
 Ala Cys Gly Arg Leu Val Ile Gly Gly Ala Leu Gly Leu Ala Leu Thr
 215 220 225

tac ggt 793
 Tyr Gly
 230

<210> 546
 <211> 231
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 546
 Met Ile Ile Ser Thr Asn Thr Ala His Pro Leu His Glu Pro His Val
 1 5 10 15

Pro Ser His His Asn Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly
 20 25 30

Ala Asn Asp Gly Ile Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile
 35 40 45

Ala Thr Gly Ala Ser Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser
 50 55 60

Thr Ile Ala Gly Ala Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val
 65 70 75 80

Ser Ser Gln Arg Asp Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys
 85 90 95

Glu Leu Ala Glu Asp Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile
 100 105 110

Leu His Ser Tyr Gly Ile Ser Pro Glu Thr Ala Asn Gln Ala Ala Thr
 115 120 125

Glu Ile Gly Gln Gly Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu
 130 135 140

Gly Ile Asp Asn Glu Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser
 145 150 155 160

Ser Ala Val Ala Phe Leu Leu Gly Ala Leu Leu Pro Met Val Ser Val
 165 170 175

Phe Ile Ala Pro Ala Gly Trp Asp Ala Gly Val Val Phe Val Val Thr
 180 185 190

Leu Leu Val Leu Ala Val Thr Gly Phe Ile Ser Ala Gln Ile Ser Gly
 195 200 205

Thr Ser Pro Met Arg Ala Cys Gly Arg Leu Val Ile Gly Gly Ala Leu
 210 215 220

Gly Leu Ala Leu Thr Tyr Gly

Pro Ala Leu Pro

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<210> 548
<211> 169
<212> PRT
<213> Corynebacterium glutamicum
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<400> 548
Met Lys Arg Thr Ile Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu
  1             5             10             15

Val Leu Ser Ala Cys Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr
      20             25             30

Thr Thr Ile Ala Thr Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly
      35             40             45

Ala Thr Thr Asp Pro Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser
      50             55             60

Ala Glu His Asn Asp Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro
  65             70             75             80

His His Gln Gln Ala Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp
      85             90             95

Asp Ile Pro Ala Glu Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala
      100            105            110

Gln Gly Pro Glu Ile Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu
      115            120            125

Glu Asp Pro Val Thr Gly Asp Met Gly Glu Met Asp His Gly Gly Met
  130            135            140

Ser Gly Met Met Ser Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln
  145            150            155            160

Gly Thr Arg Gly Cys Pro Ala Leu Pro
      165

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<210> 549
<211> 739
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(739)  
<223> FRXA01246
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<400> 549
gggaaggagg agaaggctgc tgtgagctct gcagcccccg tccgctgact ttcaatgctt 60
catggactcc ccgatacaca acctccgaaa gggaaccccc atg aag cgc act atc 115
Met Lys Arg Thr Ile
1 5

```

acc atc gcc gct ctc gcc ttg acc tcc acc ctg gtt ttg tcc gcc tgc 163
Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu Val Leu Ser Ala Cys
      10                      15                      20

gca gat aac act gag gga gaa aac acc gac acc acg acc atc gcc act 211
Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr Thr Thr Ile Ala Thr
      25                      30                      35

acg tcc gcc ccc gac acc acc gaa acg acc ggg gcc acc acg gat cct 259
Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly Ala Thr Thr Asp Pro
      40                      45                      50

gag aca gag acg ggg gcg gcc gga gag gtc tcc gcc gag cac aat gat 307
Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser Ala Glu His Asn Asp
      55                      60                      65

gcg gac atc atg ttc gcg cag atg atg atc ccg cat cac caa cag gcc 355
Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro His His Gln Gln Ala
      70                      75                      80                      85

gtg gag atg agt gaa atc ctc ctg gcc aag gac gat atc ccg gcc gag 403
Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp Asp Ile Pro Ala Glu
      90                      95                      100

gtc atc gag ttc acc cag ggt gtt atc gat gcc cag ggc ccg gag atc 451
Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala Gln Gly Pro Glu Ile
      105                      110                      115

gac cgg atg aat acc atg ctc gag acc tgg gaa gaa gat ccg gtc acc 499
Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu Glu Asp Pro Val Thr
      120                      125                      130

ggt gat atg ggt gag atg gac cat ggc ggg atg agt gga atg atg agc 547
Gly Asp Met Gly Glu Met Asp His Gly Gly Met Ser Gly Met Met Ser
      135                      140                      145

gag gag gac atg aca gcc ctc gag gac gcc cag ggc acc gag gct gcc 595
Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln Gly Thr Glu Ala Ala
      150                      155                      160                      165

cgg ctc tac ctt gag cag atg acc gcc cac cat gag ggc gcg gtc gat 643
Arg Leu Tyr Leu Glu Gln Met Thr Ala His His Glu Gly Ala Val Asp
      170                      175                      180

atg gcc cgc gat gag gtc act gat ggc cag aac ccg cag gcc atc gct 691
Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn Pro Gln Ala Ile Ala
      185                      190                      195

ctg gct gag cag gtc att gaa gat cag gag gcc gag atc gcc gag att 739
Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala Glu Ile Ala Glu Ile
      200                      205                      210

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<210> 550

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

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Met Lys Arg Thr Ile Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu
  1              5              10              15

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Val Leu Ser Ala Cys Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr
 20 25 30
 Thr Thr Ile Ala Thr Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly
 35 40 45
 Ala Thr Thr Asp Pro Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser
 50 55 60
 Ala Glu His Asn Asp Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro
 65 70 75 80
 His His Gln Gln Ala Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp
 85 90 95
 Asp Ile Pro Ala Glu Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala
 100 105 110
 Gln Gly Pro Glu Ile Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu
 115 120 125
 Glu Asp Pro Val Thr Gly Asp Met Gly Glu Met Asp His Gly Gly Met
 130 135 140
 Ser Gly Met Met Ser Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln
 145 150 155 160
 Gly Thr Glu Ala Ala Arg Leu Tyr Leu Glu Gln Met Thr Ala His His
 165 170 175
 Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn
 180 185 190
 Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala
 195 200 205
 Glu Ile Ala Glu Ile
 210

<210> 551
 <211> 471
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(471)
 <223> RXN01249

<400> 551
 tct cag att gtg gcg gtg tct tct cac ggt ctt acc acg atc cag gag 48
 Ser Gln Ile Val Ala Val Ser Ser His Gly Leu Thr Thr Ile Gln Glu
 1 5 10 15
 att gac gtg aaa cga gca gcg atc gca gcc gcc gcc ctt acc ctc gcc 96
 Ile Asp Val Lys Arg Ala Ala Ile Ala Ala Ala Ala Leu Thr Leu Ala
 20 25 30
 ctc acg ggg tgt tcg gcc gcc gac ccg gaa ccc acc gcc gac ggg acg 144

Leu Thr Gly Cys Ser Ala Ala Asp Pro Glu Pro Thr Ala Asp Gly Thr
 35 40 45
 gtg tcc cag gat aca ttc ctg act acc cat ggc ctg gcc gcc atg gac 192
 Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
 50 55 60
 gcg gtg gag atc att gat cac ctc gac cgg cag aag gtc act gag cgt 240
 Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg.
 65 70 75 80
 ccc acg gat ctg atc gcc tca gtg cgt gcc gat gaa ctg ctg ctc tcg 288
 Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
 85 90 95
 agc gat gac cag gaa gtc gtg gtc gat ctt ccc gac aat cag acg tat 336
 Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
 100 105 110
 gtc tcg atc gca ccc tac ctc aac tcc acc cac gac tgc ttc tac cac 384
 Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
 115 120 125
 agc ctc acg acc tgc ctg ggg gat ctc gac aat gag gat atc cat gtc 432
 Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
 130 135 140
 atg atc acc gat gaa gcg acc ggc gag gtc ctg ttc gat 471
 Met Ile Thr Asp Glu Ala Thr Gly Glu Val Leu Phe Asp
 145 150 155

<210> 552

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 552

Ser Gln Ile Val Ala Val Ser Ser His Gly Leu Thr Thr Ile Gln Glu
 1 5 10 15
 Ile Asp Val Lys Arg Ala Ala Ile Ala Ala Ala Ala Leu Thr Leu Ala
 20 25 30
 Leu Thr Gly Cys Ser Ala Ala Asp Pro Glu Pro Thr Ala Asp Gly Thr
 35 40 45
 Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
 50 55 60
 Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
 65 70 75 80
 Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
 85 90 95
 Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
 100 105 110
 Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
 115 120 125

Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
 130 135 140

Met Ile Thr Asp Glu Ala Thr Gly Glu Val Leu Phe Asp
 145 150 155

<210> 553
 <211> 400
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(400)
 <223> FRXA01249

<400> 553
 gaattgacgt ggaaccgagc agcgatcgca gccgcgcgcc cttaccctcg ccctcacggg 60
 gtgttcgggcc gccgaccgag aaccacccgc cgacgggacg gtg tcc cag gat aca 115
 Val Ser Gln Asp Thr
 1 5
 ttc ctg act acc cat ggc ctg gcc gcc atg gac gcg gtg gag atc att 163
 Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp Ala Val Glu Ile Ile
 10 15 20
 gat cac ctc gac cgg cag aag gtc act gag cgt ccc acg gat ctg atc 211
 Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg Pro Thr Asp Leu Ile
 25 30 35
 gcc tca gtg cgt gcc gat gaa ctg ctg ctc tcg agc gat gac cag gaa 259
 Ala Ser Val Arg Ala Asp Glu Leu Leu Ser Ser Asp Asp Gln Glu
 40 45 50
 gtc gtg gtc gat ctt ccc gac aat cag acg tat gtc tcg atc gca ccc 307
 Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr Val Ser Ile Ala Pro
 55 60 65
 tac ctc aac tcc acc cac gac tgc ttc tac cac agc ctc acg acc tgc 355
 Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His Ser Leu Thr Thr Cys
 70 75 80 85
 ctg ggg gat ctc gac aat gag gat atc cat gtc atg atc acc gat 400
 Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val Met Ile Thr Asp
 90 95 100

<210> 554
 <211> 100
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 554
 Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
 1 5 10 15
 Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
 20 25 30

Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
 35 40 45

Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
 50 55 60

Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
 65 70 75 80

Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
 85 90 95

Met Ile Thr Asp
 100

<210> 555
 <211> 432
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(409)
 <223> RXN01251

<400> 555
 tgtaagccga gagcgaacct gccaaaagta aggggcgggg tgcggtgac gtcggttagga 60

tcgagcgaag aaaccaacaa acttcttagg agccattctc atg acc cag cca gat 115
 Met Thr Gln Pro Asp
 1 5

atg tcc cag atc ctc gcc caa gct cag cag atg cag gct caa cta cag 163
 Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met Gln Ala Gln Leu Gln
 10 15 20

gcc gct cag cag gaa atc ctg gca acc acc gtt gtc gga aat gca gga 211
 Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val Val Gly Asn Ala Gly
 25 30 35

aac ggg ctg gtt acc gtc act atg gcc ggc aac ggc gag gtc tcc gca 259
 Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn Gly Glu Val Ser Ala
 40 45 50

gtg acc gtt gac cca aag gtc gtt gac cct gaa gat gtc gaa acc cta 307
 Val Thr Val Asp Pro Lys Val Val Asp Pro Glu Asp Val Glu Thr Leu
 55 60 65

cag gac ctt ctg ctc ggt gca ttc aag gat gcc cat aac aag gtc gca 355
 Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala His Asn Lys Val Ala
 70 75 80 85

aac gtt gct gaa gag aag atg ggc cca cta tcc cag ggc atg ggt ggc 403
 Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser Gln Gly Met Gly Gly
 90 95 100

ctc ttc taattagttg ctaaacgcag ggc 432
 Leu Phe

<210> 556
 <211> 103
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 556
 Met Thr Gln Pro Asp Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met
 1 5 10 15
 Gln Ala Gln Leu Gln Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val
 20 25 30
 Val Gly Asn Ala Gly Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn
 35 40 45
 Gly Glu Val Ser Ala Val Thr Val Asp Pro Lys Val Val Asp Pro Glu
 50 55 60
 Asp Val Glu Thr Leu Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala
 65 70 75 80
 His Asn Lys Val Ala Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser
 85 90 95
 Gln Gly Met Gly Gly Leu Phe
 100

<210> 557
 <211> 432
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(409)
 <223> FRXA01251

<400> 557
 tgtaagccga gagcgaacct gccaaaagta aggggcgggt tcgcggtgac gtcggttagga 60
 tcgagcgaag aaaccaacaa acttcttagg agccattctc atg acc cag cca gat 115
 Met Thr Gln Pro Asp
 1 5
 atg tcc cag atc ctc gcc caa gct cag cag atg cag gct caa cta cag 163
 Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met Gln Ala Gln Leu Gln
 10 15 20
 gcc gct cag cag gaa atc ctg gca acc acc gtt gtc gga aat gca gga 211
 Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val Val Gly Asn Ala Gly
 25 30 35
 aac ggg ctg gtt acc gtc act atg gcc ggc aac ggc gag gtc ttc gca 259
 Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn Gly Glu Val Phe Ala
 40 45 50
 gtg acc gtt gac cca aag gtc gtt gac cct gaa gat gtc gaa acc cta 307
 Val Thr Val Asp Pro Lys Val Val Asp Pro Glu Asp Val Glu Thr Leu

55	60	65	
cag gac ctt ctg ctc ggt gca ttc aag gat gcc cat aac aag gtc gca			355
Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala His Asn Lys Val Ala			
70	75	80	85
aac gtt gct gaa gag aag atg ggc cca cta tcc cag ggc atg ggt ggc			403
Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser Gln Gly Met Gly Gly			
	90	95	100
ctc ttc taattagttg ctaaacgcag ggc			432
Leu Phe			

<210> 558
 <211> 103
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 558
 Met Thr Gln Pro Asp Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met
 1 5 10 15
 Gln Ala Gln Leu Gln Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val
 20 25 30
 Val Gly Asn Ala Gly Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn
 35 40 45
 Gly Glu Val Phe Ala Val Thr Val Asp Pro Lys Val Val Asp Pro Glu
 50 55 60
 Asp Val Glu Thr Leu Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala
 65 70 75 80
 His Asn Lys Val Ala Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser
 85 90 95
 Gln Gly Met Gly Gly Leu Phe
 100

<210> 559
 <211> 1035
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> RXN01263

<400> 559
 agtggccttt ggagttatatt tgatgacggt atcggcgact gctgggatcc tcctcttttt 60
 atctccaaat agaagccaag ctgcgccacc ccaatttagt ttg acc ccg tat gat 115
 Leu Thr Pro Tyr Asp
 1 5
 cca acc gct gta aat aag gag tcg gaa aaa gaa gca gca aag aat ctg 163

Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu Ala Ala Lys Asn Leu	
10 15 20	
ttt ggc gct gag gcg ttg aca gtg gat ccg gat gcc ggt gag gtt gtt	211
Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp Ala Gly Glu Val Val	
25 30 35	
gat cga gta gat aat ttt tat ccg acg act gct aag gca aaa cga gat	259
Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala Lys Ala Lys Arg Asp	
40 45 50	
tac cca agt aac tat gca gcg ggt tgt cac caa gaa gtc aat gag act	307
Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln Glu Val Asn Glu Thr	
55 60 65	
agt cct gag tca tgt gtt tat ggt gat aaa aat tct gat ttt tct gta	355
Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn Ser Asp Phe Ser Val	
70 75 80 85	
gca ctt gtc ggt gac tcc cac gct ggt cat tgg ctt cct gcc ttg gaa	403
Ala Leu Val Gly Asp Ser His Ala Gly His Trp Leu Pro Ala Leu Glu	
90 95 100	
cca att gct gaa gca cag ggg tgg aga ttg gaa gtt tat aca aag tca	451
Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu Val Tyr Thr Lys Ser	
105 110 115	
cag tgt cca ctc ata agc act gcg atc aaa ctt ggt gaa act ttt tat	499
Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu Gly Glu Thr Phe Tyr	
120 125 130	
gca gaa tgc tat gag tgg aat gaa aaa tta ctt gct aag cta act gga	547
Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu Ala Lys Leu Thr Gly	
135 140 145	
cct tct gca cca aat cat gtg att gta agt agc caa cgt tac gct tct	595
Pro Ser Ala Pro Asn His Val Ile Val Ser Ser Gln Arg Tyr Ala Ser	
150 155 160 165	
gca aat ccg tta atc gat agt gtc gcg acg gga acc gtt tcc gaa gga	643
Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly Thr Val Ser Glu Gly	
170 175 180	
tat gaa atg gca tgg aat tca tta aaa gat gca ggt gtt tct att tct	691
Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala Gly Val Ser Ile Ser	
185 190 195	
gta ctt ctt gat act cct cgg ccg caa att gat atc cca gaa tgt gta	739
Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp Ile Pro Glu Cys Val	
200 205 210	
gca tca aac cgc gat aat ctc tca gaa tgt tca gtt cac cgg agc gtt	787
Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser Val His Arg Ser Val	
215 220 225	
gcg ctt ggg act gaa gct cat cct cag caa aaa act gca gct caa aat	835
Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys Thr Ala Ala Gln Asn	
230 235 240 245	
ata gac gtg cct gta ttg gat ttg agt aat tgg att tgt ccg gaa gaa	883
Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp Ile Cys Pro Glu Glu	

250	255	260	
tat tgc tcc gct gtt atc gga aat gtt ttg gta tac agg gat tca cat			931
Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val Tyr Arg Asp Ser His			
265	270	275	
cat ttg acc gct acg tat gct cgt agt ctc tct agc gca tta tgg aat			979
His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser Ser Ala Leu Trp Asn			
280	285	290	
gag ttg gtt gcc tca aat ggt gag cct ttt aag taagaggtag ttgttcaagt			1032
Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys			
295	300		
agc			1035

<210> 560

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Leu Thr Pro Tyr Asp Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu
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Ala Ala Lys Asn Leu Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp
20 25 30

Ala Gly Glu Val Val Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala
35 40 45

Lys Ala Lys Arg Asp Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln
50 55 60

Glu Val Asn Glu Thr Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn
65 70 75 80

Ser Asp Phe Ser Val Ala Leu Val Gly Asp Ser His Ala Gly His Trp
85 90 95

Leu Pro Ala Leu Glu Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu
100 105 110

Val Tyr Thr Lys Ser Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu
115 120 125

Gly Glu Thr Phe Tyr Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu
130 135 140

Ala Lys Leu Thr Gly Pro Ser Ala Pro Asn His Val Ile Val Ser Ser
145 150 155 160

Gln Arg Tyr Ala Ser Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly
165 170 175

Thr Val Ser Glu Gly Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala
180 185 190

Gly Val Ser Ile Ser Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp
195 200 205

Ile Pro Glu Cys Val Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser
 210 215 220
 Val His Arg Ser Val Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys
 225 230 235 240
 Thr Ala Ala Gln Asn Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp
 245 250 255
 Ile Cys Pro Glu Glu Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val
 260 265 270
 Tyr Arg Asp Ser His His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser
 275 280 285
 Ser Ala Leu Trp Asn Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
 290 295 300

<210> 561
 <211> 1035
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> FRXA01263

<400> 561
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 atctccaaat agaagccaag ctgcgccacc ccaatttagt ttg acc ccg tat gat 115
 Leu Thr Pro Tyr Asp
 1 5
 cca acc gct gta aat aag gag tcg gaa aaa gaa gca gca aag aat ctg 163
 Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu Ala Ala Lys Asn Leu
 10 15 20
 ttt ggc gct gag gcg ttg aca gtg gat ccg gat gcc ggt gag gtt gtt 211
 Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp Ala Gly Glu Val Val
 25 30 35
 gat cga gta gat aat ttt tat ccg acg act gct aag gca aaa cga gat 259
 Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala Lys Ala Lys Arg Asp
 40 45 50
 tac cca agt aac tat gca gcg ggt tgt cac caa gaa gtc aat gag act 307
 Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln Glu Val Asn Glu Thr
 55 60 65
 agt cct gag tca tgt gtt tat ggt gat aaa aat tct gat ttt tct gta 355
 Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn Ser Asp Phe Ser Val
 70 75 80 85
 gca ctt gtc ggt gac tcc cac gct ggt cat tgg ctt cct gcc ttg gaa 403
 Ala Leu Val Gly Asp Ser His Ala Gly His Trp Leu Pro Ala Leu Glu
 90 95 100

cca att gct gaa gca cag ggg tgg aga ttg gaa gtt tat aca aag tca 451
Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu Val Tyr Thr Lys Ser
105 110 115

cag tgt cca ctc ata agc act gcg atc aaa ctt ggt gaa act ttt tat 499
Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu Gly Glu Thr Phe Tyr
120 125 130

gca gaa tgc tat gag tgg aat gaa aaa tta ctt gct aag cta act gga 547
Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu Ala Lys Leu Thr Gly
135 140 145

cct tct gca cca aat cat gtg att gta agt agc caa cgt tac gct tct 595
Pro Ser Ala Pro Asn His Val Ile Val Ser Ser Gln Arg Tyr Ala Ser
150 155 160 165

gca aat ccg tta atc gat agt gtc gcg acg gga acc gtt tcc gaa gga 643
Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly Thr Val Ser Glu Gly
170 175 180

tat gaa atg gca tgg aat tca tta aaa gat gca ggt gtt tct att tct 691
Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala Gly Val Ser Ile Ser
185 190 195

gta ctt ctt gat act cct cgg ccg caa att gat atc cca gaa tgt gta 739
Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp Ile Pro Glu Cys Val
200 205 210

gca tca aac cgc gat aat ctc tca gaa tgt tca gtt cac cgg agc gtt 787
Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser Val His Arg Ser Val
215 220 225

gcg ctt ggg act gaa gct cat cct cag caa aaa act gca gct caa aat 835
Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys Thr Ala Ala Gln Asn
230 235 240 245

ata gac gtg cct gta ttg gat ttg agt aat tgg att tgt ccg gaa gaa 883
Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp Ile Cys Pro Glu Glu
250 255 260

tat tgc tcc gct gtt atc gga aat gtt ttg gta tac agg gat tca cat 931
Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val Tyr Arg Asp Ser His
265 270 275

cat ttg acc gct acg tat gct cgt agt ctc tct agc gca tta tgg aat 979
His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser Ser Ala Leu Trp Asn
280 285 290

gag ttg gtt gcc tca aat ggt gag cct ttt aag taagaggtag ttgttcaagt 1032
Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
295 300

agc 1035

<210> 562

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 562

Leu Thr Pro Tyr Asp Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu
 1 5 10 15
 Ala Ala Lys Asn Leu Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp
 20 25 30
 Ala Gly Glu Val Val Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala
 35 40 45
 Lys Ala Lys Arg Asp Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln
 50 55 60
 Glu Val Asn Glu Thr Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn
 65 70 75 80
 Ser Asp Phe Ser Val Ala Leu Val Gly Asp Ser His Ala Gly His Trp
 85 90 95
 Leu Pro Ala Leu Glu Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu
 100 105 110
 Val Tyr Thr Lys Ser Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu
 115 120 125
 Gly Glu Thr Phe Tyr Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu
 130 135 140
 Ala Lys Leu Thr Gly Pro Ser Ala Pro Asn His Val Ile Val Ser Ser
 145 150 155 160
 Gln Arg Tyr Ala Ser Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly
 165 170 175
 Thr Val Ser Glu Gly Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala
 180 185 190
 Gly Val Ser Ile Ser Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp
 195 200 205
 Ile Pro Glu Cys Val Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser
 210 215 220
 Val His Arg Ser Val Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys
 225 230 235 240
 Thr Ala Ala Gln Asn Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp
 245 250 255
 Ile Cys Pro Glu Glu Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val
 260 265 270
 Tyr Arg Asp Ser His His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser
 275 280 285
 Ser Ala Leu Trp Asn Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
 290 295 300

<210> 563

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1135)

<223> RXN01266

<400> 563

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gattgtgaag ttttatatct gtcataattct ggtgattttc gccctgctca tgaagtggcg 60

gacgagcaat ggcccgatat agatttagta aggaactaaa atg cca aaa gta agt 115
               Met Pro Lys Val Ser
               1 5

gtg gtt act ggt ttt tat aac cgc tgt gag cat tta gaa cga acc att 163
Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His Leu Glu Arg Thr Ile
               10 15 20

gag tct att ctt aac caa act tat agc gat ttt gaa tta att gtt ttt 211
Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe Glu Leu Ile Val Phe
               25 30 35

gat gat gca tcg aca gat gga aca gct tca cga ttg tta gag tta aaa 259
Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg Leu Leu Glu Leu Lys
               40 45 50

gaa aaa tat gat gat ccg cgt ttc cga ttt atc att cat gaa gag aat 307
Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile Ile His Glu Glu Asn
               55 60 65

aaa ggt ttc gta aaa ggg tta tca gaa gca att tct gga gct aaa ggg 355
Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile Ser Gly Ala Lys Gly
               70 75 80 85

cag tat att gca gtc cag gga tca ggc gat gta tct ctt cct cgc cgt 403
Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val Ser Leu Pro Arg Arg
               90 95 100

tta gag ctt cag gta gag ttt cta gac gcg aat cct tcg gta ggt gct 451
Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn Pro Ser Val Gly Ala
               105 110 115

gtg ggt ggt gct atc tat aat att caa gaa gat acg gga aca cgc aac 499
Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp Thr Gly Thr Arg Asn
               120 125 130

cca cag aga ttt gaa aag cca att gct aca ttc gat gat tta ttg aca 547
Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe Asp Asp Leu Leu Thr
               135 140 145

tct aat ccg ttc act cac gga gaa gtg atg tat cgc tta gac ctt tat 595
Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr Arg Leu Asp Leu Tyr
               150 155 160 165

aag agt ata ggt ggg tat cga agt ggc ttt act ttt gct caa gat cgt 643
Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr Phe Ala Gln Asp Arg
               170 175 180

gat tta tgg ttg agg atg gcg aaa aaa gca gat ctg ggt atc att cca 691
Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp Leu Gly Ile Ile Pro
               185 190 195

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gat ttt ctt tat cac cgt tac aca ctt tta gat ggt gtc tct ttc gtc 739
Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp Gly Val Ser Phe Val
200 205 210

ccg gat aaa act ata cgt cag cga tgc ttt tca gaa gct gcg gtg cga 787
Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser Glu Ala Ala Val Arg
215 220 225

ctg gca tta atg cca gaa gag gaa gga gct tta gcc tac tct agg ctg 835
Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu Ala Tyr Ser Arg Leu
230 235 240 245

gaa gct gaa ggg cct act gcc gta gtt cct atc gct gat aga gct gtt 883
Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile Ala Asp Arg Ala Val
250 255 260

cag aaa ttt gtc cct aaa gcg gct att cgc tta tgt cta tat ggt gct 931
Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu Cys Leu Tyr Gly Ala
265 270 275

ccg gaa act ggt tta cac atg gct cga gac tat atc cag aac cct ctg 979
Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr Ile Gln Asn Pro Leu
280 285 290

cgc cgt acc ata gtt gta gtt ttg atc agc atc tat tcg tct aga tta 1027
Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile Tyr Ser Ser Arg Leu
295 300 305

att aag cct ctt caa gat att cta tat aag tct att ttt aag ggg gtc 1075
Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser Ile Phe Lys Gly Val
310 315 320 325

tcg att tct aaa cct att aag agt tca ctc gtg aag ttt aca aga aga 1123
Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val Lys Phe Thr Arg Arg
330 335 340 345

att caa ggg aag tagcgaaaaa ccgcatctac caa 1158
Ile Gln Gly Lys
345

<210> 564

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

Met Pro Lys Val Ser Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His
1 5 10 15

Leu Glu Arg Thr Ile Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe
20 25 30

Glu Leu Ile Val Phe Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg
35 40 45

Leu Leu Glu Leu Lys Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile
50 55 60

Ile His Glu Glu Asn Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile

65	70	75	80
Ser Gly Ala Lys Gly Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val	85	90	95
Ser Leu Pro Arg Arg Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn	100	105	110
Pro Ser Val Gly Ala Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp	115	120	125
Thr Gly Thr Arg Asn Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe	130	135	140
Asp Asp Leu Leu Thr Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr	145	150	155
Arg Leu Asp Leu Tyr Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr	165	170	175
Phe Ala Gln Asp Arg Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp	180	185	190
Leu Gly Ile Ile Pro Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp	195	200	205
Gly Val Ser Phe Val Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser	210	215	220
Glu Ala Ala Val Arg Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu	225	230	235
Ala Tyr Ser Arg Leu Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile	245	250	255
Ala Asp Arg Ala Val Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu	260	265	270
Cys Leu Tyr Gly Ala Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr	275	280	285
Ile Gln Asn Pro Leu Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile	290	295	300
Tyr Ser Ser Arg Leu Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser	305	310	315
Ile Phe Lys Gly Val Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val	325	330	335
Lys Phe Thr Arg Arg Ile Gln Gly Lys	340	345	

<210> 565

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1135)

<223> FRXA01266

<400> 565

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gacgagcaat ggccccgatat agatttagta aggaactaaa atg cca aaa gta agt 115
Met Pro Lys Val Ser
1 5

gtg gtt act ggt ttt tat aac cgc tgt gag cat tta gaa cga acc att 163
Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His Leu Glu Arg Thr Ile
10 15 20

gag tct att ctt aac caa act tat agc gat ttt gaa tta att gtt ttt 211
Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe Glu Leu Ile Val Phe
25 30 35

gat gat gca tcg aca gat gga aca gct tca cga ttg tta gag tta aaa 259
Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg Leu Leu Glu Leu Lys
40 45 50

gaa aaa tat gat gat ccg cgt ttc cga ttt atc att cat gaa gag aat 307
Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile Ile His Glu Glu Asn
55 60 65

aaa ggt ttc gta aaa ggg tta tca gaa gca att tct gga gct aaa ggg 355
Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile Ser Gly Ala Lys Gly
70 75 80 85

cag tat att gca gtc cag gga tca ggc gat gta tct ctt cct cgc cgt 403
Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val Ser Leu Pro Arg Arg
90 95 100

tta gag ctt cag gta gag ttt cta gac gcg aat cct tcg gta ggt gct 451
Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn Pro Ser Val Gly Ala
105 110 115

gtg ggt ggt gct atc tat aat att caa gaa gat acg gga aca cgc aac 499
Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp Thr Gly Thr Arg Asn
120 125 130

cca cag aga ttt gaa aag cca att gct aca ttc gat gat tta ttg aca 547
Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe Asp Asp Leu Leu Thr
135 140 145

tct aat ccg ttc act cac gga gaa gtg atg tat cgc tta gac ctt tat 595
Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr Arg Leu Asp Leu Tyr
150 155 160 165

aag agt ata ggt ggg tat cga agt ggc ttt act ttt gct caa gat cgt 643
Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr Phe Ala Gln Asp Arg
170 175 180

gat tta tgg ttg agg atg gcg aaa aaa gca gat ctg ggt atc att cca 691
Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp Leu Gly Ile Ile Pro
185 190 195

gat ttt ctt tat cac cgt tac aca ctt tta gat ggt gtc tct ttc gtc 739
Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp Gly Val Ser Phe Val
200 205 210

ccg gat aaa act ata cgt cag cga tgc ttt tca gaa gct gcg gtg cga 787
 Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser Glu Ala Ala Val Arg
 215 220 225
 ctg gca tta atg cca gaa gag gaa gga gct tta gcc tac tct agg ctg 835
 Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu Ala Tyr Ser Arg Leu
 230 235 240 245
 gaa gct gaa ggg cct act gcc gta gtt cct atc gct gat aga gct gtt 883
 Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile Ala Asp Arg Ala Val
 250 255 260
 cag aaa ttt gtc cct aaa gcg gct att cgc tta tgt cta tat ggt gct 931
 Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu Cys Leu Tyr Gly Ala
 265 270 275
 ccg gaa act ggt tta cac atg gct cga gac tat atc cag aac cct ctg 979
 Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr Ile Gln Asn Pro Leu
 280 285 290
 cgc cgt acc ata gtt gta gtt ttg atc agc atc tat tcg tct aga tta 1027
 Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile Tyr Ser Ser Arg Leu
 295 300 305
 att aag cct ctt caa gat att cta tat aag tct att ttt aag ggg gtc 1075
 Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser Ile Phe Lys Gly Val
 310 315 320 325
 tcg att tct aaa cct att aag agt tca ctc gtg aag ttt aca aga aga 1123
 Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val Lys Phe Thr Arg Arg
 330 335 340
 att caa ggg aag tagcgaaaaa ccgcatctac caa 1158
 Ile Gln Gly Lys
 345

<210> 566

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 566

Met Pro Lys Val Ser Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His
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 Leu Glu Arg Thr Ile Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe
 20 25 30
 Glu Leu Ile Val Phe Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg
 35 40 45
 Leu Leu Glu Leu Lys Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile
 50 55 60
 Ile His Glu Glu Asn Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile
 65 70 75 80
 Ser Gly Ala Lys Gly Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val
 85 90 95

Ser Leu Pro Arg Arg Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn
 100 105 110
 Pro Ser Val Gly Ala Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp
 115 120 125
 Thr Gly Thr Arg Asn Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe
 130 135 140
 Asp Asp Leu Leu Thr Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr
 145 150 155 160
 Arg Leu Asp Leu Tyr Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr
 165 170 175
 Phe Ala Gln Asp Arg Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp
 180 185 190
 Leu Gly Ile Ile Pro Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp
 195 200 205
 Gly Val Ser Phe Val Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser
 210 215 220
 Glu Ala Ala Val Arg Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu
 225 230 235 240
 Ala Tyr Ser Arg Leu Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile
 245 250 255
 Ala Asp Arg Ala Val Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu
 260 265 270
 Cys Leu Tyr Gly Ala Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr
 275 280 285
 Ile Gln Asn Pro Leu Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile
 290 295 300
 Tyr Ser Ser Arg Leu Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser
 305 310 315 320
 Ile Phe Lys Gly Val Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val
 325 330 335
 Lys Phe Thr Arg Arg Ile Gln Gly Lys
 340 345

<210> 567
 <211> 1041
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1018)
 <223> RXN01275

<400> 567

cgccatacta ggctcggcct ttctgacggg aactcggata ggcttctgta aaaccatccc 60

cggtgaagag agactcgtgg ctgaaataac caccaccatta atg gaa aaa att cgc 115
Met Glu Lys Ile Arg
1 5

tca ccc gca gtc caa tca gat gca ctg cag gtt ttt aaa tca gca ctt 163
Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val Phe Lys Ser Ala Leu
10 15 20

gct gcg aca gtc acg tgg tgg att tcg gtt aac ctc ctt aac tcc caa 211
Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn Leu Leu Asn Ser Gln
25 30 35

cta ccc ttt tta gct ccc tgg gta gcg tta atg acg atg caa ttc acc 259
Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met Thr Met Gln Phe Thr
40 45 50

gtc tac cac acc ttt atc agt gga att cag act gca att gct tct gtc 307
Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr Ala Ile Ala Ser Val
55 60 65

atc gga gtt gga ctt tcc ttt gtc ata ggc act tac tta gac gta agt 355
Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr Tyr Leu Asp Val Ser
70 75 80 85

gtg tgg act ttt ggc ctt gca atg gtc ata gga tta ata ggt gca cga 403
Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly Leu Ile Gly Ala Arg
90 95 100

gta cca aag ctc cgc gcg gaa gga ata ggt att gct act aca tcc att 451
Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile Ala Thr Thr Ser Ile
105 110 115

ttt ctt ctt gcc tcc ggg ttt gat gat caa caa ccc ctt cta tac gac 499
Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln Pro Leu Leu Tyr Asp
120 125 130

cgt att tta gag atc ctg ctc ggc gtg gct gtt gcc ata gcc atc aac 547
Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val Ala Ile Ala Ile Asn
135 140 145

ctc atc atc ttt cct ccc tta cgc gac cag gag gca aac atg gtg gta 595
Leu Ile Ile Phe Pro Leu Arg Asp Gln Glu Ala Asn Met Val Val
150 155 160 165

gga aac tta gat cgg agg atg ggt gag gtt tta caa aaa atg gcc gat 643
Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu Gln Lys Met Ala Asp
170 175 180

gag ctt gca gaa aag tgg aat atc gac aat gca gat gag tgg ctg gaa 691
Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala Asp Glu Trp Leu Glu
185 190 195

gaa att aat tct att aac aat gac cta gaa aaa gcg tgg cac tcc gtg 739
Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys Ala Trp His Ser Val
200 205 210

cgg ttc gtt cgc gaa agc cgt cga gtt aat cct cgt aaa atc cgc atc 787
Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro Arg Lys Ile Arg Ile
215 220 225

caa gag ggc cgc ccc cag cct acg gaa aca agt tat gaa tca aac ctc 835
 Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser Tyr Glu Ser Asn Leu
 230 235 240 245
 acc agc att gat gaa ggg atc gct cat tta cgc cac ctt gcc cgt act 883
 Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg His Leu Ala Arg Thr
 250 255 260
 ctt cgt gat acc ccg att ata gat tcc gac tgg gga tcc agt att cca 931
 Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp Gly Ser Ser Ile Pro
 265 270 275
 gca aca gtg ggt atc cct tat gca cga tgc cgg agc ttt gct cgc aga 979
 Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg Ser Phe Ala Arg Arg
 280 285 290
 tcc gaa tca gga aat aga tcc tat ccg cga ccg gct ctc taaactttca 1028
 Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro Ala Leu
 295 300 305
 agtgagatga gtg 1041

<210> 568
 <211> 306
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 568
 Met Glu Lys Ile Arg Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val
 1 5 10 15
 Phe Lys Ser Ala Leu Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn
 20 25 30
 Leu Leu Asn Ser Gln Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met
 35 40 45
 Thr Met Gln Phe Thr Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr
 50 55 60
 Ala Ile Ala Ser Val Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr
 65 70 75 80
 Tyr Leu Asp Val Ser Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly
 85 90 95
 Leu Ile Gly Ala Arg Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile
 100 105 110
 Ala Thr Thr Ser Ile Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln
 115 120 125
 Pro Leu Leu Tyr Asp Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val
 130 135 140
 Ala Ile Ala Ile Asn Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu
 145 150 155 160
 Ala Asn Met Val Val Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu

55	60	65	
atc gga gtt gga ctt tcc ttt gtc ata ggc act tac tta gac gta agt			355
Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr Tyr Leu Asp Val Ser			
70	75	80	85
gtg tgg act ttt ggc ctt gca atg gtc ata gga tta ata ggt gca cga			403
Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly Leu Ile Gly Ala Arg			
	90	95	100
gta cca aag ctc cgc gcg gaa gga ata ggt att gct act aca tcc att			451
Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile Ala Thr Thr Ser Ile			
	105	110	115
ttt ctt ctt gcc tcc ggg ttt gat gat caa caa ccc ctt cta tac gac			499
Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln Pro Leu Leu Tyr Asp			
	120	125	130
cgt att tta gag atc ctg ctc ggc gtg gct gtt gcc ata gcc atc aac			547
Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val Ala Ile Ala Ile Asn			
	135	140	145
ctc atc atc ttt cct ccc tta cgc gac cag gag gca aac atg gtg gta			595
Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu Ala Asn Met Val Val			
	150	155	160
gga aac tta gat cgg agg atg ggt gag gtt tta caa aaa atg gcc gat			643
Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu Gln Lys Met Ala Asp			
	170	175	180
gag ctt gca gaa aag tgg aat atc gac aat gca gat gag tgg ctg gaa			691
Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala Asp Glu Trp Leu Glu			
	185	190	195
gaa att aat tct att aac aat gac cta gaa aaa gcg tgg cac tcc gtg			739
Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys Ala Trp His Ser Val			
	200	205	210
cgg ttc gtt cgc gaa agc cgt cga gtt aat cct cgt aaa atc cgc atc			787
Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro Arg Lys Ile Arg Ile			
	215	220	225
caa gag ggc cgc ccc cag cct acg gaa aca agt tat gaa tca aac ctc			835
Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser Tyr Glu Ser Asn Leu			
	230	235	240
acc agc att gat gaa ggg atc gct cat tta cgc cac ctt gcc cgt act			883
Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg His Leu Ala Arg Thr			
	250	255	260
ctt cgt gat acc ccg att ata gat tcc gac tgg gga tcc agt att cca			931
Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp Gly Ser Ser Ile Pro			
	265	270	275
gca aca gtg ggt atc cct tat gca cga tgc cgg agc ttt gct cgc aga			979
Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg Ser Phe Ala Arg Arg			
	280	285	290
tcc gaa tca gga aat aga tcc tat ccg cga ccg gct ctc taaactttca			1028
Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro Ala Leu			
	295	300	305

agtgagatga gtg

1041

<210> 570

<211> 306

<212> PRT

<213> Corynebacterium glutamicum

<400> 570

Met Glu Lys Ile Arg Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val
1 5 10 15

Phe Lys Ser Ala Leu Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn
20 25 30

Leu Leu Asn Ser Gln Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met
35 40 45

Thr Met Gln Phe Thr Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr
50 55 60

Ala Ile Ala Ser Val Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr
65 70 75 80

Tyr Leu Asp Val Ser Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly
85 90 95

Leu Ile Gly Ala Arg Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile
100 105 110

Ala Thr Thr Ser Ile Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln
115 120 125

Pro Leu Leu Tyr Asp Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val
130 135 140

Ala Ile Ala Ile Asn Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu
145 150 155 160

Ala Asn Met Val Val Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu
165 170 175

Gln Lys Met Ala Asp Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala
180 185 190

Asp Glu Trp Leu Glu Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys
195 200 205

Ala Trp His Ser Val Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro
210 215 220

Arg Lys Ile Arg Ile Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser
225 230 235 240

Tyr Glu Ser Asn Leu Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg
245 250 255

His Leu Ala Arg Thr Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp
260 265 270

Gly Ser Ser Ile Pro Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg
 275 280 285

Ser Phe Ala Arg Arg Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro
 290 295 300

Ala Leu
 305

<210> 571
 <211> 885
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(862)
 <223> RXN01281

<400> 571
 ggacaacctc atcaaattgca aacatgcgcc accgcgtccc ggaaaaccag gggcgataacc 60
 gcgcttgagt gcgaggtgcc gtcaattccc aactacaaga gtg gga ctc agc cgt 115
 Val Gly Leu Ser Arg
 1 5
 tca cat tat cag cta gcc gca gaa aac acc aaa tcc ctt gtt aga atg 163
 Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys Ser Leu Val Arg Met
 10 15 20
 gtt ccc atg act gtt cct caa gga aac gaa cca gca aag aag ctc gcc 211
 Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro Ala Lys Lys Leu Ala
 25 30 35
 act gac ctt aac cga aac caa gtc gtg gat gaa ctt tct gca gct gtt 259
 Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu Leu Ser Ala Ala Val
 40 45 50
 tcc cga ggt caa ctc act ttg gag gaa ttt gaa gat cgc tcc tcc aaa 307
 Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu Asp Arg Ser Ser Lys
 55 60 65
 gca tgg aat gcc cgc cac tta gac act ctt gta gag ctg atc tct gat 355
 Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val Glu Leu Ile Ser Asp
 70 75 80 85
 gtg aac gac aat ccc tac act ctg ctt ggt cag caa ttt ccc ggc gcc 403
 Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln Gln Phe Pro Gly Ala
 90 95 100
 tcc tat gcg ccg gcg gcc tac gag acc act ccc cca gcg atg ccc aat 451
 Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro Pro Ala Met Pro Asn
 105 110 115
 gtg tca gat cct gta aat att gtc cgc aac agg att acc ggc aac ccg 499
 Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg Ile Thr Gly Asn Pro
 120 125 130
 aat ggc tcc aaa atg tcg gtc tcg ttt atg ggt ggc acc gtg cgc aaa 547
 Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly Gly Thr Val Arg Lys

135	140	145	
ggt gga tgg cat gtg cct aat gtt cac aca tcc ttc gcc atg atg ggc			595
Gly Gly Trp His Val Pro Asn Val His Thr Ser Phe Ala Met Met Gly			
150	155	160	165
ggc aat cag atc gat ttg cgc gac gcc ttc ctg gaa agc gac cgc att			643
Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu Glu Ser Asp Arg Ile			
	170	175	180
cag atc aac gcc tac aca ttc atg ggt ggc atc gag att att gtt ccc			691
Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile Glu Ile Ile Val Pro			
	185	190	195
gag ggt gtt ttt gtc att tgt gat ggc atg ggc att ttc ggc ggc ttc			739
Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly Ile Phe Gly Gly Phe			
	200	205	210
gaa cag tct gtg gac aag gcc ggt gca ctc aat ccc gcg cgc ctg cca			787
Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn Pro Ala Arg Leu Pro			
	215	220	225
agc aac gcg ccc acg gtc cac atc aaa ggc ctg gcg ttc atg ggc gga			835
Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu Ala Phe Met Gly Gly			
230	235	240	245
gtc agc gta gtc acc aag aaa aac att taaaaagctt gtcgacgcgc			882
Val Ser Val Val Thr Lys Lys Asn Ile			
	250		
ccc			885

<210> 572

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

Val Gly Leu Ser Arg Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys
1 5 10 15

Ser Leu Val Arg Met Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro
20 25 30

Ala Lys Lys Leu Ala Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu
35 40 45

Leu Ser Ala Ala Val Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu
50 55 60

Asp Arg Ser Ser Lys Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val
65 70 75 80

Glu Leu Ile Ser Asp Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln
85 90 95

Gln Phe Pro Gly Ala Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro
100 105 110

Pro Ala Met Pro Asn Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg

115	120	125
Ile Thr Gly Asn Pro Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly 130 135 140		
Gly Thr Val Arg Lys Gly Gly Trp His Val Pro Asn Val His Thr Ser 145 150 155 160		
Phe Ala Met Met Gly Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu 165 170 175		
Glu Ser Asp Arg Ile Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile 180 185 190		
Glu Ile Ile Val Pro Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly 195 200 205		
Ile Phe Gly Gly Phe Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn 210 215 220		
Pro Ala Arg Leu Pro Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu 225 230 235 240		
Ala Phe Met Gly Gly Val Ser Val Val Thr Lys Lys Asn Ile 245 250		

<210> 573
 <211> 885
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(862)
 <223> FRXA01281

<400> 573
 ggacaacctc atcaaatgca aacatgcgcc accgcgtccc ggaaaaccag gggcgatacc 60

gcgcttgagt gcgaggtgcc gtcaattccc aactacaaga gtg gga ctc agc cgt 115
 Val Gly Leu Ser Arg
 1 5

tca cat tat cag cta gcc gca gaa aac acc aaa tcc ctt gtt aga atg 163
 Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys Ser Leu Val Arg Met
 10 15 20

gtt ccc atg act gtt cct caa gga aac gaa cca gca aag aag ctc gcc 211
 Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro Ala Lys Lys Leu Ala
 25 30 35

act gac ctt aac cga aac caa gtc gtg gat gaa ctt tct gca gct gtt 259
 Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu Leu Ser Ala Ala Val
 40 45 50

tcc cga ggt caa ctc act ttg gag gaa ttt gaa gat cgc tcc tcc aaa 307
 Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu Asp Arg Ser Ser Lys
 55 60 65

gca tgg aat gcc cgc cac tta gac act ctt gta gag ctg atc tct gat 355

Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val Glu Leu Ile Ser Asp
70 75 80 85

gtg aac gac aat ccc tac act ctg ctt ggt cag caa ttt ccc ggc gcc 403
Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln Gln Phe Pro Gly Ala
90 95 100

tcc tat gcg ccg gcg gcc tac gag acc act ccc cca gcg atg ccc aat 451
Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro Pro Ala Met Pro Asn
105 110 115

gtg tca gat cct gta aat att gtc cgc aac agg att acc ggc aac ccg 499
Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg Ile Thr Gly Asn Pro
120 125 130

aat ggc tcc aaa atg tcg gtc tcg ttt atg ggt ggc acc gtg cgc aaa 547
Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly Gly Thr Val Arg Lys
135 140 145

ggg gga tgg cat gtg cct aat gtt cac aca tcc ttc gcc atg atg ggc 595
Gly Gly Trp His Val Pro Asn Val His Thr Ser Phe Ala Met Met Gly
150 155 160 165

ggc aat cag atc gat ttg cgc gac gcc ttc ctg gaa agc gac cgc att 643
Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu Glu Ser Asp Arg Ile
170 175 180

cag atc aac gcc tac aca ttc atg ggt ggc atc gag att att gtt ccc 691
Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile Glu Ile Ile Val Pro
185 190 195

gag ggt gtt ttt gtc att tgt gat ggc atg ggc att ttc ggc ggc ttc 739
Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly Ile Phe Gly Gly Phe
200 205 210

gaa cag tct gtg gac aag gcc ggt gca ctc aat ccc gcg cgc ctg cca 787
Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn Pro Ala Arg Leu Pro
215 220 225

agc aac gcg ccc acg gtc cac atc aaa ggc ctg gcg ttc atg ggc gga 835
Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu Ala Phe Met Gly Gly
230 235 240 245

gtc agc gta gtc acc aag aaa aac att taaaaagctt gtgcacgcgc 882
Val Ser Val Val Thr Lys Lys Asn Ile
250

ccc 885

<210> 574

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 574

Val Gly Leu Ser Arg Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys
1 5 10 15

Ser Leu Val Arg Met Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro
20 25 30

Ala Lys Lys Leu Ala Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu
35 40 45

Leu Ser Ala Ala Val Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu
50 55 60

Asp Arg Ser Ser Lys Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val
65 70 75 80

Glu Leu Ile Ser Asp Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln
85 90 95

Gln Phe Pro Gly Ala Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro
100 105 110

Pro Ala Met Pro Asn Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg
115 120 125

Ile Thr Gly Asn Pro Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly
130 135 140

Gly Thr Val Arg Lys Gly Gly Trp His Val Pro Asn Val His Thr Ser
145 150 155 160

Phe Ala Met Met Gly Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu
165 170 175

Glu Ser Asp Arg Ile Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile
180 185 190

Glu Ile Ile Val Pro Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly
195 200 205

Ile Phe Gly Gly Phe Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn
210 215 220

Pro Ala Arg Leu Pro Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu
225 230 235 240

Ala Phe Met Gly Gly Val Ser Val Val Thr Lys Lys Asn Ile
245 250

<210> 575
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXN01296

<400> 575
taaaactcct gttcgaaatt gccagacag gtgtccacca acactgctac attgcattgg 60
agatccagaa tcgatcactc tacgaccagg aaaaactttc atg tcc atc gag caa 115
Met Ser Ile Glu Gln
1 5

gca atc act tca ctc tcc gca aga gtg cgg gaa cta aag ccc atc atc	163
Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu Leu Lys Pro Ile Ile	
10 15 20	
gag act gaa gaa gcc acc aaa acc gca ctg atc atc ccc ttt atc agc	211
Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile Ile Pro Phe Ile Ser	
25 30 35	
aac gtt ctc ggc tac gac gtc act gat cct cgt gaa gtc att ccg gaa	259
Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg Glu Val Ile Pro Glu	
40 45 50	
tac act gct gat gtt ggc gtc aaa aag ggt gag aag gtc gac ttc gct	307
Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu Lys Val Asp Phe Ala	
55 60 65	
atc aaa acc ggc gat gat ttc cac ttc ctc atc gaa tgc aaa aag gtc	355
Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile Glu Cys Lys Lys Val	
70 75 80 85	
ggc tcc cca ctc agc ctc gat cac gct aac cag ctc gtc cgc tat ttc	403
Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln Leu Val Arg Tyr Phe	
90 95 100	
aat gtc aca gac acc gaa ttt gcc att ctc acc aac ggc gaa atc tac	451
Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr Asn Gly Glu Ile Tyr	
105 110 115	
caa ttc tat gga caa ctc gat gca gcc aac cgc atg gat gca aaa cca	499
Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg Met Asp Ala Lys Pro	
120 125 130	
ttc atg acc ttg gat ttg aac aat att gat gcc cgt cag ttc cct cat	547
Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala Arg Gln Phe Pro His	
135 140 145	
ttg gaa atg tgt acc cgc aag cat ttc aac cca caa gcg cta gcc gcc	595
Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro Gln Ala Leu Ala Ala	
150 155 160 165	
aac gct gaa gaa ctg aag tac att gct gaa ttg aag aaa gtc atc gcg	643
Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu Lys Lys Val Ile Ala	
170 175 180	
aat caa ttc caa gaa cct gac gta gaa atc gtc aag atg ctt gcg gcg	691
Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val Lys Met Leu Ala Ala	
185 190 195	
aca gtc acc aca aag cgt atg act gca caa aat ctg gaa ttc ttc acc	739
Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn Leu Glu Phe Phe Thr	
200 205 210	
cgc ttg gtt aat act gcg tct tcc cag ttc ctc aaa gac gag gtc aat	787
Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu Lys Asp Glu Val Asn	
215 220 225	
cgt aga ttg cgc tcc gcc caa gtc ttt gag gat cct gtc caa aca caa	835
Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp Pro Val Gln Thr Gln	
230 235 240 245	
ggg gct gat gca gaa aca cca gca gag gac gaa gca gta atc gaa gaa	883

Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu Ala Val Ile Glu Glu
 250 255 260
 gtg gtt tca gaa atc gtg acg aca gaa gag gaa atc cac ggt cat tca 931
 Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu Ile His Gly His Ser
 265 270 275
 att gtc cgt gca att tgc tgc tca gag gta tcg gca caa gaa atc acc 979
 Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser Ala Gln Glu Ile Thr
 280 285 290
 atg cgt gac gca aaa tcc tac tgc gct att ctc ttc caa gac aac aac 1027
 Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu Phe Gln Asp Asn Asn
 295 300 305
 cga aag cca atc gcc cgt ttc tac ttt gat cgc aag att cca cgc atc 1075
 Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg Lys Ile Pro Arg Ile
 310 315 320 325
 ggc atc ttc aat gct gaa ggc gag cag gaa cac ttt gat ttg gaa tcc 1123
 Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His Phe Asp Leu Glu Ser
 330 335 340
 atc gaa gat atc tac aac cac gct gat ctt ctg cat tcc cgc gtc gta 1171
 Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu His Ser Arg Val Val
 345 350 355
 gca ttg aac gct taagttctgc ctttagttct gca 1206
 Ala Leu Asn Ala
 360

<210> 576

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

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 20 25 30
 Ile Pro Phe Ile Ser Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg
 35 40 45
 Glu Val Ile Pro Glu Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu
 50 55 60
 Lys Val Asp Phe Ala Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile
 65 70 75 80
 Glu Cys Lys Lys Val Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln
 85 90 95
 Leu Val Arg Tyr Phe Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr
 100 105 110
 Asn Gly Glu Ile Tyr Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg
 115 120 125

Met Asp Ala Lys Pro Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala
 130 135 140
 Arg Gln Phe Pro His Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro
 145 150 155 160
 Gln Ala Leu Ala Ala Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu
 165 170 175
 Lys Lys Val Ile Ala Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val
 180 185 190
 Lys Met Leu Ala Ala Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn
 195 200 205
 Leu Glu Phe Phe Thr Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu
 210 215 220
 Lys Asp Glu Val Asn Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp
 225 230 235 240
 Pro Val Gln Thr Gln Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu
 245 250 255
 Ala Val Ile Glu Glu Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu
 260 265 270
 Ile His Gly His Ser Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser
 275 280 285
 Ala Gln Glu Ile Thr Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu
 290 295 300
 Phe Gln Asp Asn Asn Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg
 305 310 315 320
 Lys Ile Pro Arg Ile Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His
 325 330 335
 Phe Asp Leu Glu Ser Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu
 340 345 350
 His Ser Arg Val Val Ala Leu Asn Ala
 355 360

<210> 577

<211> 1206

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1183)

<223> FRXA01296

<400> 577

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Met Ser Ile Glu Gln
1 5

230	235	240	245	
ggt gct gat gca gaa aca cca gca gag gac gaa gca gta atc gaa gaa				883
Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu Ala Val Ile Glu Glu				
	250	255	260	
gtg gtt tca gaa atc gtg acg aca gaa gag gaa atc cac ggt cat tca				931
Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu Ile His Gly His Ser				
	265	270	275	
att gtc cgt gca att tgc tgc tca gag gta tcg gca caa gaa atc acc				979
Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser Ala Gln Glu Ile Thr				
	280	285	290	
atg cgt gac gca aaa tcc tac tgc gct att ctc ttc caa gac aac aac				1027
Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu Phe Gln Asp Asn Asn				
	295	300	305	
cga aag cca atc gcc cgt ttc tac ttt gat cgc aag att cca cgc atc				1075
Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg Lys Ile Pro Arg Ile				
	310	315	320	325
ggc atc ttc aat gct gaa ggc gag cag gaa cac ttt gat ttg gaa tcc				1123
Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His Phe Asp Leu Glu Ser				
	330	335	340	
atc gaa gat atc tac aac cac gct gat ctt ctg cat tcc cgc gtc gta				1171
Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu His Ser Arg Val Val				
	345	350	355	
gca ttg aac gct taagttctgc ctttagttct gca				1206
Ala Leu Asn Ala				
	360			

<210> 578

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 578

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			20					25					30		

Ile	Pro	Phe	Ile	Ser	Asn	Val	Leu	Gly	Tyr	Asp	Val	Thr	Asp	Pro	Arg
		35					40					45			

Glu	Val	Ile	Pro	Glu	Tyr	Thr	Ala	Asp	Val	Gly	Val	Lys	Lys	Gly	Glu
	50					55				60					

Lys	Val	Asp	Phe	Ala	Ile	Lys	Thr	Gly	Asp	Asp	Phe	His	Phe	Leu	Ile
65					70				75					80	

Glu	Cys	Lys	Lys	Val	Gly	Ser	Pro	Leu	Ser	Leu	Asp	His	Ala	Asn	Gln
				85				90						95	

Leu	Val	Arg	Tyr	Phe	Asn	Val	Thr	Asp	Thr	Glu	Phe	Ala	Ile	Leu	Thr
			100					105					110		

Asn Gly Glu Ile Tyr Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg
115 120 125

Met Asp Ala Lys Pro Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala
130 135 140

Arg Gln Phe Pro His Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro
145 150 155 160

Gln Ala Leu Ala Ala Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu
165 170 175

Lys Lys Val Ile Ala Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val
180 185 190

Lys Met Leu Ala Ala Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn
195 200 205

Leu Glu Phe Phe Thr Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu
210 215 220

Lys Asp Glu Val Asn Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp
225 230 235 240

Pro Val Gln Thr Gln Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu
245 250 255

Ala Val Ile Glu Glu Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu
260 265 270

Ile His Gly His Ser Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser
275 280 285

Ala Gln Glu Ile Thr Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu
290 295 300

Phe Gln Asp Asn Asn Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg
305 310 315 320

Lys Ile Pro Arg Ile Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His
325 330 335

Phe Asp Leu Glu Ser Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu
340 345 350

His Ser Arg Val Val Ala Leu Asn Ala
355 360

<210> 579

<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1108)

<223> RXN01306

<400> 579


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ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac      883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His
                250                      255                      260

gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct      931
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala
                265                      270                      275

tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta      979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu
                280                      285                      290

cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg      1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala
                295                      300                      305

gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat      1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp
310                      315                      320                      325

cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct 1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
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gaa                                                                    1131

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<210> 580
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<212> PRT
<213> Corynebacterium glutamicum

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  20                      25                      30

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
  35                      40                      45

Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
  50                      55                      60

Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
  65                      70                      75                      80

Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
  85                      90                      95

Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
 100                      105                      110

Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
 115                      120                      125

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Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
 130 135 140
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
 145 150 155 160
 Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
 165 170 175
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
 180 185 190
 Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
 195 200 205
 Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
 210 215 220
 Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
 225 230 235 240
 Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
 245 250 255
 His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
 260 265 270
 Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
 275 280 285
 Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
 290 295 300
 Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
 305 310 315 320
 Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
 325 330 335

<210> 581
 <211> 1107
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (77)..(1084)
 <223> FRXA01306

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 Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile
 1 5 10
 cta ctc atc gcg ctg tct gcg ttt ttc gtc atc att gag ttc gct ttg 160
 Leu Leu Ile Ala Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu
 15 20 25

ctt gca gct agg cgg aac cgg tta gag gag act gtg gaa acc tcg cgg	208
Leu Ala Ala Arg Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg	
30 35 40	
tct tcc cgc gct gcg ttg cga agc ctc aat gaa ctt act ctc atg ctc	256
Ser Ser Arg Ala Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu	
45 50 55 60	
gcg ggc gcg cag ttg gga atc acc atg gtg act ttc gcg ttg ggt gct	304
Ala Gly Ala Gln Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala	
65 70 75	
atc acg aag ccg tgg gtt cat tat gct ttg atg ccg ctc ttc gaa tgg	352
Ile Thr Lys Pro Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp	
80 85 90	
gcg cgt ata ccg ctg gtt atg gca gat gtc att gcg ttt att ttg tcg	400
Ala Arg Ile Pro Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser	
95 100 105	
ctg ttt atc gta acg ttt ctg cac ttg gtc atc ggc gaa atg gct ccg	448
Leu Phe Ile Val Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro	
110 115 120	
aaa tcc tgg gca atc gcg cat ccg gag acg gca ctt cga act atc gcg	496
Lys Ser Trp Ala Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala	
125 130 135 140	
att ccc gca cgg ggc ttc att aac ctg ttt cgt cca ttg ctg cag tgg	544
Ile Pro Ala Arg Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp	
145 150 155	
atc aac aaa atg gcg aac gat ttg gtc cgc aaa gtt ggt gaa act ccc	592
Ile Asn Lys Met Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro	
160 165 170	
gtt gat cga gct gca gct ggt ggc tat gac acc gat acc ctc cat gcc	640
Val Asp Arg Ala Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala	
175 180 185	
ctc att gag cat tcc cga gaa act ggc gct ctg gat cag caa tcc gcc	688
Leu Ile Glu His Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala	
190 195 200	
gcc caa atc agc gga att atc aag ctg gat aaa atc acg gtc ggt caa	736
Ala Gln Ile Ser Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln	
205 210 215 220	
acc ctg acc gca tct cca ttt acg cac agc gcc agc gcc acg gtt gct	784
Thr Leu Thr Ala Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala	
225 230 235	
gag gtg caa gcc gca gct cag cgc agt ggc agc ttg cgt gtg ctt atc	832
Glu Val Gln Ala Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile	
240 245 250	
gac gcc ccc tcc cac ctt ttc cca cac gtc att cat gtg cga gac acc	880
Asp Ala Pro Ser His Leu Phe Pro His Val Ile His Val Arg Asp Thr	
255 260 265	

ctt ggt gcc tcg cca gac gag aag gct tcg aag tgg tct cgc cca atc 928
 Leu Gly Ala Ser Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile
 270 275 280
 ctc acc gtt gct gag acc gac acg tta cac caa gcg ctg gaa tac atg 976
 Leu Thr Val Ala Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met
 285 290 295 300
 cgg gag cat aac gag cag atc agt gcg gtg ctt tcc gct gat ggg aaa 1024
 Arg Glu His Asn Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys
 305 310 315
 acg gtg ctt ggt gta ata act tgg gat cac atc ttg aaa tac ctg tgg 1072
 Thr Val Leu Gly Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp
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 cct gca tcg gtg tagctaattt gaggtgcgct gaa 1107
 Pro Ala Ser Val
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<210> 582

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 582

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 Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
 35 40 45
 Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
 50 55 60
 Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65 70 75 80
 Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
 85 90 95
 Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
 100 105 110
 Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
 115 120 125
 Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
 130 135 140
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
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 165 170 175
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His

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Met Ser Asn Ser Glu																
1 5																
tgc cac acc cac ggt tac atc gaa gaa aag cag cgt tac ctc gca cgc																163
Cys	His	Thr	His	Gly	Tyr	Ile	Glu	Glu	Lys	Gln	Arg	Tyr	Leu	Ala	Arg	
10 15 20																
ctc aaa aga atc gaa ggc caa acc cga ggc att cac cgc atg atc gac																211
Leu	Lys	Arg	Ile	Glu	Gly	Gln	Thr	Arg	Gly	Ile	His	Arg	Met	Ile	Asp	
25 30 35																
gag gaa caa tac tgc atc gac atc ctc acg cag atc tcc gca gtg aac																259
Glu	Glu	Gln	Tyr	Cys	Ile	Asp	Ile	Leu	Thr	Gln	Ile	Ser	Ala	Val	Asn	
40 45 50																
tcc gca ctc aaa aac gtg gcg ttc ggc ctc ctc gac gat cac ctc gct																307
Ser	Ala	Leu	Lys	Asn	Val	Ala	Phe	Gly	Leu	Leu	Asp	Asp	His	Leu	Ala	

55	60	65	
cac tgt gtc aaa gaa gca gct gac ctc ggc ggc gac gaa ctc gac gca			355
His Cys Val Lys Glu Ala Ala Asp Leu Gly Gly Asp Glu Leu Asp Ala			
70	75	80	85
aaa ctc aaa gaa gtt tcc gac gcc atc gcc cgc ttc agt aag gcc			400
Lys Leu Lys Glu Val Ser Asp Ala Ile Ala Arg Phe Ser Lys Ala			
	90	95	100
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 584
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 35 40 45
 Ile Ser Ala Val Asn Ser Ala Leu Lys Asn Val Ala Phe Gly Leu Leu
 50 55 60
 Asp Asp His Leu Ala His Cys Val Lys Glu Ala Ala Asp Leu Gly Gly
 65 70 75 80
 Asp Glu Leu Asp Ala Lys Leu Lys Glu Val Ser Asp Ala Ile Ala Arg
 85 90 95
 Phe Ser Lys Ala
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<210> 585
 <211> 2520
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2497)
 <223> RXN01331

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 Met Leu Thr Thr Leu
 1 5
 tgg att gcg gtg ttg gta ttt acc gtt cca gga ttg gtc gtc tcg tgg 163
 Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly Leu Val Val Ser Trp
 10 15 20

gtt tct ggc ctt aaa gtg ccc tgg gct atc gca gcc tcc atc cca gcc	211
Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala Ala Ser Ile Pro Ala	
25 30 35	
acc ttc ggt att tac ggc ctg tcc gcc tgg ttg ctg ggc ttg tgg gag	259
Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu Leu Gly Leu Trp Glu	
40 45 50	
atg cgt ttt gat ctc cat tct gta gtt att tcc aca ttg gtt ttc gct	307
Met Arg Phe Asp Leu His Ser Val Val Ile Ser Thr Leu Val Phe Ala	
55 60 65	
gcg gtt gct ttg gta tgg cgc ttg ttt ttt gtc ggt ggt tgg ctt gta	355
Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val Gly Gly Trp Leu Val	
70 75 80 85	
cgt cgg cgt aaa gca cgt atc cgc agg cag acg ctc gcg gat gaa gag	403
Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr Leu Ala Asp Glu Glu	
90 95 100	
cgg gca gaa aat gct gag gta tct gca ggg gag cct gcc gaa tcg agc	451
Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu Pro Ala Glu Ser Ser	
105 110 115	
aca aac gaa gca gcc gaa tct gaa tct gaa acc tcg gag cgt cgc gga	499
Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr Ser Glu Arg Arg Gly	
120 125 130	
atc tgg cgc gtg atc ttt gat tac atg cgc gac ggt ggc atc ttg gat	547
Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp Gly Gly Ile Leu Asp	
135 140 145	
cac cgt tgg ctg ctg cct gcc gca ggt gct atc act ggt gcg tgg ctg	595
His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile Thr Gly Ala Trp Leu	
150 155 160 165	
atc att gat cgt gcc gtt gat ctg ctc ttg agc acc gag cat ggt ttg	643
Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser Thr Glu His Gly Leu	
170 175 180	
ggc gat atc gtc caa ggc tgg gat gtc cat tgg cat gct tcg act gtc	691
Gly Asp Ile Val Gln Gly Trp Asp Val His Trp His Ala Ser Thr Val	
185 190 195	
cgt ttt ata gat gag acc ggc att gcg tca tcc acg atg atg ggg cag	739
Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser Thr Met Met Gly Gln	
200 205 210	
ctg cgc aat att gaa acg cag caa gat ctg ttc tac cca agc gca tgg	787
Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe Tyr Pro Ser Ala Trp	
215 220 225	
cat gct ggt gca tgg gtg ctg tcg gat gtc gga aat ctg acg att gtt	835
His Ala Gly Ala Trp Val Leu Ser Asp Val Gly Asn Leu Thr Ile Val	
230 235 240 245	
gaa gcc acc aac ctc act ggc att gtg ctg tcc gga ttg ttg ctg ccg	883
Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser Gly Leu Leu Leu Pro	
250 255 260	

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acc gcg cag att ggt gcg ggc ttt gct gga ctg atc acc att gcc tct Thr Ala Gln Ile Gly Ala Gly Phe Ala Gly Leu Ile Thr Ile Ala Ser 280 285 290	979
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gct gcg atc ggt gct tca ggt gtg gtg ctt gcg ctg ttt atg tcc act Ala Ala Ile Gly Ala Ser Gly Val Val Leu Ala Leu Phe Met Ser Thr 310 315 320 325	1075
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ctg gcc atc acg ggc atc atc ggt gtg ctc ttc atg ctg cct cag gtg Leu Ala Ile Thr Gly Ile Ile Gly Val Leu Phe Met Leu Pro Gln Val 390 395 400 405	1315
att tca ggt tcc gaa caa acc gaa gat gtg ctg tca tat tct gct gag Ile Ser Gly Ser Glu Gln Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu 410 415 420	1363
gaa caa gtc acc cgc agc gag tcc tgg ttg gtg tct att ttc atg gag Glu Gln Val Thr Arg Ser Glu Ser Trp Leu Val Ser Ile Phe Met Glu 425 430 435	1411
acc cgc cat gtt gat ttc ttc gga aat att gac atc gtc cca gtg ctg Thr Arg His Val Asp Phe Phe Gly Asn Ile Asp Ile Val Pro Val Leu 440 445 450	1459
gta ttc gca gca atc ggt ggc gtg gtt gct ttg gtg tgg cgc gga aac Val Phe Ala Ala Ile Gly Gly Val Val Ala Leu Val Trp Arg Gly Asn 455 460 465	1507
ttg tgg gcg ccg gtg ttt tac ttc gcc agc gtt gcg ttg acc gct aac Leu Trp Ala Pro Val Phe Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn 470 475 480 485	1555
tcg ctg aag cct ttt gaa gag ccg tgg ggt gat tgg ctc aac atc gtg Ser Leu Lys Pro Phe Glu Glu Pro Trp Gly Asp Trp Leu Asn Ile Val 490 495 500	1603
ggc ggt ctg cat tac tcc aca gga cac cgt ttg atc atg cct gtc gcc	1651

Gly	Gly	Leu	His	Tyr	Ser	Thr	Gly	His	Arg	Leu	Ile	Met	Pro	Val	Ala		
			505					510					515				
atg	ttc	act	ttt	gct	gcc	gca	ggg	atc	ggc	gct	gcc	gca	gtg	atc	cgt		1699
Met	Phe	Thr	Phe	Ala	Ala	Ala	Gly	Ile	Gly	Ala	Ala	Ala	Val	Ile	Arg		
		520					525					530					
ttg	atc	tgc	ttg	gga	cca	ata	aag	aag	ttc	acc	act	gtt	tcc	ggg	gtt		1747
Leu	Ile	Cys	Leu	Gly	Pro	Ile	Lys	Lys	Phe	Thr	Thr	Val	Ser	Gly	Val		
	535					540					545						
gtt	tct	gtg	gtg	atg	gct	ctt	gtt	gtg	gct	gtg	cca	ttg	cag	act	tgg		1795
Val	Ser	Val	Val	Met	Ala	Leu	Val	Val	Ala	Val	Pro	Leu	Gln	Thr	Trp		
550					555					560					565		
gcg	aag	gat	ttt	gta	gag	gaa	gga	tcc	gaa	acc	aca	atc	ctt	gcg	cca		1843
Ala	Lys	Asp	Phe	Val	Glu	Glu	Gly	Ser	Glu	Thr	Thr	Ile	Leu	Ala	Pro		
			570					575						580			
cac	aat	gat	gaa	cgt	atg	gtg	agc	aac	aac	gac	ttg	gct	gcc	tgg	gac		1891
His	Asn	Asp	Glu	Arg	Met	Val	Ser	Asn	Asn	Asp	Leu	Ala	Ala	Trp	Asp		
			585					590					595				
tgg	tta	atc	caa	cag	cca	ggg	gga	gct	gac	atg	aac	atc	atg	ggg	gac		1939
Trp	Leu	Ile	Gln	Gln	Pro	Gly	Gly	Ala	Asp	Met	Asn	Ile	Met	Gly	Asp		
	600					605						610					
ccc	gca	gat	ggg	aac	ggc	tgg	atg	tat	gcc	tac	aac	ggc	ttg	cac	tcc		1987
Pro	Ala	Asp	Gly	Asn	Gly	Trp	Met	Tyr	Ala	Tyr	Asn	Gly	Leu	His	Ser		
	615					620					625						
gtg	gcc	cgc	cac	tat	gca	tgg	cca	gca	gca	ggc	gaa	ggc	tct	gcc	acc		2035
Val	Ala	Arg	His	Tyr	Ala	Trp	Pro	Ala	Ala	Gly	Glu	Gly	Ser	Ala	Thr		
630					635					640					645		
gcg	atg	ctg	ttc	tgg	tgg	cct	caa	ctt	cta	ggg	gtg	ggc	acc	gat	gaa		2083
Ala	Met	Leu	Phe	Trp	Trp	Pro	Gln	Leu	Leu	Gly	Val	Gly	Thr	Asp	Glu		
			650					655						660			
aac	cca	gat	caa	gtc	aac	gat	gtg	gat	cag	gct	gct	cgt	gat	ctc	aac		2131
Asn	Pro	Asp	Gln	Val	Asn	Asp	Val	Asp	Gln	Ala	Ala	Arg	Asp	Leu	Asn		
			665				670						675				
gtc	ggc	tac	ttc	atg	atc	agt	ccg	tgg	acg	ttc	tgg	gat	ttc	cag	atc		2179
Val	Gly	Tyr	Phe	Met	Ile	Ser	Pro	Trp	Thr	Phe	Trp	Asp	Phe	Gln	Ile		
	680						685					690					
ccc	aac	ttc	cgc	cag	atc	gat	ctg	ctg	tgg	caa	acc	cca	ggc	gtg	aca		2227
Pro	Asn	Phe	Arg	Gln	Ile	Asp	Leu	Leu	Trp	Gln	Thr	Pro	Gly	Val	Thr		
	695					700					705						
ccg	gtg	tgc	aag	aag	ggc	gac	tcg	gtg	atc	ttc	gca	gtc	aac	gat	atg		2275
Pro	Val	Cys	Lys	Lys	Gly	Asp	Ser	Val	Ile	Phe	Ala	Val	Asn	Asp	Met		
710					715					720					725		
ttc	act	gac	gcc	gaa	ctg	gat	cag	atg	cgt	gca	cct	ggg	aat	tct	cca		2323
Phe	Thr	Asp	Ala	Glu	Leu	Asp	Gln	Met	Arg	Ala	Pro	Gly	Asn	Ser	Pro		
			730						735					740			
gaa	cca	ctg	cca	gag	ctt	cct	acc	ttg	ggc	gag	ctt	ggg	ttg	gct	gaa		2371
Glu	Pro	Leu	Pro	Glu	Leu	Pro	Thr	Leu	Gly	Glu	Leu	Gly	Leu	Ala	Glu		

745	750	755	
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Thr Glu Asp Glu Val Asp Gln	Thr Tyr Tyr His Arg Pro Thr Val Pro		
760	765	770	
gct ggt gtg aac tca gag atg cct tca gcc gaa act ctg tat gca ccg			2467
Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu Thr Leu Tyr Ala Pro			
775	780	785	
gat cca acg aag ccg cat acg gtc cct aac taatcacaaa gagtattcag			2517
Asp Pro Thr Lys Pro His Thr Val Pro Asn			
790	795		
taa			2520

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<211> 799

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

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			20					25					30		

Ala	Ser	Ile	Pro	Ala	Thr	Phe	Gly	Ile	Tyr	Gly	Leu	Ser	Ala	Trp	Leu
		35					40					45			

Leu	Gly	Leu	Trp	Glu	Met	Arg	Phe	Asp	Leu	His	Ser	Val	Val	Ile	Ser
	50					55					60				

Thr	Leu	Val	Phe	Ala	Ala	Val	Ala	Leu	Val	Trp	Arg	Leu	Phe	Phe	Val
65					70					75					80

Gly	Gly	Trp	Leu	Val	Arg	Arg	Arg	Lys	Ala	Arg	Ile	Arg	Arg	Gln	Thr
			85						90					95	

Leu	Ala	Asp	Glu	Glu	Arg	Ala	Glu	Asn	Ala	Glu	Val	Ser	Ala	Gly	Glu
		100						105					110		

Pro	Ala	Glu	Ser	Ser	Thr	Asn	Glu	Ala	Ala	Glu	Ser	Glu	Ser	Glu	Thr
		115					120					125			

Ser	Glu	Arg	Arg	Gly	Ile	Trp	Arg	Val	Ile	Phe	Asp	Tyr	Met	Arg	Asp
	130					135					140				

Gly	Gly	Ile	Leu	Asp	His	Arg	Trp	Leu	Leu	Pro	Ala	Ala	Gly	Ala	Ile
145					150					155					160

Thr	Gly	Ala	Trp	Leu	Ile	Ile	Asp	Arg	Ala	Val	Asp	Leu	Leu	Leu	Ser
			165						170					175	

Thr	Glu	His	Gly	Leu	Gly	Asp	Ile	Val	Gln	Gly	Trp	Asp	Val	His	Trp
			180					185					190		

His	Ala	Ser	Thr	Val	Arg	Phe	Ile	Asp	Glu	Thr	Gly	Ile	Ala	Ser	Ser
		195					200					205			

Thr Met Met Gly Gln Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe
 210 215 220
 Tyr Pro Ser Ala Trp His Ala Gly Ala Trp Val Leu Ser Asp Val Gly
 225 230 235 240
 Asn Leu Thr Ile Val Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser
 245 250 255
 Gly Leu Leu Leu Pro Leu Ala Val Ala Leu Ile Ala Trp Arg Met Ile
 260 265 270
 Asn Asn Arg Gly Leu Thr Ala Gln Ile Gly Ala Gly Phe Ala Gly Leu
 275 280 285
 Ile Thr Ile Ala Ser Pro Val Leu Phe Trp Val Gly Asn Tyr Val Gly
 290 295 300
 Ala Trp Pro Tyr Val Ala Ala Ile Gly Ala Ser Gly Val Val Leu Ala
 305 310 315 320
 Leu Phe Met Ser Thr Pro Ser Val Pro Val Arg Ile Phe Ala Ala Ala
 325 330 335
 Leu Ala Phe Met Gly Met Phe Gln Leu His Pro Ala Pro Ser Thr Ile
 340 345 350
 Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu Lys Leu Val Val Val
 355 360 365
 Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly Ile Gly Ile Arg Leu
 370 375 380
 Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile Ile Gly Val Leu Phe
 385 390 395 400
 Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln Thr Glu Asp Val Leu
 405 410 415
 Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser Glu Ser Trp Leu Val
 420 425 430
 Ser Ile Phe Met Glu Thr Arg His Val Asp Phe Phe Gly Asn Ile Asp
 435 440 445
 Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly Gly Val Val Ala Leu
 450 455 460
 Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe Tyr Phe Ala Ser Val
 465 470 475 480
 Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu Glu Pro Trp Gly Asp
 485 490 495
 Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser Thr Gly His Arg Leu
 500 505 510
 Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala Ala Gly Ile Gly Ala
 515 520 525

Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro Ile Lys Lys Phe Thr
530 535 540
Thr Val Ser Gly Val Val Ser Val Val Met Ala Leu Val Val Ala Val
545 550 555 560
Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu Glu Gly Ser Glu Thr
565 570 575
Thr Ile Leu Ala Pro His Asn Asp Glu Arg Met Val Ser Asn Asn Asp
580 585 590
Leu Ala Ala Trp Asp Trp Leu Ile Gln Gln Pro Gly Gly Ala Asp Met
595 600 605
Asn Ile Met Gly Asp Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr
610 615 620
Asn Gly Leu His Ser Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly
625 630 635 640
Glu Gly Ser Ala Thr Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly
645 650 655
Val Gly Thr Asp Glu Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala
660 665 670
Ala Arg Asp Leu Asn Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe
675 680 685
Trp Asp Phe Gln Ile Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln
690 695 700
Thr Pro Gly Val Thr Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe
705 710 715 720
Ala Val Asn Asp Met Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala
725 730 735
Pro Gly Asn Ser Pro Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu
740 745 750
Leu Gly Leu Ala Glu Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His
755 760 765
Arg Pro Thr Val Pro Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu
770 775 780
Thr Leu Tyr Ala Pro Asp Pro Thr Lys Pro His Thr Val Pro Asn
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (40)..(615)

<223> FRXA01331

<400> 587

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Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr Asn Gly Leu His Ser
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gtg gcc cgc cac tat gca tgg cca gca gca ggc gaa ggc tct gcc acc 153
Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly Glu Gly Ser Ala Thr
          25           30           35

gcg atg ctg ttc tgg tgg cct caa ctt cta ggt gtg ggc acc gat gaa 201
Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly Val Gly Thr Asp Glu
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aac cca gat caa gtc aac gat gtg gat cag gct gct cgt gat ctc aac 249
Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala Ala Arg Asp Leu Asn
          55           60           65           70

gtc ggc tac ttc atg atc agt ccg tgg acg ttc tgg gat ttc cag atc 297
Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe Trp Asp Phe Gln Ile
          75           80           85

ccc aac ttc cgc cag atc gat ctg ctg tgg caa acc cca ggc gtg aca 345
Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln Thr Pro Gly Val Thr
          90           95           100

ccg gtg tgc aag aag ggc gac tcg gtg atc ttc gca gtc aac gat atg 393
Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe Ala Val Asn Asp Met
          105           110           115

ttc act gac gcc gaa ctg gat cag atg cgt gca cct ggt aat tct cca 441
Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala Pro Gly Asn Ser Pro
          120           125           130

gaa cca ctg cca gag ctt cct acc ttg ggc gag ctt ggg ttg gct gaa 489
Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu Leu Gly Leu Ala Glu
          135           140           145           150

act gaa gac gag gta gat cag act tat tac cat cgt cca acg gtt cct 537
Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His Arg Pro Thr Val Pro
          155           160           165

gct ggt gtg aac tca gag atg cct tca gcc gaa act ctg tat gca ccg 585
Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu Thr Leu Tyr Ala Pro
          170           175           180

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Asp Pro Thr Lys Pro His Thr Val Pro Asn
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taa 638

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<400> 588

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Tyr Asn Gly Leu His Ser Val Ala Arg His Tyr Ala Trp Pro Ala Ala
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Gly Glu Gly Ser Ala Thr Ala Met Leu Phe Trp Trp Pro Gln Leu Leu
 35 40 45

Gly Val Gly Thr Asp Glu Asn Pro Asp Gln Val Asn Asp Val Asp Gln
 50 55 60

Ala Ala Arg Asp Leu Asn Val Gly Tyr Phe Met Ile Ser Pro Trp Thr
 65 70 75 80

Phe Trp Asp Phe Gln Ile Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp
 85 90 95

Gln Thr Pro Gly Val Thr Pro Val Cys Lys Lys Gly Asp Ser Val Ile
 100 105 110

Phe Ala Val Asn Asp Met Phe Thr Asp Ala Glu Leu Asp Gln Met Arg
 115 120 125

Ala Pro Gly Asn Ser Pro Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly
 130 135 140

Glu Leu Gly Leu Ala Glu Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr
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His Arg Pro Thr Val Pro Ala Gly Val Asn Ser Glu Met Pro Ser Ala
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Glu Thr Leu Tyr Ala Pro Asp Pro Thr Lys Pro His Thr Val Pro Asn
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<212> DNA

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 Met Leu Thr Thr Leu
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tgg att gcg gtg ttg gta ttt acc gtt cca gga ttg gtc gtc tcg tgg 163
 Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly Leu Val Val Ser Trp
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Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala Ala Ser Ile Pro Ala	
25 30 35	
acc ttc ggt att tac ggc ctg tcc gcc tgg ttg ctg ggc ttg tgg gag	259
Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu Leu Gly Leu Trp Glu	
40 45 50	
atg cgt ttt gat ctc cat tct gta gtt att tcc aca ttg gtt ttc gct	307
Met Arg Phe Asp Leu His Ser Val Val Ile Ser Thr Leu Val Phe Ala	
55 60 65	
gcg gtt gct ttg gta tgg cgc ttg ttt ttt gtc ggt ggt tgg ctt gta	355
Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val Gly Gly Trp Leu Val	
70 75 80 85	
cgt cgg cgt aaa gca cgt atc cgc agg cag acg ctc gcg gat gaa gag	403
Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr Leu Ala Asp Glu Glu	
90 95 100	
cgg gca gaa aat gct gag gta tct gca ggg gag cct gcc gaa tcg agc	451
Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu Pro Ala Glu Ser Ser	
105 110 115	
aca aac gaa gca gcc gaa tct gaa tct gaa acc tcg gag cgt cgc gga	499
Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr Ser Glu Arg Arg Gly	
120 125 130	
atc tgg cgc gtg atc ttt gat tac atg cgc gac ggt ggc atc ttg gat	547
Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp Gly Gly Ile Leu Asp	
135 140 145	
cac cgt tgg ctg ctg cct gcc gca ggt gct atc act ggt gcg tgg ctg	595
His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile Thr Gly Ala Trp Leu	
150 155 160 165	
atc att gat cgt gcc gtt gat ctg ctc ttg agc acc gag cat ggt ttg	643
Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser Thr Glu His Gly Leu	
170 175 180	
ggc gat atc gtc caa ggc tgg gat gtc cat tgg cat gct tcg act gtc	691
Gly Asp Ile Val Gln Gly Trp Asp Val His Trp His Ala Ser Thr Val	
185 190 195	
cgt ttt ata gat gag acc ggc att gcg tca tcc acg atg atg ggg cag	739
Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser Thr Met Met Gly Gln	
200 205 210	
ctg cgc aat att gaa acg cag caa gat ctg ttc tac cca agc gca tgg	787
Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe Tyr Pro Ser Ala Trp	
215 220 225	
cat gct ggt gca tgg gtg ctg tcg gat gtc gga aat ctg acg att gtt	835
His Ala Gly Ala Trp Val Leu Ser Asp Val Gly Asn Leu Thr Ile Val	
230 235 240 245	
gaa gcc acc aac ctc act ggc att gtg ctg tcc gga ttg ttg ctg ccg	883
Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser Gly Leu Leu Leu Pro	
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Leu Ala Val	

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<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 590

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20 25 30

Ala Ser Ile Pro Ala Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu
35 40 45

Leu Gly Leu Trp Glu Met Arg Phe Asp Leu His Ser Val Val Ile Ser
50 55 60

Thr Leu Val Phe Ala Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val
65 70 75 80

Gly Gly Trp Leu Val Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr
85 90 95

Leu Ala Asp Glu Glu Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu
100 105 110

Pro Ala Glu Ser Ser Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr
115 120 125

Ser Glu Arg Arg Gly Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp
130 135 140

Gly Gly Ile Leu Asp His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile
145 150 155 160

Thr Gly Ala Trp Leu Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser
165 170 175

Thr Glu His Gly Leu Gly Asp Ile Val Gln Gly Trp Asp Val His Trp
180 185 190

His Ala Ser Thr Val Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser
195 200 205

Thr Met Met Gly Gln Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe
210 215 220

Tyr Pro Ser Ala Trp His Ala Gly Ala Trp Val Leu Ser Asp Val Gly
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Gly Leu Leu Leu Pro Leu Ala Val
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 Ala Pro Ser Thr Ile Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu
 20 25 30
 aaa ctc gtg gtg gtt cca agc cag aaa gtg aag ggc tgg aag gcg ggc 144
 Lys Leu Val Val Val Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly
 35 40 45
 atc ggt atc cgt ttg aag gat gtc ggc atc ctg gcc atc acg ggc atc 192
 Ile Gly Ile Arg Leu Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile
 50 55 60
 atc ggt gtg ctc ttc atg ctg cct cag gtg att tca ggt tcc gaa caa 240
 Ile Gly Val Leu Phe Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln
 65 70 75 80
 acc gaa gat gtg ctg tca tat tct gct gag gaa caa gtc acc cgc agc 288
 Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser
 85 90 95
 gag tcc tgg ttg gtg tct att ttc atg gag acc cgc cat gtt gat ttc 336
 Glu Ser Trp Leu Val Ser Ile Phe Met Glu Thr Arg His Val Asp Phe
 100 105 110
 ttc gga aat att gac atc gtc cca gtg ctg gta ttc gca gca atc ggt 384
 Phe Gly Asn Ile Asp Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly
 115 120 125
 ggc gtg gtt gct ttg gtg tgg cgc gga aac ttg tgg gcg ccg gtg ttt 432
 Gly Val Val Ala Leu Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe
 130 135 140
 tac ttc gcc agc gtt gcg ttg acc gct aac tcg ctg aag cct ttt gaa 480
 Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu
 145 150 155 160
 gag ccg tgg ggt gat tgg ctc aac atc gtg ggc ggt ctg cat tac tcc 528
 Glu Pro Trp Gly Asp Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser
 165 170 175
 aca gga cac cgt ttg atc atg cct gtc gcc atg ttc act ttt gct gcc 576
 Thr Gly His Arg Leu Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala
 180 185 190
 gca ggt atc ggc gct gcc gca gtg atc cgt ttg atc tgc ttg gga cca 624
 Ala Gly Ile Gly Ala Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro

195	200	205	
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Ile Lys Lys Phe Thr Thr Val Ser Gly Val Val Ser Val Val Met Ala			
210	215	220	
ctt gtt gtg gct gtg cca ttg cag act tgg gcg aag gat ttt gta gag			720
Leu Val Val Ala Val Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu			
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gaa gga tcc gaa acc aca atc ctt gcg cca			750
Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro			
245	250		

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<212> PRT

<213> Corynebacterium glutamicum

<400> 592

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Lys Leu Val Val Val Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly
35 40 45

Ile Gly Ile Arg Leu Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile
50 55 60

Ile Gly Val Leu Phe Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln
65 70 75 80

Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser
85 90 95

Glu Ser Trp Leu Val Ser Ile Phe Met Glu Thr Arg His Val Asp Phe
100 105 110

Phe Gly Asn Ile Asp Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly
115 120 125

Gly Val Val Ala Leu Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe
130 135 140

Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu
145 150 155 160

Glu Pro Trp Gly Asp Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser
165 170 175

Thr Gly His Arg Leu Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala
180 185 190

Ala Gly Ile Gly Ala Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro
195 200 205

Ile Lys Lys Phe Thr Thr Val Ser Gly Val Val Ser Val Val Met Ala

210

215

220

Leu Val Val Ala Val Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu
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Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
 245 250

<210> 593

<211> 1536

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1513)

<223> RXN01337

<400> 593

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tacgcaagaa aaagtttctt agcagggttaa cctaaatgtc gtg aca ttt cga ggc 115
 Val Thr Phe Arg Gly
 1 5

gga aac act ggc gca aag cac gcg gtc gtt gtt ggt tct ggc ccc aat 163
 Gly Asn Thr Gly Ala Lys His Ala Val Val Val Gly Ser Gly Pro Asn
 10 15 20

ggg ttg acc acg gcg gcg gtg ctg gcc aaa gca ggt tgg caa gta gat 211
 Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala Gly Trp Gln Val Asp
 25 30 35

gtg tat gag gcg gcg cca acc cct gga ggg gcg gcg cgc tca gaa agc 259
 Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala Ala Arg Ser Glu Ser
 40 45 50

gtt ctg ggg gag ggg act atc agc gat ttg ggt gcc gca ggg cat cct 307
 Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly Ala Ala Gly His Pro
 55 60 65

ttc ggg gtg gca agc cca gct ttt cac tat ttg ggt ctg gaa gat cac 355
 Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu Gly Leu Glu Asp His
 70 75 80 85

ggc ctg gaa tgg gcg tat tct ccc ttt gcg atg gcc cac ccg tta gat 403
 Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met Ala His Pro Leu Asp
 90 95 100

tat ggc agg gcc gga ctg ctg gaa acg tca ctc cca gag acc gcc aaa 451
 Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu Pro Glu Thr Ala Lys
 105 110 115

aag ctt gga cct gat gca cgt cgt tgg aag aat ttg cac cag ggc tta 499
 Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn Leu His Gln Gly Leu
 120 125 130

acc aaa aac att gat aaa cac ttg gcc aat cta tta ggg ccg gtg ctg 547
 Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu Leu Gly Pro Val Leu
 135 140 145

aaa tgg cca gca cat ccg att cgg atg gca aag ttt ggc cca ttt gcg Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys Phe Gly Pro Phe Ala 150 155 160 165	595
ttg ctg ccc gcg aaa cgt cta gcc agt gcc gct ttt gaa aca gaa gaa Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala Phe Glu Thr Glu Glu 170 175 180	643
gcc cga tcc ctg ttt atc ggt tcg gcg atg cac tcg gtg act cca cca Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His Ser Val Thr Pro Pro 185 190 195	691
cac aag ccg atg acc gca tca ctt gga ttg ctt ttt ggc gct ctg ggg His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu Phe Gly Ala Leu Gly 200 205 210	739
atg tcg cga gga tgg ccg gtt gca gtt ggg gga agc gga cgg atc gtc Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly Ser Gly Arg Ile Val 215 220 225	787
gat gct ctg gtc aat gtc ata aac cat cac ggt ggc acc att cac tgc Asp Ala Leu Val Asn Val Ile Asn His His Gly Gly Thr Ile His Cys 230 235 240 245	835
gat tca cag att gat tcc ctc tca caa ttc cgc gac acc gat gcc att Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg Asp Thr Asp Ala Ile 250 255 260	883
att ctg aac caa acc ccc tca cag gtg ctg aaa ctc aaa gga act gac Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys Leu Lys Gly Thr Asp 265 270 275	931
ctt aat gca ggg ctt ccg caa cgc atg agc acc tgg aaa cac gga cca Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr Trp Lys His Gly Pro 280 285 290	979
agt tcc tac aaa gtg gac tac ctc ctt gac gaa cca att ccc tgg agc Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu Pro Ile Pro Trp Ser 295 300 305	1027
aat ccc cag gta ggc cag gcc aca acc gtc cat gtg ggc gga agc tct Asn Pro Gln Val Gly Gln Ala Thr Thr Val His Val Gly Gly Ser Ser 310 315 320 325	1075
gag gaa atc gct ttc gca gaa gca gaa gtc gca gcg ggg cgg atg ccc Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala Ala Gly Arg Met Pro 330 335 340	1123
gaa cgc ccg ttt atc att ttg tgc caa caa caa gtg gcg gat cct tca Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln Val Ala Asp Pro Ser 345 350 355	1171
cgc gcc cgg gag ggg cgc cac gtc gtg tgg gcc tac gcg cat gtg ccg Arg Ala Arg Glu Gly Arg His Val Val Trp Ala Tyr Ala His Val Pro 360 365 370	1219
cgg ggt ttc gtc gat aag cga gct gct tta tta atc act gcg cag att Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu Ile Thr Ala Gln Ile 375 380 385	1267

gaa cgc ttc gcc ccc ggt ttc cgt gat cgc atc gtg cat tca gtg gat 1315
 Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile Val His Ser Val Asp
 390 395 400 405

acc aac gcg gag gat tta gag gcg tgg aac ccc aat ctt gtt ggc gga 1363
 Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro Asn Leu Val Gly Gly
 410 415 420

gac atc acc gca ggg tcc gcg ctg ctt cgg cga atg ccg acc aaa atc 1411
 Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg Met Pro Thr Lys Ile
 425 430 435

ggc gag aaa acg tac atg gca tcc gcc tcc aac gcg ccg ggc ggg gga 1459
 Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn Ala Pro Gly Gly Gly
 440 445 450

gtc cac gga atg ccc ggc tgg tgg gca gcg caa gcc gtt tta gca gat 1507
 Val His Gly Met Pro Gly Trp Trp Ala Ala Gln Ala Val Leu Ala Asp
 455 460 465

cac agg tagaattgcg acatggagcc cac 1536
 His Arg
 470

<210> 594

<211> 471

<212> PRT

<213> Corynebacterium glutamicum

<400> 594

Val Thr Phe Arg Gly Gly Asn Thr Gly Ala Lys His Ala Val Val Val
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Gly Ser Gly Pro Asn Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala
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Gly Trp Gln Val Asp Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala
 35 40 45

Ala Arg Ser Glu Ser Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly
 50 55 60

Ala Ala Gly His Pro Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu
 65 70 75 80

Gly Leu Glu Asp His Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met
 85 90 95

Ala His Pro Leu Asp Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu
 100 105 110

Pro Glu Thr Ala Lys Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn
 115 120 125

Leu His Gln Gly Leu Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu
 130 135 140

Leu Gly Pro Val Leu Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys
 145 150 155 160

Phe Gly Pro Phe Ala Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala
165 170 175

Phe Glu Thr Glu Glu Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His
180 185 190

Ser Val Thr Pro Pro His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu
195 200 205

Phe Gly Ala Leu Gly Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly
210 215 220

Ser Gly Arg Ile Val Asp Ala Leu Val Asn Val Ile Asn His His Gly
225 230 235 240

Gly Thr Ile His Cys Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg
245 250 255

Asp Thr Asp Ala Ile Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys
260 265 270

Leu Lys Gly Thr Asp Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr
275 280 285

Trp Lys His Gly Pro Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu
290 295 300

Pro Ile Pro Trp Ser Asn Pro Gln Val Gly Gln Ala Thr Thr Val His
305 310 315 320

Val Gly Gly Ser Ser Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala
325 330 335

Ala Gly Arg Met Pro Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln
340 345 350

Val Ala Asp Pro Ser Arg Ala Arg Glu Gly Arg His Val Val Trp Ala
355 360 365

Tyr Ala His Val Pro Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu
370 375 380

Ile Thr Ala Gln Ile Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile
385 390 395 400

Val His Ser Val Asp Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro
405 410 415

Asn Leu Val Gly Gly Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg
420 425 430

Met Pro Thr Lys Ile Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn
435 440 445

Ala Pro Gly Gly Gly Val His Gly Met Pro Gly Trp Trp Ala Ala Gln
450 455 460

Ala Val Leu Ala Asp His Arg
465 470

gcc cga tcc ctg ttt atc ggt tgc gcg atg cac tgc gtg act cca cca	691
Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His Ser Val Thr Pro Pro	
185 190 195	
cac aag ccg atg acc gca tca ctt gga ttg ctt ttt ggc gct ctg ggg	739
His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu Phe Gly Ala Leu Gly	
200 205 210	
atg tgc cga gga tgg ccg gtt gca gtt ggg gga agc gga cgg atc gtc	787
Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly Ser Gly Arg Ile Val	
215 220 225	
gat gct ctg gtc aat gtc ata aac cat cac ggt ggc acc att cac tgc	835
Asp Ala Leu Val Asn Val Ile Asn His His Gly Gly Thr Ile His Cys	
230 235 240 245	
gat tca cag att gat tcc ctg tca caa ttc cgc gac acc gat gcc att	883
Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg Asp Thr Asp Ala Ile	
250 255 260	
att ctg aac caa acc ccc tca cag gtg ctg aaa ctg aaa gga act gac	931
Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys Leu Lys Gly Thr Asp	
265 270 275	
ctt aat gca ggg ctt ccg caa cgc atg agc acc tgg aaa cac gga cca	979
Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr Trp Lys His Gly Pro	
280 285 290	
agt tcc tac aaa gtg gac tac ctg ctt gac gaa cca att ccc tgg agc	1027
Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu Pro Ile Pro Trp Ser	
295 300 305	
aat ccc cag gta ggc cag gcc aca acc gtc cat gtg ggc gga agc tct	1075
Asn Pro Gln Val Gly Gln Ala Thr Thr Val His Val Gly Gly Ser Ser	
310 315 320 325	
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Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala Ala Gly Arg Met Pro	
330 335 340	
gaa cgc ccg ttt atc att ttg tgc caa caa caa gtg gcg gat cct tca	1171
Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln Val Ala Asp Pro Ser	
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cgc gcc ccg gag ggg cgc cac gtc gtg tgg gcc tac gcg cat gtg ccg	1219
Arg Ala Arg Glu Gly Arg His Val Val Trp Ala Tyr Ala His Val Pro	
360 365 370	
cgg ggt ttc gtc gat aag cga gct gct tta tta atc act gcg cag att	1267
Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu Ile Thr Ala Gln Ile	
375 380 385	
gaa cgc ttc gcc ccc ggt ttc cgt gat cgc atc gtg cat tca gtg gat	1315
Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile Val His Ser Val Asp	
390 395 400 405	
acc aac gcg gag gat tta gag gcg tgg aac ccc aat ctt gtt ggc gga	1363
Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro Asn Leu Val Gly Gly	
410 415 420	
gac atc acc gca ggg tcc gcg ctg ctt ccg cga atg ccg acc aaa atc	1411

Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg Met Pro Thr Lys Ile
 425 430 435

ggc gag aaa acg tac atg gca tcc gcc tcc aac gcg ccg ggc ggg gga 1459
 Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn Ala Pro Gly Gly Gly
 440 445 450

gtc cac gga atg ccc ggc tgg tgg gca gcg caa gcc gtt tta gca gat 1507
 Val His Gly Met Pro Gly Trp Trp Ala Ala Gln Ala Val Leu Ala Asp
 455 460 465

cac agg tagaattgcg acatggagcc cac 1536
 His Arg
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<210> 596

<211> 471

<212> PRT

<213> Corynebacterium glutamicum

<400> 596

Val Thr Phe Arg Gly Gly Asn Thr Gly Ala Lys His Ala Val Val Val
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 20 25 30

Gly Trp Gln Val Asp Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala
 35 40 45

Ala Arg Ser Glu Ser Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly
 50 55 60

Ala Ala Gly His Pro Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu
 65 70 75 80

Gly Leu Glu Asp His Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met
 85 90 95

Ala His Pro Leu Asp Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu
 100 105 110

Pro Glu Thr Ala Lys Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn
 115 120 125

Leu His Gln Gly Leu Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu
 130 135 140

Leu Gly Pro Val Leu Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys
 145 150 155 160

Phe Gly Pro Phe Ala Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala
 165 170 175

Phe Glu Thr Glu Glu Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His
 180 185 190

Ser Val Thr Pro Pro His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu
 195 200 205

Phe Gly Ala Leu Gly Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly
210 215 220
Ser Gly Arg Ile Val Asp Ala Leu Val Asn Val Ile Asn His His Gly
225 230 235 240
Gly Thr Ile His Cys Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg
245 250 255
Asp Thr Asp Ala Ile Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys
260 265 270
Leu Lys Gly Thr Asp Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr
275 280 285
Trp Lys His Gly Pro Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu
290 295 300
Pro Ile Pro Trp Ser Asn Pro Gln Val Gly Gln Ala Thr Thr Val His
305 310 315 320
Val Gly Gly Ser Ser Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala
325 330 335
Ala Gly Arg Met Pro Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln
340 345 350
Val Ala Asp Pro Ser Arg Ala Arg Glu Gly Arg His Val Val Trp Ala
355 360 365
Tyr Ala His Val Pro Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu
370 375 380
Ile Thr Ala Gln Ile Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile
385 390 395 400
Val His Ser Val Asp Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro
405 410 415
Asn Leu Val Gly Gly Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg
420 425 430
Met Pro Thr Lys Ile Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn
435 440 445
Ala Pro Gly Gly Gly Val His Gly Met Pro Gly Trp Trp Ala Ala Gln
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Ala Val Leu Ala Asp His Arg
465 470

<210> 597

<211> 708

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(685)

<223> RXN01351

<400> 597

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gagcgcgagg cagtgcgcga cttgctctaa tctttaacgc atg act tcg ctt ttc 115
 Met Thr Ser Leu Phe
 1 5

gac gcc cca acc ctc caa cgc gtc acc gtt ttc acg ggc tcg gcg ctc 163
 Asp Ala Pro Thr Leu Gln Arg Val Thr Val Phe Thr Gly Ser Ala Leu
 10 15 20

ggc agt tcc tcg ctg tac acg caa gcg gct caa acc ttg gcg aaa acc 211
 Gly Ser Ser Ser Leu Tyr Thr Gln Ala Ala Gln Thr Leu Ala Lys Thr
 25 30 35

gcg gta gac cgc ggc atc gac ttg gtt tac ggt ggc gga aaa gtg ggg 259
 Ala Val Asp Arg Gly Ile Asp Leu Val Tyr Gly Gly Gly Lys Val Gly
 40 45 50

ctc atg ggt atc gtc gcg gat gcg ttc ctg gaa tca ggt ggc gaa gcc 307
 Leu Met Gly Ile Val Ala Asp Ala Phe Leu Glu Ser Gly Gly Glu Ala
 55 60 65

ttt ggc gtc atc acg gaa tca ctt atg aag ggt gag ctt ggg cat gaa 355
 Phe Gly Val Ile Thr Gln Ser Leu Met Lys Gly Glu Leu Gly His Glu
 70 75 80 85

aag ctc acc gaa ctt gaa atc gtt cct gat atg cac atc cgc aag cgt 403
 Lys Leu Thr Glu Leu Glu Ile Val Pro Asp Met His Ile Arg Lys Arg
 90 95 100

cgc atg gca gaa ctt ggc gat ggt ttt atc gcc atg ccc ggt ggc gcc 451
 Arg Met Ala Glu Leu Gly Asp Gly Phe Ile Ala Met Pro Gly Gly Ala
 105 110 115

ggc acc ttg gaa gaa ctt ttc gag gtc tgg acc tgg caa cag ctg ggc 499
 Gly Thr Leu Glu Glu Leu Phe Glu Val Trp Thr Trp Gln Gln Leu Gly
 120 125 130

att cat caa aag ccc gtc gca ctt tat gat gtc gat ggt ttt tgg cag 547
 Ile His Gln Lys Pro Val Ala Leu Tyr Asp Val Asp Gly Phe Trp Gln
 135 140 145

ccc ctg ctg gaa atg ctt gag cag atg acc cag cgt gga ttt atc aag 595
 Pro Leu Leu Glu Met Leu Glu Gln Met Thr Gln Arg Gly Phe Ile Lys
 150 155 160 165

cga gac ttc ttt gag tgc ctc atc gtg gaa tcc gac ccg cat gcc ctg 643
 Arg Asp Phe Phe Glu Cys Leu Ile Val Glu Ser Asp Pro His Ala Leu
 170 175 180

cta aag gca atg cag acc tgg act cca cca gca cca aaa tgg 685
 Leu Lys Ala Met Gln Thr Trp Thr Pro Pro Ala Pro Lys Trp
 185 190 195

taactaaatt gtgtgctcga cgg 708

<210> 598

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 598

Met Thr Ser Leu Phe Asp Ala Pro Thr Leu Gln Arg Val Thr Val Phe
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 20 25 30

Thr Leu Ala Lys Thr Ala Val Asp Arg Gly Ile Asp Leu Val Tyr Gly
 35 40 45

Gly Gly Lys Val Gly Leu Met Gly Ile Val Ala Asp Ala Phe Leu Glu
 50 55 60

Ser Gly Gly Glu Ala Phe Gly Val Ile Thr Glu Ser Leu Met Lys Gly
 65 70 75 80

Glu Leu Gly His Glu Lys Leu Thr Glu Leu Glu Ile Val Pro Asp Met
 85 90 95

His Ile Arg Lys Arg Arg Met Ala Glu Leu Gly Asp Gly Phe Ile Ala
 100 105 110

Met Pro Gly Gly Ala Gly Thr Leu Glu Glu Leu Phe Glu Val Trp Thr
 115 120 125

Trp Gln Gln Leu Gly Ile His Gln Lys Pro Val Ala Leu Tyr Asp Val
 130 135 140

Asp Gly Phe Trp Gln Pro Leu Leu Glu Met Leu Glu Gln Met Thr Gln
 145 150 155 160

Arg Gly Phe Ile Lys Arg Asp Phe Phe Glu Cys Leu Ile Val Glu Ser
 165 170 175

Asp Pro His Ala Leu Leu Lys Ala Met Gln Thr Trp Thr Pro Pro Ala
 180 185 190

Pro Lys Trp
 195

<210> 599

<211> 3677

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(3654)

<223> RXN01362

<400> 599

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 1 5 10 15

acc cag cat gct cgc acg ggc acc cac ctt tat gat tcc ctg cag ctg 96
 Thr Gln His Ala Arg Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu

20	25	30	
ctg ttc act ctg gtg gat aaa ggc cac cac cca aca gat gct aag gct Leu Phe Thr Leu Val Asp Lys Gly His His Pro Thr Asp Ala Lys Ala 35 40 45			144
gta gct ttt gat gcc gag gct gga gaa gaa ggc ctg cac ttc cgc aac Val Ala Phe Asp Ala Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn 50 55 60			192
ctt tca gcg gat ctc ttc ctc cct gca gcc aca gaa ctt att gat cga Leu Ser Ala Asp Leu Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg 65 70 75 80			240
gtt ggt ctt tcc aat gaa gcc cta aac aag gtc ttg gaa aac ctc ctg Val Gly Leu Ser Asn Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu 85 90 95			288
ctc tcc cgg gtg caa tcc ggt aaa gac cgc ggc ttt atc tcc tat gcc Leu Ser Arg Val Gln Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala 100 105 110			336
acc ttg ggt gtt acc gag ctt ggc caa gtt tat gag ggt ctg atg tcc Thr Leu Gly Val Thr Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser 115 120 125			384
tat acc ggc ttt atc gcc cag gaa gat ctt ttt gag gtt gca cca cat Tyr Thr Gly Phe Ile Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His 130 135 140			432
ggc aaa gcc gat aaa ggt tcc tgg atg ctc ccg gtc tca aag gct gat Gly Lys Ala Asp Lys Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp 145 150 155 160			480
gaa gtc cct gcc gat agc ttt atc gaa gtt gat caa gaa gcc cct ggt Glu Val Pro Ala Asp Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly 165 170 175			528
ggc ggc gta atc aag gtg cgt aaa cgc cac ccg cgc gga tca ttt gtg Gly Gly Val Ile Lys Val Arg Lys Arg His Pro Arg Gly Ser Phe Val 180 185 190			576
ttc cgt cag tcc tct cgt gac cgc gaa cgc tca gcg tcc ttc tac acc Phe Arg Gln Ser Ser Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr 195 200 205			624
cca caa gta ctc acc agc ttt act gtc acc cag gct att gaa gaa ctc Pro Gln Val Leu Thr Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu 210 215 220			672
cag gca tca aag cgc atc acc aca gcc aat gat gtt ctc agc ctc acc Gln Ala Ser Lys Arg Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr 225 230 235 240			720
atc tgt gaa cct gcc atg ggt tcc ggc gcc ttc gct gtg gaa gca gta Ile Cys Glu Pro Ala Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val 245 250 255			768
cgc caa tta gca gag ctt tat ttg gaa ttg cgc caa gaa gaa cta gag Arg Gln Leu Ala Glu Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu 260 265 270			816

cag cag att cca gcg gaa gac cgt gcc aag gaa ctc caa aag gtc aaa Gln Gln Ile Pro Ala Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys 275 280 285	864
gcg cac att gcg ctg cac cag gtt tat ggt gtg gac ctt aac agc act Ala His Ile Ala Leu His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr 290 295 300	912
gct gtg gag ttg gcg gaa atc tcg ctg tgg cta gac acc atg aat gca Ala Val Glu Leu Ala Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala 305 310 315 320	960
gaa atg gac gca cct tgg tat ggc ctg cac ctg cgt aat ggt aac tcc Glu Met Asp Ala Pro Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser 325 330 335	1008
ctc gtt ggt gcc acc cgt tcg ctg tat gca cct agt ctg ctt aat aaa Leu Val Gly Ala Thr Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys 340 345 350	1056
aaa gcc tgg tta act gct act cca acc cgc tat cgg ctt gat gat atc Lys Ala Trp Leu Thr Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile 355 360 365	1104
gcg cag gct att gat gaa aac aaa gca gaa ccc ctc ttc aac cac ggc Ala Gln Ala Ile Asp Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly 370 375 380	1152
atc cac cac ttc ctc ttg ccc tct act ggc tgg gga gcc act gca gat Ile His His Phe Leu Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp 385 390 395 400	1200
gcc aaa gat ctt aaa gat ctt atg gct act gaa atc aag gag ctt aaa Ala Lys Asp Leu Lys Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys 405 410 415	1248
tct tgg cgt act tcc atc cgt gcg tct ttg agt aaa act cag att aag Ser Trp Arg Thr Ser Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys 420 425 430	1296
cag ctc aat aac ctt gcc cta cgc gtg gaa aca cta tgg cga ttt gtg Gln Leu Asn Asn Leu Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val 435 440 445	1344
ctg atg cgt att cgc att gca gaa tcc cag atc tca cgt agc act act Leu Met Arg Ile Arg Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr 450 455 460	1392
ctc tgg ggt caa gag cca gct gag gtt tcg gag gtt gtc aca cgt gag Leu Trp Gly Gln Glu Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu 465 470 475 480	1440
caa att gaa caa gac ctc ttt ggc aat att gat ggt gca tat aac cgt Gln Ile Glu Gln Asp Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg 485 490 495	1488
cta cgc ttg gtg atg gat gct tgg tgt gcg ctg tgg ttc tgg cct ttg Leu Arg Leu Val Met Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu 500 505 510	1536

gat gct gtt gct acc gct gag cat ccg gag cgt cca gcc ctt cca gat	1584
Asp Ala Val Ala Thr Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp	
515 520 525	
ctt gat gag tgg cta gcc acc ctg acg gag att ctg ggt att gat ctc	1632
Leu Asp Glu Trp Leu Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu	
530 535 540	
cct ctg aag tcc aaa aac gaa aat cag att gtc tta ggt cca gat acc	1680
Pro Leu Lys Ser Lys Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr	
545 550 555 560	
aat tgg cta gcc att aat gat gcc gag gct act gat ctt ggt ttt tct	1728
Asn Trp Leu Ala Ile Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser	
565 570 575	
ggg gca ttg agc ttt gag cgt gtt agc gcg aat cac ccg tgg atc aat	1776
Gly Ala Leu Ser Phe Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn	
580 585 590	
gtt gcc cgc caa gtg gct aaa caa cag agc ttc ttc cac tgg gat cta	1824
Val Ala Arg Gln Val Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu	
595 600 605	
gac ttc gcc cac gtt ttt gcc aag ggt gga ttt gat ctg cag gtt ggt	1872
Asp Phe Ala His Val Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly	
610 615 620	
aat cca cca tgg gtg cga cca gat gtg aac ttt gag gat ctg ctt gct	1920
Asn Pro Pro Trp Val Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala	
625 630 635 640	
gaa cat gat ccg tgg tgg gct gta atg agt aaa cca acc cag gca tcc	1968
Glu His Asp Pro Trp Trp Ala Val Met Ser Lys Pro Thr Gln Ala Ser	
645 650 655	
aaa aaa gaa cgc cag aag aat ttt cac aac aat cct aag agc ctc gaa	2016
Lys Lys Glu Arg Gln Lys Asn Phe His Asn Asn Pro Lys Ser Leu Glu	
660 665 670	
cat gtg gtc agt ggt gca ggt gaa ccc gtg gct act tct gcg atc ctc	2064
His Val Val Ser Gly Ala Gly Glu Pro Val Ala Thr Ser Ala Ile Leu	
675 680 685	
ggt tgg gtt act ctc tat ccg cat ctt aaa gat caa cgc ccg gac ctc	2112
Gly Ser Val Thr Leu Tyr Pro His Leu Lys Asp Gln Arg Pro Asp Leu	
690 695 700	
tac cgg ggc ttt atg gaa aag act tgg tct aat gcc tcc ccg gca ggt	2160
Tyr Arg Gly Phe Met Glu Lys Thr Trp Ser Asn Ala Ser Pro Ala Gly	
705 710 715 720	
gcg atc tca ctg atc cac ccc gaa tcc cac ttc act gag aaa aaa gct	2208
Ala Ile Ser Leu Ile His Pro Glu Ser His Phe Thr Glu Lys Lys Ala	
725 730 735	
gcc ccg cta cgt cgg gga gca tat gag cgt ctg cgc cgc cac tgg cag	2256
Ala Pro Leu Arg Arg Gly Ala Tyr Glu Arg Leu Arg Arg His Trp Gln	
740 745 750	
ttc att aat gag ttg att ctt ttt gac gtc cac gac ttg gtt aaa tat	2304

Phe Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr	
755 760 765	
ggc gta cat gtc tat ggc gct ccg cag gaa tct att aac ttt tta agt	2352
Gly Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser	
770 775 780	
gct gcg tcg ctt tat cac cca caa aca gtg ctt gat tca ttt gat cat	2400
Ala Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His	
785 790 795 800	
gac ggt tca ggt aat ctc cct ggt ctt aaa gac gac aat ggc aac tgg	2448
Asp Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp	
805 810 815	
gac cgt cgc cca cac aag gac cgt atc caa ctg gtc aat gcc gat act	2496
Asp Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr	
820 825 830	
ttg acg gtg tgg aag tcc atc ctg gag gat gaa caa acg cca tac ttg	2544
Leu Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu	
835 840 845	
gat acc cgc atg gtt tat acc gtc aac acg gaa gca gca gca gcg ttg	2592
Asp Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Leu	
850 855 860	
gaa aag ttg gct tct gca cct cgt atc aaa gaa ctc ggg ctg cag ttc	2640
Glu Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe	
865 870 875 880	
tcc agt ggc tgg aat gaa acc acc gat aag aaa aag gga tac ttt gac	2688
Ser Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp	
885 890 895	
gtt ggt tgg ggc tac cca gct tcc tgg tct gat gcc att ttg cag ggg	2736
Val Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly	
900 905 910	
ccg cac ctg ggt gtt gct aca cca atg atc aag cag ccc aat ccg aca	2784
Pro His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr	
915 920 925	
atg aag cat aat caa gat tgg tct gaa att gat ttc gag gcc att cct	2832
Met Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro	
930 935 940	
gca aac ttc ata cct gca acg gcg tac cag ccc gat cgc caa aca aag	2880
Ala Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys	
945 950 955 960	
ccc act tat gat gct gac tac ggc acc tgg act ttc ggg gac aag cag	2928
Pro Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln	
965 970 975	
gta cca gtt gca gac act ttc cga att gca tgg agg gag atg gct gcc	2976
Val Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala	
980 985 990	
acc acg gga ttt agg act gtc tac cca tca gta att cca ccg gga gcc	3024
Thr Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala	

995	1000	1005	
aac cat gtg cac aca gtt aat agc gct gca tca cgt tca aac tta aaa			3072
Asn His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys			
1010	1015	1020	
acc att ctc gtt gga gca cag ctt ggt gca att cta agt gac tat ttt			3120
Thr Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe			
1025	1030	1035	1040
gct cgg tcc tcg ggt tca agc cac ata ttt aac gac att gtt cgc aag			3168
Ala Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys			
1045	1050	1055	
att cca ctt cca aat ttc aca tcc ttg gaa aag cag ttc gcc cgc aca			3216
Ile Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr			
1060	1065	1070	
tac ctc cgc ctc aac tgc ctg acc tca gct tat gcc cca ttg tgg gaa			3264
Tyr Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu			
1075	1080	1085	
gag atc acc ggt gag ccg tgg gat gtt cag gtg cct ttg cgc aat gcc			3312
Glu Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala			
1090	1095	1100	
gag caa cgt cga gca gcg caa aac gat att gat gcc atg gtg gca ttg			3360
Glu Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu			
1105	1110	1115	1120
tct ttg ggt att agt gct gat gag ctg tgc atg att tat cgc act caa			3408
Ser Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln			
1125	1130	1135	
ttc cca gtg atg cgt aga tat gat caa gaa gat cat ttt gat gcc aat			3456
Phe Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn			
1140	1145	1150	
ggc cgt aaa gtt cct aaa gag atc atc aag ctg cag cag aaa ctt aaa			3504
Gly Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys			
1155	1160	1165	
gat ggc caa gag ctc agc gtg gaa aag cgc acc tgg gtg cat ccc caa			3552
Asp Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln			
1170	1175	1180	
tca gaa gtg tcc tat acc ttt gaa tat cct ttc cgg gtg ttg gat cgt			3600
Ser Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg			
1185	1190	1195	1200
gaa gct gat ctg cgt gct gca tat gca aaa ttt gaa aac cag ctt aag			3648
Glu Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys			
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gag cca tagagcgctt atgtcctcac tca			3677
Glu Pro			

<210> 600

<211> 1218

<212> PRT

<213> Corynebacterium glutamicum

<400> 600

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20 25 30

Leu Phe Thr Leu Val Asp Lys Gly His His Pro Thr Asp Ala Lys Ala
35 40 45

Val Ala Phe Asp Ala Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn
50 55 60

Leu Ser Ala Asp Leu Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg
65 70 75 80

Val Gly Leu Ser Asn Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu
85 90 95

Leu Ser Arg Val Gln Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala
100 105 110

Thr Leu Gly Val Thr Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser
115 120 125

Tyr Thr Gly Phe Ile Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His
130 135 140

Gly Lys Ala Asp Lys Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp
145 150 155 160

Glu Val Pro Ala Asp Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly
165 170 175

Gly Gly Val Ile Lys Val Arg Lys Arg His Pro Arg Gly Ser Phe Val
180 185 190

Phe Arg Gln Ser Ser Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr
195 200 205

Pro Gln Val Leu Thr Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu
210 215 220

Gln Ala Ser Lys Arg Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr
225 230 235 240

Ile Cys Glu Pro Ala Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val
245 250 255

Arg Gln Leu Ala Glu Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu
260 265 270

Gln Gln Ile Pro Ala Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys
275 280 285

Ala His Ile Ala Leu His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr
290 295 300

Ala Val Glu Leu Ala Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala
305 310 315 320

Glu Met Asp Ala Pro Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser
325 330 335

Leu Val Gly Ala Thr Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys
340 345 350

Lys Ala Trp Leu Thr Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile
355 360 365

Ala Gln Ala Ile Asp Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly
370 375 380

Ile His His Phe Leu Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp
385 390 395 400

Ala Lys Asp Leu Lys Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys
405 410 415

Ser Trp Arg Thr Ser Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys
420 425 430

Gln Leu Asn Asn Leu Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val
435 440 445

Leu Met Arg Ile Arg Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr
450 455 460

Leu Trp Gly Gln Glu Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu
465 470 475 480

Gln Ile Glu Gln Asp Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg
485 490 495

Leu Arg Leu Val Met Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu
500 505 510

Asp Ala Val Ala Thr Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp
515 520 525

Leu Asp Glu Trp Leu Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu
530 535 540

Pro Leu Lys Ser Lys Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr
545 550 555 560

Asn Trp Leu Ala Ile Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser
565 570 575

Gly Ala Leu Ser Phe Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn
580 585 590

Val Ala Arg Gln Val Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu
595 600 605

Asp Phe Ala His Val Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly
610 615 620

Asn Pro Pro Trp Val Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala

625	630	635	640
Glu His Asp Pro Trp Trp Ala Val Met Ser Lys Pro Thr Gln Ala Ser	645	650	655
Lys Lys Glu Arg Gln Lys Asn Phe His Asn Asn Pro Lys Ser Leu Glu	660	665	670
His Val Val Ser Gly Ala Gly Glu Pro Val Ala Thr Ser Ala Ile Leu	675	680	685
Gly Ser Val Thr Leu Tyr Pro His Leu Lys Asp Gln Arg Pro Asp Leu	690	695	700
Tyr Arg Gly Phe Met Glu Lys Thr Trp Ser Asn Ala Ser Pro Ala Gly	705	710	715
Ala Ile Ser Leu Ile His Pro Glu Ser His Phe Thr Glu Lys Lys Ala	725	730	735
Ala Pro Leu Arg Arg Gly Ala Tyr Glu Arg Leu Arg Arg His Trp Gln	740	745	750
Phe Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr	755	760	765
Gly Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser	770	775	780
Ala Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His	785	790	795
Asp Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp	805	810	815
Asp Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr	820	825	830
Leu Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu	835	840	845
Asp Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu	850	855	860
Glu Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe	865	870	875
Ser Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp	885	890	895
Val Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly	900	905	910
Pro His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr	915	920	925
Met Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro	930	935	940
Ala Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys	945	950	955
			960

Pro Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln
965 970 975

Val Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala
980 985 990

Thr Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala
995 1000 1005

Asn His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys
1010 1015 1020

Thr Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe
1025 1030 1035 1040

Ala Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys
1045 1050 1055

Ile Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr
1060 1065 1070

Tyr Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu
1075 1080 1085

Glu Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala
1090 1095 1100

Glu Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu
1105 1110 1115 1120

Ser Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln
1125 1130 1135

Phe Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn
1140 1145 1150

Gly Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys
1155 1160 1165

Asp Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln
1170 1175 1180

Ser Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg
1185 1190 1195 1200

Glu Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys
1205 1210 1215

Glu Pro

<210> 601
<211> 1418
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(1395)

<223> FRXA01362

<400> 601

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Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr Gly	
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gta cat gtc tat ggc gct ccg cag gaa tct att aac ttt tta agt gct	96
Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser Ala	
20 25 30	
gcg tcg ctt tat cac cca caa aca gtg ctt gat tca ttt gat cat gac	144
Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His Asp	
35 40 45	
ggt tca ggt aat ctc cct ggt ctt aaa gac gac aat ggc aac tgg gac	192
Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp Asp	
50 55 60	
cgt cgc cca cac aag gac cgt atc caa ctg gtc aat gcc gat act ttg	240
Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr Leu	
65 70 75 80	
acg gtg tgg aag tcc atc ctg gag gat gaa caa acg cca tac ttg gat	288
Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu Asp	
85 90 95	
acc cgc atg gtt tat acc gtc aac acg gaa gca gca gca gcg ttg gaa	336
Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu Glu	
100 105 110	
aag ttg gct tct gca cct cgt atc aaa gaa ctc ggg ctg cag ttc tcc	384
Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe Ser	
115 120 125	
agt ggc tgg aat gaa acc acc gat aag aaa aag gga tac ttt gac gtt	432
Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp Val	
130 135 140	
ggt tgg ggc tac cca gct tcc tgg tct gat gcc att ttg cag ggg ccg	480
Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly Pro	
145 150 155 160	
cac ctg ggt gtt gct aca cca atg atc aag cag ccc aat ccg aca atg	528
His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr Met	
165 170 175	
aag cat aat caa gat tgg tct gaa att gat ttc gag gcc att cct gca	576
Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro Ala	
180 185 190	
aac ttc ata cct gca acg gcg tac cag ccc gat cgc caa aca aag ccc	624
Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys Pro	
195 200 205	
act tat gat gct gac tac ggc acc tgg act ttc ggg gac aag cag gta	672
Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln Val	
210 215 220	
cca gtt gca gac act ttc cga att gca tgg agg gag atg gct gcc acc	720
Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala Thr	

225	230	235	240	
acg gga ttt agg act gtc tac cca tca gta att cca ccg gga gcc aac	Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala Asn	768		
245	250	255		
cat gtg cac aca gtt aat agc gct gca tca cgt tca aac tta aaa acc	His Val His Thr Val Asn Ser Ala Ser Arg Ser Asn Leu Lys Thr	816		
260	265	270		
att ctc gtt gga gca cag ctt ggt gca att cta agt gac tat ttt gct	Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe Ala	864		
275	280	285		
cgg tcc tcg ggt tca agc cac ata ttt aac gac att gtt cgc aag att	Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys Ile	912		
290	295	300		
cca ctt cca aat ttc aca tcc ttg gaa aag cag ttc gcc cgc aca tac	Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr Tyr	960		
305	310	315		320
ctc cgc ctc aac tgc ctg acc tca gct tat gcc cca ttg tgg gaa gag	Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu Glu	1008		
325	330	335		
atc acc ggt gag ccg tgg gat gtt cag gtg cct ttg cgc aat gcc gag	Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala Glu	1056		
340	345	350		
caa cgt cga gca gcg caa aac gat att gat gcc atg gtg gca ttg tct	Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu Ser	1104		
355	360	365		
ttg ggt att agt gct gat gag ctg tgc atg att tat cgc act caa ttc	Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln Phe	1152		
370	375	380		
cca gtg atg cgt aga tat gat caa gaa gat cat ttt gat gcc aat ggc	Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn Gly	1200		
385	390	395		400
cgt aaa gtt cct aaa gag atc atc aag ctg cag cag aaa ctt aaa gat	Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys Asp	1248		
405	410	415		
ggc caa gag ctc agc gtg gaa aag cgc acc tgg gtg cat ccc caa tca	Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln Ser	1296		
420	425	430		
gaa gtg tcc tat acc ttt gaa tat cct ttc cgg gtg ttg gat cgt gaa	Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg Glu	1344		
435	440	445		
gct gat ctg cgt gct gca tat gca aaa ttt gaa aac cag ctt aag gag	Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys Glu	1392		
450	455	460		
cca tagagcgctt atgtcctcac tca	Pro	1418		
465				

<210> 602

<211> 465

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 602

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 Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser Ala
 20 25 30
 Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His Asp
 35 40 45
 Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp Asp
 50 55 60
 Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr Leu
 65 70 75 80
 Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu Asp
 85 90 95
 Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu Glu
 100 105 110
 Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe Ser
 115 120 125
 Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp Val
 130 135 140
 Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly Pro
 145 150 155 160
 His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr Met
 165 170 175
 Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro Ala
 180 185 190
 Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys Pro
 195 200 205
 Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln Val
 210 215 220
 Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala Thr
 225 230 235 240
 Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala Asn
 245 250 255
 His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys Thr
 260 265 270
 Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe Ala
 275 280 285

Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys Ile
 290 295 300

Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr Tyr
 305 310 315 320

Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu Glu
 325 330 335

Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala Glu
 340 345 350

Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu Ser
 355 360 365

Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln Phe
 370 375 380

Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn Gly
 385 390 395 400

Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys Asp
 405 410 415

Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln Ser
 420 425 430

Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg Glu
 435 440 445

Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys Glu
 450 455 460

Pro
 465

<210> 603
 <211> 1866
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1866)
 <223> FRXA01364

<400> 603

acg ggc acc cac ctt tat gat tcc ctg cag ctg ctg ttc act ctg gtg	48
Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu Leu Phe Thr Leu Val	
1 5 10 15	
gat aaa ggc cac cac cca aca gat gct aag gct gta gct ttt gat gcc	96
Asp Lys Gly His His Pro Thr Asp Ala Lys Ala Val Ala Phe Asp Ala	
20 25 30	
gag gct gga gaa gaa ggc ctg cac ttc cgc aac ctt tca gcg gat ctc	144
Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn Leu Ser Ala Asp Leu	
35 40 45	

ttc ctc cct gca gcc aca gaa ctt att gat cga gtt ggt ctt tcc aat	192
Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg Val Gly Leu Ser Asn	
50 55 60	
gaa gcc cta aac aag gtc ttg gaa aac ctc ctg ctc tcc cgg gtg caa	240
Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu Leu Ser Arg Val Gln	
65 70 75 80	
tcc ggt aaa gac cgc ggc ttt atc tcc tat gcc acc ttg ggt gtt acc	288
Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala Thr Leu Gly Val Thr	
85 90 95	
gag ctt ggc caa gtt tat gag ggt ctg atg tcc tat acc ggc ttt atc	336
Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser Tyr Thr Gly Phe Ile	
100 105 110	
gcc cag gaa gat ctt ttt gag gtt gca cca cat ggc aaa gcc gat aaa	384
Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His Gly Lys Ala Asp Lys	
115 120 125	
ggt tcc tgg atg ctc ccg gtc tca aag gct gat gaa gtc cct gcc gat	432
Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp Glu Val Pro Ala Asp	
130 135 140	
agc ttt atc gaa gtt gat caa gaa gcc cct ggt ggc ggc gta atc aag	480
Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly Gly Gly Val Ile Lys	
145 150 155 160	
gtg cgt aaa cgc cac ccg cgc gga tca ttt gtg ttc cgt cag tcc tct	528
Val Arg Lys Arg His Pro Arg Gly Ser Phe Val Phe Arg Gln Ser Ser	
165 170 175	
cgt gac cgc gaa cgc tca gcg tcc ttc tac acc cca caa gta ctc acc	576
Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr Pro Gln Val Leu Thr	
180 185 190	
agc ttt act gtc acc cag gct att gaa gaa ctc cag gca tca aag cgc	624
Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu Gln Ala Ser Lys Arg	
195 200 205	
atc acc aca gcc aat gat gtt ctc agc ctc acc atc tgt gaa cct gcc	672
Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr Ile Cys Glu Pro Ala	
210 215 220	
atg ggt tcc ggc gcc ttc gct gtg gaa gca gta cgc caa tta gca gag	720
Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val Arg Gln Leu Ala Glu	
225 230 235 240	
ctt tat ttg gaa ttg cgc caa gaa gaa cta gag cag cag att cca gcg	768
Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu Gln Gln Ile Pro Ala	
245 250 255	
gaa gac cgt gcc aag gaa ctc caa aag gtc aaa gcg cac att gcg ctg	816
Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys Ala His Ile Ala Leu	
260 265 270	
cac cag gtt tat ggt gtg gac ctt aac agc act gct gtg gag ttg gcg	864
His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr Ala Val Glu Leu Ala	
275 280 285	
gaa atc tcg ctg tgg cta gac acc atg aat gca gaa atg gac gca cct	912

Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala Glu Met Asp Ala Pro 290 295 300	
tgg tat ggc ctg cac ctg cgt aat ggt aac tcc ctc gtt ggt gcc acc Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser Leu Val Gly Ala Thr 305 310 315 320	960
cgt tcg ctg tat gca cct agt ctg ctt aat aaa aaa gcc tgg tta act Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys Lys Ala Trp Leu Thr 325 330 335	1008
gct act cca acc cgc tat cgg ctt gat gat atc gcg cag gct att gat Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile Ala Gln Ala Ile Asp 340 345 350	1056
gaa aac aaa gca gaa ccc ctc ttc aac cac ggc atc cac cac ttc ctc Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly Ile His His Phe Leu 355 360 365	1104
ttg ccc tct act ggc tgg gga gcc act gca gat gcc aaa gat ctt aaa Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp Ala Lys Asp Leu Lys 370 375 380	1152
gat ctt atg gct act gaa atc aag gag ctt aaa tct tgg cgt act tcc Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys Ser Trp Arg Thr Ser 385 390 395 400	1200
atc cgt gcg tct ttg agt aaa act cag att aag cag ctc aat aac ctt Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys Gln Leu Asn Asn Leu 405 410 415	1248
gcc cta cgc gtg gaa aca cta tgg cga ttt gtg ctg atg cgt att cgc Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val Leu Met Arg Ile Arg 420 425 430	1296
att gca gaa tcc cag atc tca cgt agc act act ctc tgg ggt caa gag Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr Leu Trp Gly Gln Glu 435 440 445	1344
cca gct gag gtt tcg gag gtt gtc aca cgt gag caa att gaa caa gac Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu Gln Ile Glu Gln Asp 450 455 460	1392
ctc ttt ggc aat att gat ggt gca tat aac cgt cta cgc ttg gtg atg Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg Leu Arg Leu Val Met 465 470 475 480	1440
gat gct tgg tgt gcg ctg tgg ttc tgg cct ttg gat gct gtt gct acc Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu Asp Ala Val Ala Thr 485 490 495	1488
gct gag cat ccg gag cgt cca gcc ctt cca gat ctt gat gag tgg cta Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp Leu Asp Glu Trp Leu 500 505 510	1536
gcc acc ctg acg gag att ctg ggt att gat ctc cct ctg aag tcc aaa Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu Pro Leu Lys Ser Lys 515 520 525	1584
aac gaa aat cag att gtc tta ggt cca gat acc aat tgg cta gcc att Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr Asn Trp Leu Ala Ile 530 535 540	1632

530 535 540
 aat gat gcc gag gct act gat ctt ggt ttt tct ggg gca ttg agc ttt 1680
 Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser Gly Ala Leu Ser Phe
 545 550 555 560
 gag cgt gtt agc gcg aat cac ccg tgg atc aat gtt gcc cgc caa gtg 1728
 Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn Val Ala Arg Gln Val
 565 570 575
 gct aaa caa cag agc ttc ttc cac tgg gat cta gac ttc gcc cac gtt 1776
 Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu Asp Phe Ala His Val
 580 585 590
 ttt gcc aag ggt gga ttt gat ctg cag gtt ggt aat cca cca tgg gtg 1824
 Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly Asn Pro Pro Trp Val
 595 600 605
 cga cca gat gtg aac ttt gag gat ctg ctt gct gaa cat gat 1866
 Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala Glu His Asp
 610 615 620

 <210> 604
 <211> 622
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 604
 Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu Leu Phe Thr Leu Val
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 Asp Lys Gly His His Pro Thr Asp Ala Lys Ala Val Ala Phe Asp Ala
 20 25 30
 Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn Leu Ser Ala Asp Leu
 35 40 45
 Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg Val Gly Leu Ser Asn
 50 55 60
 Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu Leu Ser Arg Val Gln
 65 70 75 80
 Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala Thr Leu Gly Val Thr
 85 90 95
 Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser Tyr Thr Gly Phe Ile
 100 105 110
 Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His Gly Lys Ala Asp Lys
 115 120 125
 Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp Glu Val Pro Ala Asp
 130 135 140
 Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly Gly Gly Val Ile Lys
 145 150 155 160
 Val Arg Lys Arg His Pro Arg Gly Ser Phe Val Phe Arg Gln Ser Ser
 165 170 175

Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr Pro Gln Val Leu Thr
 180 185 190
 Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu Gln Ala Ser Lys Arg
 195 200 205
 Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr Ile Cys Glu Pro Ala
 210 215 220
 Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val Arg Gln Leu Ala Glu
 225 230 235 240
 Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu Gln Gln Ile Pro Ala
 245 250 255
 Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys Ala His Ile Ala Leu
 260 265 270
 His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr Ala Val Glu Leu Ala
 275 280 285
 Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala Glu Met Asp Ala Pro
 290 295 300
 Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser Leu Val Gly Ala Thr
 305 310 315 320
 Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys Lys Ala Trp Leu Thr
 325 330 335
 Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile Ala Gln Ala Ile Asp
 340 345 350
 Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly Ile His His Phe Leu
 355 360 365
 Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp Ala Lys Asp Leu Lys
 370 375 380
 Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys Ser Trp Arg Thr Ser
 385 390 395 400
 Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys Gln Leu Asn Asn Leu
 405 410 415
 Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val Leu Met Arg Ile Arg
 420 425 430
 Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr Leu Trp Gly Gln Glu
 435 440 445
 Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu Gln Ile Glu Gln Asp
 450 455 460
 Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg Leu Arg Leu Val Met
 465 470 475 480
 Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu Asp Ala Val Ala Thr
 485 490 495

tat ggt gtc ccc agc gcg cgc cac gcg cag cgc ggc tcc gac aca ata	403
Tyr Gly Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile	
90 95 100	
tcc tat tcc tct tgg gtg gga aat gcc ggc agt gtg gaa ttt ctt gca	451
Ser Tyr Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala	
105 110 115	
gcg act ccc gct gaa agc ttt gaa gag aac ttc cga tcc ctt ccc ctt	499
Ala Thr Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu	
120 125 130	
gag cca gta gcg gtc aat gac aag ccc cag gat atc acc gca gcc aaa	547
Glu Pro Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys	
135 140 145	
ttg gtg ggc cag att ttc ctt agt gat act ccc cct gct ttt gtt gtt	595
Leu Val Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val	
150 155 160 165	
atc acc gct ggt aaa tgg gtg gtt tta gcc gag cgt gaa acc tgg cct	643
Ile Thr Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro	
170 175 180	
cta ggc cgc cac cta gct att gat att tcc ctg gtg gtg gaa cgt aat	691
Leu Gly Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn	
185 190 195	
gac acc aaa gcc cag ggt gag atg cag cag acg gtc gta gca cta gcc	739
Asp Thr Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala	
200 205 210	
cgc gaa aat acc gag cgt gcc gcc gat ggc acc acc tgg tgg gaa gaa	787
Arg Glu Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu	
215 220 225	
acc att gag caa tcc cgc gaa cat gct gtc aag gtt tct ggc gag cta	835
Thr Ile Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu	
230 235 240 245	
cgc agt gcg gtg cgt gaa tcc att gaa atc ctg ggc aat gac gtg ctc	883
Arg Ser Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu	
250 255 260	
aca cgc tat gaa gct aaa gag ctc tcc acc gct gag atc gac ggt ggc	931
Thr Arg Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly	
265 270 275	
gag cta gct aag caa tct ttg cgc tat ctc tac cgc att ttg ttc ctg	979
Glu Leu Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu	
280 285 290	
ctt ttt gcc gag gct tca cca gag ctt gaa atc ctg cca acc ggc acc	1027
Leu Phe Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr	
295 300 305	
ccg gaa tat gac gag	1042
Pro Glu Tyr Asp Glu	
310	

<210> 606

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

Met Ser Ala Phe Asp Ser Ile Leu Asn Val Glu Glu Trp Ile Ser Asp
1 5 10 15

His Tyr Leu Thr Asn Asp Asp Ala Lys Gly Ala Ser Phe Ser Lys Arg
20 25 30

Val Arg Glu Arg Ile Lys Glu Trp Lys Thr Thr Glu Asp Ala Thr Gln
35 40 45

Gln Ser Gly Pro Leu Thr Arg Phe Ser Ser Asn Arg Leu Gln Leu Gln
50 55 60

His Ala Leu Ser Glu Leu Asp Asp Ala Thr Thr Ala Ala Ser Leu Val
65 70 75 80

Ala Ser Ala Leu Gly Tyr Gly Val Pro Ser Ala Arg His Ala Gln Arg
85 90 95

Gly Ser Asp Thr Ile Ser Tyr Ser Ser Trp Val Gly Asn Ala Gly Ser
100 105 110

Val Glu Phe Leu Ala Ala Thr Pro Ala Glu Ser Phe Glu Glu Asn Phe
115 120 125

Arg Ser Leu Pro Leu Glu Pro Val Ala Val Asn Asp Lys Pro Gln Asp
130 135 140

Ile Thr Ala Ala Lys Leu Val Gly Gln Ile Phe Leu Ser Asp Thr Pro
145 150 155 160

Pro Ala Phe Val Val Ile Thr Ala Gly Lys Trp Val Val Leu Ala Glu
165 170 175

Arg Glu Thr Trp Pro Leu Gly Arg His Leu Ala Ile Asp Ile Ser Leu
180 185 190

Val Val Glu Arg Asn Asp Thr Lys Ala Gln Gly Glu Met Gln Gln Thr
195 200 205

Val Val Ala Leu Ala Arg Glu Asn Thr Glu Arg Ala Ala Asp Gly Thr
210 215 220

Thr Trp Trp Glu Glu Thr Ile Glu Gln Ser Arg Glu His Ala Val Lys
225 230 235 240

Val Ser Gly Glu Leu Arg Ser Ala Val Arg Glu Ser Ile Glu Ile Leu
245 250 255

Gly Asn Asp Val Leu Thr Arg Tyr Glu Ala Lys Glu Leu Ser Thr Ala
260 265 270

Glu Ile Asp Gly Gly Glu Leu Ala Lys Gln Ser Leu Arg Tyr Leu Tyr
275 280 285

Arg Ile Leu Phe Leu Leu Phe Ala Glu Ala Ser Pro Glu Leu Glu Ile
 290 295 300

Leu Pro Thr Gly Thr Pro Glu Tyr Asp Glu
 305 310

<210> 607

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(921)

<223> FRXA01379

<400> 607

cta aat gtt gaa gag tgg atc agt gac cac tac ctc acc aat gac gat 48
 Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn Asp Asp
 1 5 10 15

gcc aaa ggt gcc tca ttt tcc aag cgg gtg cgc gag cgc att aaa gaa 96
 Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile Lys Glu
 20 25 30

tgg aaa acc acc gag gac gca acc cag cag agt ggc cct tta act cgt 144
 Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu Thr Arg
 35 40 45

ttt tcc agc aac cgc ctg cag ttg cag cat gct ctt tct gag ctt gac 192
 Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu Leu Asp
 50 55 60

gac gcc acc acc gcc gcc agt tta gtg gcc tct gca ctg ggg tat ggt 240
 Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly Tyr Gly
 65 70 75 80

gtc ccc agc gcg cgc cac gcg cag cgc ggc tcc gac aca ata tcc tat 288
 Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile Ser Tyr
 85 90 95

tcc tct tgg gtg gga aat gcc ggc agt gtg gaa ttt ctt gca gcg act 336
 Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala Ala Thr
 100 105 110

ccc gct gaa agc ttt gaa gag aac ttc cga tcc ctt ccc ctt gag cca 384
 Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu Glu Pro
 115 120 125

gta gcg gtc aat gac aag ccc cag gat atc acc gca gcc aaa ttg gtg 432
 Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys Leu Val
 130 135 140

ggc cag att ttc ctt agt gat act ccc cct gct ttt gtt gtt atc acc 480
 Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val Ile Thr
 145 150 155 160

gct ggt aaa tgg gtg gtt tta gcc gag cgt gaa acc tgg cct cta ggc 528
 Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro Leu Gly
 165 170 175

cgc cac cta gct att gat att tcc ctg gtg gtg gaa cgt aat gac acc 576
 Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn Asp Thr
 180 185 190
 aaa gcc cag ggt gag atg cag cag acg gtc gta gca cta gcc cgc gaa 624
 Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala Arg Glu
 195 200 205
 aat acc gag cgt gcc gcc gat ggc acc acc tgg tgg gaa gaa acc att 672
 Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu Thr Ile
 210 215 220
 gag caa tcc cgc gaa cat gct gtc aag gtt tct ggc gag cta cgc agt 720
 Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu Arg Ser
 225 230 235 240
 gcg gtg cgt gaa tcc att gaa atc ctg ggc aat gac gtg ctc 'aca cgc 768
 Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu Thr Arg
 245 250 255
 tat gaa gct aaa gag ctc tcc acc gct gag atc gac ggt ggc gag cta 816
 Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly Glu Leu
 260 265 270
 gct aag caa tct ttg cgc tat ctc tac cgc att ttg ttc ctg ctt ttt 864
 Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu Leu Phe
 275 280 285
 gcc gag gct tca cca gag ctt gaa atc ctg cca acc ggc acc ccg gaa 912
 Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr Pro Glu
 290 295 300
 tat gac gag 921
 Tyr Asp Glu
 305

<210> 608
 <211> 307
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 608
 Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn Asp Asp
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 Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile Lys Glu
 20 25 30
 Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu Thr Arg
 35 40 45
 Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu Leu Asp
 50 55 60
 Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly Tyr Gly
 65 70 75 80
 Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile Ser Tyr
 85 90 95

Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala Ala Thr
 100 105 110
 Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu Glu Pro
 115 120 125
 Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys Leu Val
 130 135 140
 Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val Ile Thr
 145 150 155 160
 Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro Leu Gly
 165 170 175
 Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn Asp Thr
 180 185 190
 Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala Arg Glu
 195 200 205
 Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu Thr Ile
 210 215 220
 Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu Arg Ser
 225 230 235 240
 Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu Thr Arg
 245 250 255
 Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly Glu Leu
 260 265 270
 Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu Leu Phe
 275 280 285
 Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr Pro Glu
 290 295 300
 Tyr Asp Glu
 305

<210> 609
 <211> 780
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(757)
 <223> RXN01390

<400> 609
 cgtccagata atcaatctgc gaagccagtg gcttccgaag ctccaacaac tattacgccg 60
 gcaagctctg gtgcattagc atccgatgct ccgacgtctt atg ttc agg cgc agc 115
 Met Phe Arg Arg Ser
 1 5

ctt ccc agc aac aag aca tcc tca gca agt tcc gcc agc tcc gcc gac 163
 Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser Ala Ser Ser Ala Asp
 10 15 20

aca agt tac tca gtc aga tta ggc cgt cct gaa gag cct ggt tac cag 211
 Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu Glu Pro Gly Tyr Gln
 25 30 35

cca gaa ccg tct tat tcg gag cct tac act gac tct gat ttc gcg cca 259
 Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp Ser Asp Phe Ala Pro
 40 45 50

gca ggt gcg gcc gct gcg gca gct gca gta gct cca cca atg att gcg 307
 Ala Gly Ala Ala Ala Ala Ala Ala Val Ala Pro Pro Met Ile Ala
 55 60 65

gaa cag cca caa att gtt gaa gat gcc cgc cga ggt acc ctc gat ttc 355
 Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg Gly Thr Leu Asp Phe
 70 75 80 85

ggc ctg ttg att atc cgc gca gtc att ggt gtc tat ttg atc gtc cgt 403
 Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val Tyr Leu Ile Val Arg
 90 95 100

gga gtc ttt aca ttc ttc acc ctt gga gga tct gcc ggt ctt gct ggc 451
 Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser Ala Gly Leu Ala Gly
 105 110 115

ctc gag gca gag ttc gct ggt tac cag tgg cct gaa atc ctc gcg atc 499
 Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro Glu Ile Leu Ala Ile
 120 125 130

ctg ctt cca tct att gaa ctt gcg gct ggt gtc ttc ctg ctc ctt ggt 547
 Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val Phe Leu Leu Leu Gly
 135 140 145

ctg atg acc cca gtg gca gca gcg gta gcc acg gtg gcg aca tcc ttt 595
 Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr Val Ala Thr Ser Phe
 150 155 160 165

acc acc ctt cac caa gtc aac act cat gaa ggt ggt tgg ggt gaa ctt 643
 Thr Thr Leu His Gln Val Asn Thr His Glu Gly Gly Trp Gly Glu Leu
 170 175 180

agt gag cca ttg atg ctg gca ctg atc ctc act atc gtg gtt gtc gga 691
 Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr Ile Val Val Val Gly
 185 190 195

ctt cag ttc acc ggc ccc ggc aag att tcc ctt gac tct ggc cga ggt 739
 Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu Asp Ser Gly Arg Gly
 200 205 210

tgg caa agc gtc cac tgg tgagctcgtg gatcttcgtg gtc 780
 Trp Gln Ser Val His Trp
 215

<210> 610

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 610

Met Phe Arg Arg Ser Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser
 1 5 10 15

Ala Ser Ser Ala Asp Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu
 20 25 30

Glu Pro Gly Tyr Gln Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp
 35 40 45

Ser Asp Phe Ala Pro Ala Gly Ala Ala Ala Ala Ala Ala Val Ala
 50 55 60

Pro Pro Met Ile Ala Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg
 65 70 75 80

Gly Thr Leu Asp Phe Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val
 85 90 95

Tyr Leu Ile Val Arg Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser
 100 105 110

Ala Gly Leu Ala Gly Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro
 115 120 125

Glu Ile Leu Ala Ile Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val
 130 135 140

Phe Leu Leu Leu Gly Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr
 145 150 155 160

Val Ala Thr Ser Phe Thr Thr Leu His Gln Val Asn Thr His Glu Gly
 165 170 175

Gly Trp Gly Glu Leu Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr
 180 185 190

Ile Val Val Val Gly Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu
 195 200 205

Asp Ser Gly Arg Gly Trp Gln Ser Val His Trp
 210 215

<210> 611

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> FRXA01390

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 135 140 145

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<213> Corynebacterium glutamicum

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Ser Asp Phe Ala Pro Ala Gly Ala Ala Ala Ala Ala Ala Val Ala
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Pro Pro Met Ile Ala Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg
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Gly Thr Leu Asp Phe Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val
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Tyr Leu Ile Val Arg Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser
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Phe Leu Leu Leu Gly Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr
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Val Ala Thr Ser Phe Thr Thr Leu His Gln Val Asn Thr His Glu Gly
165 170 175
Gly Trp Gly Glu Leu Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr
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Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr Ala Phe Arg Cys Asp	
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Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg Tyr Asn Val Trp Val	
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Glu Leu Phe Gly Pro Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly
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His Asn Gly Cys Asp Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp
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Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp Asp Ile Gln Leu Arg	
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Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg Tyr Asn Val Trp Val	
200 205 210	

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His Asn Gly Cys Asp Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp
 85 90 95

Asp Ile Gln Leu Arg Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly
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Leu Leu Ser Asp Pro Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly
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Glu Arg Ser Gly Asp Val Gln Ile Asp His Leu Val Pro Leu His Asp
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Gln Gln Lys Gly Ala Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr
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Ala Phe Arg Cys Asp Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg
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 Ser Arg Pro Ser His Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro
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 Thr Val Ile Ile Gly Ser Asp His Ser His Val Asp Met Trp Ser Met
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Tyr Val Ser Ala Ser Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile
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His Ala Leu Asp Leu Leu Thr His Glu Ser Ser His Phe Leu Ala Val
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att tca gtg atg gct gat gtt acg gcg gcg ctg gcg gac ctt ccg ttg	787
Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu Ala Asp Leu Pro Leu	
215 220 225	
cgt gct gta ttc cca gtc cat agc cgt ttc gat cag cgc tgg cac gat	835
Arg Ala Val Phe Pro Val His Ser Arg Phe Asp Gln Arg Trp His Asp	
230 235 240 245	
agt gtc ggg tgg ttt atc tcc aat tcg gtc att gag gtg cca gat tcc	883
Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile Glu Val Pro Asp Ser	
250 255 260	
gat cct cac act gca gcc caa gct gtt cgc gag gct gtt tct ttg gga	931
Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu Ala Val Ser Leu Gly	
265 270 275	
agc tac ccg ctg gct gag ctg ctt gaa ccg tgg ggt ggc atg ccg gaa	979
Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp Gly Gly Met Pro Glu	
280 285 290	
acg cca gga atg ttt gct att tct tgg ctt gac ctg cgc cga ctc cca	1027
Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp Leu Arg Arg Leu Pro	
295 300 305	
gtg agc att gac gat att ggc ctc caa gcc cag tat gtc agc gct tca	1075
Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln Tyr Val Ser Ala Ser	
310 315 320 325	
ctg cgc acc gat ggt gtg atg ctg tgg ttt att ttg gat cgc tcc ggc	1123
Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile Leu Asp Arg Ser Gly	
330 335 340	
gcg cac ctt cgc tgt cgt tat cct gac tct ttg gtg gcg cgg gaa aat	1171
Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu Val Ala Arg Glu Asn	
345 350 355	
gta ggc cgc tgg att gat gcg att gtt gct cag atg cgc gcc gaa gct	1219
Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln Met Arg Ala Glu Ala	
360 365 370	
ggg acg gtg aat ctg cag gcc ggc ggg gaa cag ctg aca ctt cgg cat	1267
Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln Leu Thr Leu Arg His	
375 380 385	
gga act cgc gcc gat att tcc gag atc gcc ccg cta ctt gcc cga aac	1315
Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro Leu Leu Ala Arg Asn	
390 395 400 405	
gca gct gac cct tgt gag ctg gtg gat ctt gaa cat gcc ctt gac ctg	1363

Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu His Ala Leu Asp Leu
 410 415 420

ctg aca cac gag tct tcg cat ttc ctg gcg gtg gtt cga aac gct cgt 1411
 Leu Thr His Glu Ser Ser His Phe Leu Ala Val Val Arg Asn Ala Arg
 425 430 435

ggc aag ata atc gca gcg atg cag ttg act att gtt ccg gag ttt tcc 1459
 Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile Val Pro Glu Phe Ser
 440 445 450

cgc ggt ggt gcg ctt cat ctt cac atc gag ggg ccg ttc att att ccg 1507
 Arg Gly Gly Ala Leu His Leu His Ile Glu Gly Pro Phe Ile Ile Pro
 455 460 465

gaa tat cgc acc acc gat ttg gat aaa aag ctg cgc gcc tgg gct gtg 1555
 Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu Arg Ala Trp Ala Val
 470 475 480 485

gag cat ggg cgt gcg cga ggg gtg aag gtt gag gag gtg gtg gga 1600
 Glu His Gly Arg Ala Arg Gly Val Lys Val Glu Glu Val Val Gly
 490 495 500

tagttggttt attggcgcct cgt 1623

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 <213> Corynebacterium glutamicum

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Glu Arg Ala Trp Leu Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr
 20 25 30

Val Phe Ser Thr Gly Met Gly Gly Glu Val Gln Gln His Arg Ile Asp
 35 40 45

Val Gly Pro Gly Lys Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser
 50 55 60

Ile Asn Glu Ala Leu Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr
 65 70 75 80

Ser Arg Pro Ser His Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro
 85 90 95

Thr Val Ile Ile Gly Ser Asp His Ser His Val Asp Met Trp Ser Met
 100 105 110

Leu Val Ile Val Arg Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro
 115 120 125

Val Glu Pro Pro Leu Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala
 130 135 140

Ala Pro Pro Ala Pro Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu
 145 150 155 160

Glu Ala Gly Gly Gly Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp
 165 170 175
 Ala Ile Ser Met Pro Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val
 180 185 190
 Asn Gly Leu Ala Ile Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser
 195 200 205
 Ser Leu Ala Leu Thr Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu
 210 215 220
 Ala Asp Leu Pro Leu Arg Ala Val Phe Pro Val His Ser Arg Phe Asp
 225 230 235 240
 Gln Arg Trp His Asp Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile
 245 250 255
 Glu Val Pro Asp Ser Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu
 260 265 270
 Ala Val Ser Leu Gly Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp
 275 280 285
 Gly Gly Met Pro Glu Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp
 290 295 300
 Leu Arg Arg Leu Pro Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln
 305 310 315 320
 Tyr Val Ser Ala Ser Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile
 325 330 335
 Leu Asp Arg Ser Gly Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu
 340 345 350
 Val Ala Arg Glu Asn Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln
 355 360 365
 Met Arg Ala Glu Ala Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln
 370 375 380
 Leu Thr Leu Arg His Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro
 385 390 395 400
 Leu Leu Ala Arg Asn Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu
 405 410 415
 His Ala Leu Asp Leu Leu Thr His Glu Ser Ser His Phe Leu Ala Val
 420 425 430
 Val Arg Asn Ala Arg Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile
 435 440 445
 Val Pro Glu Phe Ser Arg Gly Gly Ala Leu His Leu His Ile Glu Gly
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 Pro Phe Ile Ile Pro Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu
 465 470 475 480

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Trp	Val	Asp	Phe	Pro	Asp	Val	Thr	Ala	Arg	Leu	Gly	Tyr	Glu	Tyr	Met	
1				5					10					15		
cag	ctg	acc	cct	cat	gta	gat	ttc	ggc	cct	ttc	ttc	cgc	cac	ccc	aag	96
Gln	Leu	Thr	Pro	His	Val	Asp	Phe	Gly	Pro	Phe	Phe	Arg	His	Pro	Lys	
			20					25					30			
gca	gac	gat	gat	ctc	gtg	gca	gcc	ctg	aaa	aag	cgt	gcc	aag	gat	gcc	144
Ala	Asp	Asp	Asp	Leu	Val	Ala	Ala	Leu	Lys	Lys	Arg	Ala	Lys	Asp	Ala	
			35				40					45				
gga	gtc	acc	att	cct	gca	ctg	ttg	cca	gtg	cag	cgt	att	tcc	tgg	ccg	192
Gly	Val	Thr	Ile	Pro	Ala	Leu	Leu	Pro	Val	Gln	Arg	Ile	Ser	Trp	Pro	
	50					55					60					
gag	gaa	acc	cag	cgt	gtt	gca	gca	gta	cgc	aac	atc	aag	cgc	atc	atc	240
Glu	Glu	Thr	Gln	Arg	Val	Ala	Ala	Val	Arg	Asn	Ile	Lys	Arg	Ile	Ile	
65				70						75					80	
cag	ttg	gcc	gtt	gat	ctg	gaa	gta	gac	acc	ctc	aac	acg	gag	ttt	tct	288
Gln	Leu	Ala	Val	Asp	Leu	Glu	Val	Asp	Thr	Leu	Asn	Thr	Glu	Phe	Ser	
				85					90					95		
gga	cgc	cca	gaa	cgc	tcc	gag	gat	tcc	gaa	gat	gcc	ttc	tac	cgc	tcc	336
Gly	Arg	Pro	Glu	Arg	Ser	Glu	Asp	Ser	Glu	Asp	Ala	Phe	Tyr	Arg	Ser	
			100					105					110			
atg	gaa	gaa	ctc	ctg	cca	atc	ctg	gaa	aaa	gag	ggc	atc	aag	ttc	aac	384
Met	Glu	Glu	Leu	Leu	Pro	Ile	Leu	Glu	Lys	Glu	Gly	Ile	Lys	Phe	Asn	
		115					120					125				
atc	gac	cca	cac	cct	gat	gat	ttc	gtg	gaa	aac	ggc	att	gaa	gca	tgg	432
Ile	Asp	Pro	His	Pro	Asp	Asp	Phe	Val	Glu	Asn	Gly	Ile	Glu	Ala	Trp	
	130					135					140					
cga	gtc	atc	cgc	ggc	ctg	aac	tcc	aag	cag	gtg	ggc	ttt	gtt	tac	gtg	480
Arg	Val	Ile	Arg	Gly	Leu	Asn	Ser	Lys	Gln	Val	Gly	Phe	Val	Tyr	Val	
145				150					155						160	
gca	cct	cac	tca	ttc	cac	atg	ggc	gat	cag	gct	gag	gca	atc	ctg	cca	528
Ala	Pro	His	Ser	Phe	His	Met	Gly	Asp	Gln	Ala	Glu	Ala	Ile	Leu	Pro	
				165					170					175		

gca gta ggc gat cgc ctt ggg gct gtg tac ctg tca gat acc ttc gac 576
 Ala Val Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp
 180 185 190

cac cac aaa tcc cac ggc ctg cgc tac atc act aac cct cca ggc aac 624
 His His Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn
 195 200 205

gca gtg cgc gtg cac cag cac cta aaa atc ggt gat ggc gat gtg aac 672
 Ala Val Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn
 210 215 220

ttt gaa gag atc ttc tca ctg ctg cgc tct acc ggt tac ctt gac cgt 720
 Phe Glu Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg
 225 230 235 240

gaa gat gca ctg ttg gtc tcc aac gtg ttt gca gaa gat gaa gca gca 768
 Glu Asp Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala
 245 250 255

gat gaa gta tcc cgc tac cag ctg gag aaa atc cgc tca ctc atc gaa 816
 Asp Glu Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu
 260 265 270

aac gca tagagttatc tcgaaactac caa 845
 Asn Ala

<210> 622

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 622

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Gln Leu Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys
 20 25 30

Ala Asp Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala
 35 40 45

Gly Val Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro
 50 55 60

Glu Glu Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile
 65 70 75 80

Gln Leu Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser
 85 90 95

Gly Arg Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser
 100 105 110

Met Glu Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn
 115 120 125

Ile Asp Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp

130	135	140
Arg Val Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val		
145	150	155
Ala Pro His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro		
	165	170
Ala Val Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp		
	180	185
His His Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn		
	195	200
Ala Val Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn		
	210	215
Phe Glu Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg		
225	230	235
Glu Asp Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala		
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Asp Glu Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu		
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		270

Asn Ala

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acc cct cat gta gat ttc ggt cct ttc ttc cgc cac ccc aag gca gac	96
Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys Ala Asp	
20 25 30	
gat gat ctc gtg gca gcc ctg aaa aag cgt gcc aag gat gcc gga gtc	144
Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala Gly Val	
35 40 45	
acc att cct gca ctg ttg cca gtg cag cgt att tcc tgg ccg gag gaa	192
Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro Glu Glu	
50 55 60	
acc cag cgt gtt gca gca gta cgc aac atc aag cgc atc atc cag ttg	240
Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile Gln Leu	
65 70 75 80	

gcc gtt gat ctg gaa gta gac acc ctc aac acg gag ttt tct gga cgc 288
Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser Gly Arg
85 90 95

cca gaa cgc tcc gag gat tcc gaa gat gcc ttc tac cgc tcc atg gaa 336
Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser Met Glu
100 105 110

gaa ctc ctg cca atc ctg gaa aaa gag ggc atc aag ttc aac atc gac 384
Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn Ile Asp
115 120 125

cca cac cct gat gat ttc gtg gaa aac ggt att gaa gca tgg cga gtc 432
Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp Arg Val
130 135 140

atc cgc ggt ctg aac tcc aag cag gtg ggc ttt gtt tac gtg gca cct 480
Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val Ala Pro
145 150 155 160

cac tca ttc cac atg ggt gat cag gct gag gca atc ctg cca gca gta 528
His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro Ala Val
165 170 175

ggc gat cgc ctt ggg gct gtg tac ctg tca gat acc ttc gac cac cac 576
Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp His His
180 185 190

aaa tcc cac ggc ctg cgc tac atc act aac cct cca ggc aac gca gtg 624
Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn Ala Val
195 200 205

cgc gtg cac cag cac cta aaa atc ggt gat ggc gat gtg aac ttt gaa 672
Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn Phe Glu
210 215 220

gag atc ttc tca ctg ctg cgc tct acc ggt tac ctt gac cgt gaa gat 720
Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg Glu Asp
225 230 235 240

gca ctg ttg gtc tcc aac gtg ttt gca gaa gat gaa gca gca gat gaa 768
Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala Asp Glu
245 250 255

gta tcc cgc tac cag ctg gag aaa atc cgc tca ctc atc gaa aac gca 816
Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu Asn Ala
260 265 270

tagagttatc tcgaaactac caa 839

<210> 624

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 624

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Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys Ala Asp

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Asp	Asp	Leu	Val	Ala	Ala	Leu	Lys	Lys	Arg	Ala	Lys	Asp	Ala	Gly	Val
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Thr	Ile	Pro	Ala	Leu	Leu	Pro	Val	Gln	Arg	Ile	Ser	Trp	Pro	Glu	Glu
	50					55					60				
Thr	Gln	Arg	Val	Ala	Ala	Val	Arg	Asn	Ile	Lys	Arg	Ile	Ile	Gln	Leu
	65					70					75				80
Ala	Val	Asp	Leu	Glu	Val	Asp	Thr	Leu	Asn	Thr	Glu	Phe	Ser	Gly	Arg
			85						90					95	
Pro	Glu	Arg	Ser	Glu	Asp	Ser	Glu	Asp	Ala	Phe	Tyr	Arg	Ser	Met	Glu
			100					105					110		
Glu	Leu	Leu	Pro	Ile	Leu	Glu	Lys	Glu	Gly	Ile	Lys	Phe	Asn	Ile	Asp
			115				120					125			
Pro	His	Pro	Asp	Asp	Phe	Val	Glu	Asn	Gly	Ile	Glu	Ala	Trp	Arg	Val
	130					135					140				
Ile	Arg	Gly	Leu	Asn	Ser	Lys	Gln	Val	Gly	Phe	Val	Tyr	Val	Ala	Pro
	145					150					155				160
His	Ser	Phe	His	Met	Gly	Asp	Gln	Ala	Glu	Ala	Ile	Leu	Pro	Ala	Val
			165						170					175	
Gly	Asp	Arg	Leu	Gly	Ala	Val	Tyr	Leu	Ser	Asp	Thr	Phe	Asp	His	His
			180					185					190		
Lys	Ser	His	Gly	Leu	Arg	Tyr	Ile	Thr	Asn	Pro	Pro	Gly	Asn	Ala	Val
		195					200					205			
Arg	Val	His	Gln	His	Leu	Lys	Ile	Gly	Asp	Gly	Asp	Val	Asn	Phe	Glu
	210					215					220				
Glu	Ile	Phe	Ser	Leu	Leu	Arg	Ser	Thr	Gly	Tyr	Leu	Asp	Arg	Glu	Asp
	225					230					235			240	
Ala	Leu	Leu	Val	Ser	Asn	Val	Phe	Ala	Glu	Asp	Glu	Ala	Ala	Asp	Glu
			245						250					255	
Val	Ser	Arg	Tyr	Gln	Leu	Glu	Lys	Ile	Arg	Ser	Leu	Ile	Glu	Asn	Ala
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<210> 625

<211> 3075

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3052)

<223> RXN01434

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tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu 250 255 260	883
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val 265 270 275	931
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr 280 285 290	979
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser 295 300 305	1027
ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu 310 315 320 325	1075
cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile 330 335 340	1123
gcc gcc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu 345 350 355	1171
ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn 360 365 370	1219
ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg 375 380 385	1267
aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu 390 395 400 405	1315
tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu 410 415 420	1363
ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu 425 430 435	1411
agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe 440 445 450	1459
atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val 455 460 465	1507
caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe	1555

470	475	480	485	
att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu	490	495	500	1603
cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr	505	510	515	1651
cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu	520	525	530	1699
gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp	535	540	545	1747
cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala	550	555	560	1795
acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala	570	575	580	1843
cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Gly Ile Ala Tyr Glu	585	590	595	1891
gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val	600	605	610	1939
gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val	615	620	625	1987
gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly	630	635	640	2035
gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr	650	655	660	2083
atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys	665	670	675	2131
tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro	680	685	690	2179
gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala	695	700	705	2227
tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val	710	715	720	2275

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc	2323
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro	
730 735 740	
gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc	2371
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr	
745 750 755	
gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct	2419
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro	
760 765 770	
gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg	2467
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met	
775 780 785	
gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc	2515
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala	
790 795 800 805	
ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa	2563
Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln	
810 815 820	
tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct	2611
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro	
825 830 835	
gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat	2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp	
840 845 850	
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Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser	
855 860 865	
acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc	2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser	
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acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc	2803
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser	
890 895 900	
gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc	2851
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala	
905 910 915	
tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat	2899
Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr	
920 925 930	
tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg	2947
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro	
935 940 945	
ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca	2995
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser	
950 955 960 965	

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt 3043
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<212> PRT

<213> Corynebacterium glutamicum

<400> 626

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 35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
 50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
 65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
 85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
 100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
 115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
 130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
 145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175

Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190

Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205

Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220

Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240

Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala

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Ile	Pro	Ile 275	Val	Val	Phe	Phe	Thr 280	Ala	Phe	Gly	Val	Pro 285	Ile	Ala	Asn
Gly	Leu 290	Phe	Ala	Tyr	Gly	Gln 295	Phe	Asp	Ala	Asn	Ala 300	Ala	Asn	Ile	Leu
Gly 305	Trp	Thr	Leu	Ser	Phe 310	Ser	Ala	Phe	Thr	Leu 315	Ile	Pro	Tyr	Ala	Leu 320
Val	Leu	Leu	His 325	Leu	Arg	Val	Phe	Tyr	Ala 330	Arg	Glu	Glu	Val	Trp 335	Thr
Pro	Thr	Phe	Ile 340	Ile	Ala	Gly	Ile	Thr 345	Ala	Thr	Lys	Val	Val 350	Leu	Ser
Leu	Leu	Ala 355	Pro	Leu	Leu	Ser	Ser 360	Ser	Pro	Glu	Arg	Val 365	Val	Val	Leu
Leu	Gly 370	Ala	Ala	Asn	Gly	Phe 375	Ser	Phe	Ile	Thr	Gly 380	Ala	Val	Ile	Gly
Ala 385	Tyr	Leu	Leu	Arg	Asn 390	Lys	Leu	Gly	Leu	Leu 395	Gly	Met	Arg	Ser	Leu 400
Ala	Lys	Thr	Ser 405	Leu	Trp	Ala	Leu	Gly	Ser 410	Ala	Ala	Val	Gly	Ala 415	Ala
Ala	Ala	Trp	Ala 420	Leu	Gly	Trp	Leu	Ile 425	Gln	Ala	Val	Val	Gly	Asp 430	Phe
Leu	Leu	Gly 435	Thr	Leu	Ser	Ser	Val 440	Gly	Tyr	Leu	Leu	Asn 445	Leu	Ala	Val
Leu	Gly 450	Val	Phe	Phe	Ile	Phe 455	Val	Thr	Gly	Ile	Val 460	Leu	Ser	Arg	Ser
Gly 465	Leu	Pro	Glu	Val	Gln 470	Asn	Leu	Gly	Gln	Ala 475	Leu	Thr	Arg	Ile	Pro 480
Gly	Leu	Ser	Arg 485	Phe	Ile	Arg	Pro	Asn	Thr 490	Lys	Ile	Ser	Leu	Asp 495	Val
Gly	Glu	Val	Ser 500	Glu	Gln	Asp	Phe	Ser 505	Thr	Gln	Leu	Val	Ala 510	Pro	Ser
Glu	Phe 515	Ala	Ala	Thr	Pro	Val	Pro 520	Pro	Pro	Met	Ser	Ala 525	Gly	Ile	Val
Arg	Gly 530	Pro	Arg	Leu	Val	Pro 535	Gly	Ala	Pro	Val	Gly 540	Asp	Gly	Arg	Phe
Arg 545	Leu	Leu	Ala	Asp	His 550	Gly	Gly	Val	Gln	Gly 555	Ala	Arg	Phe	Trp	Gln 560
Ala	Arg	Glu	Ile 565	Ala	Thr	Gly	Lys	Glu	Val 570	Ala	Leu	Ile	Phe	Val 575	Asp

Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
 805 810 815
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
 885 890 895

Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
 900 905 910
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
 915 920 925
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
 930 935 940
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
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 Gly Leu Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile
 20 25 30
 ttg acc acc ggc acc ggc tcc gac agc aac gtg acc tcg acc gtg aag 144
 Leu Thr Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys
 35 40 45
 atc tac gca ttc aac gac gcc tca cca cac tcc ctg tcg gaa ggc atc 192
 Ile Tyr Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile
 50 55 60
 gag atc ggc acc gtg gat tat tcc ggc cgc agt ctc agc cac agc atc 240
 Glu Ile Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile
 65 70 75 80
 cgc gat tcc tcc aag ctt ccg ggt cag gtg gaa tcc gtg gtg att ctg 288
 Arg Asp Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu
 85 90 95
 gtc gat gag gtt cgt tcc tca caa acc tca gac acc aat cca cag atg 336
 Val Asp Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met
 100 105 110
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 Gln Ile Ala Glu Val Gln Leu Val Gly Trp
 115 120

gac

389

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 20 25 30
 Leu Thr Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys
 35 40 45
 Ile Tyr Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile
 50 55 60
 Glu Ile Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile
 65 70 75 80
 Arg Asp Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu
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 Gln Ile Ala Glu Val Gln Leu Val Gly Trp
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 Met Ala Lys Lys Lys
 1 5
 ctg ggg act gtc gcc aga ctg tct gaa ctg gat aag tcc ctg cgc aat 163
 Leu Gly Thr Val Ala Arg Leu Ser Glu Leu Asp Lys Ser Leu Arg Asn
 10 15 20
 aga ttg ctg cgg gtt cgt tcc cga ctg ctg ttt att gtt cat tcc gca 211
 Arg Leu Leu Arg Val Arg Ser Arg Leu Leu Phe Ile Val His Ser Ala
 25 30 35
 att ggt gcg ggt gtg gcg tat tgg atc gcc gtg gaa gtg atc aaa cac 259

Ile	Gly	Ala	Gly	Val	Ala	Tyr	Trp	Ile	Ala	Val	Glu	Val	Ile	Lys	His		
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gga	caa	ccg	ttt	ttc	gca	ccg	atg	tcc	gcg	gtg	att	att	ttg	ggt	ctc	307	
Gly	Gln	Pro	Phe	Phe	Ala	Pro	Met	Ser	Ala	Val	Ile	Ile	Leu	Gly	Leu		
	55					60					65						
tcc	gga	gga	gac	cgc	atc	aaa	aga	gcc	acg	gaa	ctc	acc	ctg	ggc	tgt	355	
Ser	Gly	Gly	Asp	Arg	Ile	Lys	Arg	Ala	Thr	Glu	Leu	Thr	Leu	Gly	Cys		
70					75					80					85		
gct	tta	ggc	gtt	ggt	ttg	ggt	gat	tta	ctg	atc	atg	caa	atc	ggc	acg	403	
Ala	Leu	Gly	Val	Gly	Leu	Gly	Asp	Leu	Leu	Ile	Met	Gln	Ile	Gly	Thr		
			90						95					100			
ggc	tat	tgg	cag	ata	ttt	gtg	gta	gtt	gga	tta	gcg	ctg	ctg	gtg	gcc	451	
Gly	Tyr	Trp	Gln	Ile	Phe	Val	Val	Val	Gly	Leu	Ala	Leu	Leu	Val	Ala		
			105					110					115				
tcg	ttt	gtt	tca	ccg	gca	ccg	ttg	gtg	agt	aat	cag	atg	gcc	att	ggt	499	
Ser	Phe	Val	Ser	Pro	Ala	Pro	Leu	Val	Ser	Asn	Gln	Met	Ala	Ile	Gly		
		120					125					130					
ggc	att	ttg	att	gcc	acg	atg	ttc	ccg	cca	ggt	gat	ggt	gga	agc	att	547	
Gly	Ile	Leu	Ile	Ala	Thr	Met	Phe	Pro	Pro	Gly	Asp	Gly	Gly	Ser	Ile		
	135					140					145						
gac	cgt	atg	atc	gac	gcc	ttc	att	ggt	ggt	ggc	gtg	gga	att	ttg	gtc	595	
Asp	Arg	Met	Ile	Asp	Ala	Phe	Ile	Gly	Gly	Gly	Val	Gly	Ile	Leu	Val		
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atc	gca	ctt	ctt	ccc	tca	tct	cct	ctt	gac	gca	ggc	cgg	cat	caa	gtg	643	
Ile	Ala	Leu	Leu	Pro	Ser	Ser	Pro	Leu	Asp	Ala	Gly	Arg	His	Gln	Val		
				170					175					180			
gcc	aac	gtt	ttg	ggg	atc	gca	gct	agt	gtg	ctg	gaa	gac	gtg	gca	gct	691	
Ala	Asn	Val	Leu	Gly	Ile	Ala	Ala	Ser	Val	Leu	Glu	Asp	Val	Ala	Ala		
		185						190					195				
tcc	cta	aaa	gcc	aag	gat	gca	gcc	aaa	ctc	aac	aat	gct	ttg	gaa	gca	739	
Ser	Leu	Lys	Ala	Lys	Asp	Ala	Ala	Lys	Leu	Asn	Asn	Ala	Leu	Glu	Ala		
		200				205						210					
ttg	aga	agg	tcg	cag	gcg	tcg	gtg	aac	aag	ctg	gaa	act	gcg	gca	tct	787	
Leu	Arg	Arg	Ser	Gln	Ala	Ser	Val	Asn	Lys	Leu	Glu	Thr	Ala	Ala	Ser		
	215					220					225						
tca	ggc	aag	gaa	gca	acc	acc	gta	tcg	cca	ttt	tta	tgg	gga	gat	agg	835	
Ser	Gly	Lys	Glu	Ala	Thr	Thr	Val	Ser	Pro	Phe	Leu	Trp	Gly	Asp	Arg		
230					235					240				245			
gcc	cgc	gtg	aga	tcg	ctg	tat	cgc	att	ctg	gcg	cca	gtg	gac	aac	gtc	883	
Ala	Arg	Val	Arg	Ser	Leu	Tyr	Arg	Ile	Leu	Ala	Pro	Val	Asp	Asn	Val		
				250					255					260			
atc	cga	aat	gct	cga	gtc	ctt	gcg	cga	cgg	gca	gtg	gtg	ctg	acc	gaa	931	
Ile	Arg	Asn	Ala	Arg	Val	Leu	Ala	Arg	Arg	Ala	Val	Val	Leu	Thr	Glu		
			265					270					275				
gac	aat	gac	acc	gtc	agt	gat	gaa	caa	atc	cac	gtg	att	gag	gaa	atc	979	
Asp	Asn	Asp	Thr	Val	Ser	Asp	Glu	Gln	Ile	His	Val	Ile	Glu	Glu	Ile		

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Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu His His Lys Glu			
295	300	305	
atc agt gaa gca ctg gaa att cct gag ttg gtt aac cga ctg cgt caa			1075
Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val Asn Arg Leu Arg Gln			
310	315	320	325
ctg ggc agt gaa gtg ggc gag gac atc gcc gaa gat cga gtg cta tcc			1123
Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu Asp Arg Val Leu Ser			
330	335	340	
gca caa gta att ttg gcg caa tcg cga tcc atc att gtg gac ctg ttg			1171
Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile Ile Val Asp Leu Leu			
345	350	355	
cag atc tgc ggc atg tcc agg gaa tct gcg gtg gca gtg ttg gtt ccg			1219
Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val Ala Val Leu Val Pro			
360	365	370	
acc tca gag agt ccg gct tac cct ccg gag ctg tgg gat gac gaa gac			1267
Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp Asp Asp Glu Asp			
375	380	385	
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<211> 389

<212> PRT

<213> Corynebacterium glutamicum

<400> 630

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Lys	Ser	Leu	Arg	Asn	Arg	Leu	Leu	Arg	Val	Arg	Ser	Arg	Leu	Leu	Phe
			20					25					30		

Ile	Val	His	Ser	Ala	Ile	Gly	Ala	Gly	Val	Ala	Tyr	Trp	Ile	Ala	Val
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Glu	Val	Ile	Lys	His	Gly	Gln	Pro	Phe	Phe	Ala	Pro	Met	Ser	Ala	Val
	50					55					60				

Ile	Ile	Leu	Gly	Leu	Ser	Gly	Gly	Asp	Arg	Ile	Lys	Arg	Ala	Thr	Glu
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Leu	Thr	Leu	Gly	Cys	Ala	Leu	Gly	Val	Gly	Leu	Gly	Asp	Leu	Leu	Ile
				85				90						95	

Met	Gln	Ile	Gly	Thr	Gly	Tyr	Trp	Gln	Ile	Phe	Val	Val	Val	Gly	Leu
			100					105					110		

Ala	Leu	Leu	Val	Ala	Ser	Phe	Val	Ser	Pro	Ala	Pro	Leu	Val	Ser	Asn
		115					120					125			

Gln	Met	Ala	Ile	Gly	Gly	Ile	Leu	Ile	Ala	Thr	Met	Phe	Pro	Pro	Gly
	130					135					140				

Asp Gly Gly Ser Ile Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly
145 150 155 160

Val Gly Ile Leu Val Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala
165 170 175

Gly Arg His Gln Val Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu
180 185 190

Glu Asp Val Ala Ala Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn
195 200 205

Asn Ala Leu Glu Ala Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu
210 215 220

Glu Thr Ala Ala Ser Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe
225 230 235 240

Leu Trp Gly Asp Arg Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala
245 250 255

Pro Val Asp Asn Val Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala
260 265 270

Val Val Leu Thr Glu Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His
275 280 285

Val Ile Glu Glu Ile Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr
290 295 300

Glu His His Lys Glu Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val
305 310 315 320

Asn Arg Leu Arg Gln Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu
325 330 335

Asp Arg Val Leu Ser Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile
340 345 350

Ile Val Asp Leu Leu Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val
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Trp Asp Asp Glu Asp
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<223> FRXA01448

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Leu Ile Ala Thr Met Phe Pro Pro Gly Asp Gly Gly Ser Ile Asp Arg
10 15 20

atg atc gac gcc ttc att ggt ggt ggc gtg gga att ttg gtc atc gca 153
Met Ile Asp Ala Phe Ile Gly Gly Gly Val Gly Ile Leu Val Ile Ala
25 30 35

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Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly Arg His Gln Val Ala Asn
40 45 50

gtt ttg ggg atc gca gct agt gtg ctg gaa gac gtg gca gct tcc cta 249
Val Leu Gly Ile Ala Ala Ser Val Leu Glu Asp Val Ala Ala Ser Leu
55 60 65 70

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Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn Ala Leu Glu Ala Leu Arg
75 80 85

agg tcg cag gcg tcg gtg aac aag ctg gaa act gcg gca tct tca ggc 345
Arg Ser Gln Ala Ser Val Asn Lys Leu Glu Thr Ala Ala Ser Ser Gly
90 95 100

aag gaa gca acc acc gta tcg cca ttt tta tgg gga gat agg gcc cgc 393
Lys Glu Ala Thr Thr Val Ser Pro Phe Leu Trp Gly Asp Arg Ala Arg
105 110 115

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Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro Val Asp Asn Val Ile Arg
120 125 130

aat gct cga gtc ctt gcg cga cgg gca gtg gtg ctg acc gaa gac aat 489
Asn Ala Arg Val Leu Ala Arg Arg Ala Val Val Leu Thr Glu Asp Asn
135 140 145 150

gac acc gtc agt gat gaa caa atc cac gtg att gag gaa atc gca gac 537
Asp Thr Val Ser Asp Glu Gln Ile His Val Ile Glu Glu Ile Ala Asp
155 160 165

att gca ctg cga ctg tca gac ctt tat gag cac cac aaa gaa atc agt 585
Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu His His Lys Glu Ile Ser
170 175 180

gaa gca ctg gaa att cct gag ttg gtt aac cga ctg cgt caa ctg ggc 633
Glu Ala Leu Glu Ile Pro Glu Leu Val Asn Arg Leu Arg Gln Leu Gly
185 190 195

agt gaa gtg ggc gag gac atc gcc gaa gat cga gtg cta tcc gca caa 681
Ser Glu Val Gly Glu Asp Ile Ala Glu Asp Arg Val Leu Ser Ala Gln
200 205 210

gta att ttg gcg caa tcg cga tcc atc att gtg gac ctg ttg cag atc 729
Val Ile Leu Ala Gln Ser Arg Ser Ile Ile Val Asp Leu Leu Gln Ile
215 220 225 230

tgc ggc atg tcc agg gaa tct gcg gtg gca gtg ttg gtt ccg acc tca 777

Cys Gly Met Ser Arg Glu Ser Ala Val Ala Val Leu Val Pro Thr Ser
 235 240 245

gag agt ccg gct tac cct ccg gag ctg tgg gat gac gaa gac 819
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<210> 632

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 632

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Gly Ile Leu Val Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly
 35 40 45

Arg His Gln Val Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu Glu
 50 55 60

Asp Val Ala Ala Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn
 65 70 75 80

Ala Leu Glu Ala Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu Glu
 85 90 95

Thr Ala Ala Ser Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe Leu
 100 105 110

Trp Gly Asp Arg Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro
 115 120 125

Val Asp Asn Val Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala Val
 130 135 140

Val Leu Thr Glu Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His Val
 145 150 155 160

Ile Glu Glu Ile Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu
 165 170 175

His His Lys Glu Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val Asn
 180 185 190

Arg Leu Arg Gln Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu Asp
 195 200 205

Arg Val Leu Ser Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile Ile
 210 215 220

Val Asp Leu Leu Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val Ala
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Val Leu Val Pro Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp
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Asp Asp Glu Asp
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(910)
 <223> RXN01459

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 Met Asn Ser Asn Gly
 1 5
 ttt ggt ttc tct ttt ggc aac aac gat gac gac gat gac aaa aac cgc 163
 Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp Asp Lys Asn Arg
 10 15 20
 aac aac gac cca ttc ggc ctt ttc ggt ggc aac ttc gga ttc gga gga 211
 Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn Phe Gly Phe Gly Gly
 25 30 35
 caa ggt ggc gct ggt ggc ccc ggc gga tta ggc gat att tta aac cag 259
 Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Asp Ile Leu Asn Gln
 40 45 50
 ttc ggc cag atg ctg tcc gga atg gga gat tcg atg aac tcc ccc gaa 307
 Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser Met Asn Ser Pro Glu
 55 60 65
 gca gca ggc ccg gtt aat tat gat tta gca gca cgc atc gcc cgc cag 355
 Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala Arg Ile Ala Arg Gln
 70 75 80 85
 cag att ggt cgc gta gcg ccg gtg aag gat tct gag aag gaa gca gtc 403
 Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser Glu Lys Glu Ala Val
 90 95 100
 gaa gag tcc ctt cgc ctt gct gaa ctc tgg ctc gat aac gcc acc cag 451
 Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu Asp Asn Ala Thr Gln
 105 110 115
 ctc ccc act tcc ggg cac cgc gtc gaa gcg tgg aat cca gaa aac tgg 499
 Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp Asn Pro Glu Asn Trp
 120 125 130
 tta gaa aac acc ctg cct gtg tgg aag cgt ctt gtc tcc cct gtt gcg 547
 Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu Val Ser Pro Val Ala
 135 140 145
 gag caa atg aac aaa gcc caa tta gaa aac ctc cct gaa gaa gcc cgc 595

Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu Pro Glu Glu Ala Arg
 150 155 160 165
 gag atg atg ggc ccg atg tct tct ttg atg aac tcc atg tct tcg atg 643
 Glu Met Met Gly Pro Met Ser Ser Leu Met Asn Ser Met Ser Ser Met
 170 175 180
 aac ttc gga gtt caa tta gga aat gcg ctg ggc gac ctc gca aag cag 691
 Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly Asp Leu Ala Lys Gln
 185 190 195
 acc ctc acc ggc tct gac ttc ggt ttg cct atc tcc cca gtc ggc gta 739
 Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile Ser Pro Val Gly Val
 200 205 210
 tct gcc gtc ctg ccc ggc aac atc gcc gaa gca tcc aaa ggc ctc aac 787
 Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala Ser Lys Gly Leu Asn
 215 220 225
 gtg gca ccg caa gaa atg ctc gtt tac atc tgt gcc cgc gaa gcc gcc 835
 Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys Ala Arg Glu Ala Ala
 230 235 240 245
 gcc aac gcc tct tca agc acg tgc cgt ggc ttg tcg agc gcc tcg ttt 883
 Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu Ser Ser Ala Ser Phe
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 cct ccg ttg agg aat acg ccg tcg gcc tagaaatcga cacctcacac 930
 Pro Pro Leu Arg Asn Thr Pro Ser Ala
 265 270
 att 933

<210> 634
 <211> 270
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 634

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 Phe Gly Phe Gly Gly Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly
 35 40 45
 Asp Ile Leu Asn Gln Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser
 50 55 60
 Met Asn Ser Pro Glu Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala
 65 70 75 80
 Arg Ile Ala Arg Gln Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser
 85 90 95
 Glu Lys Glu Ala Val Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu
 100 105 110

Asp Asn Ala Thr Gln Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp
115 120 125

Asn Pro Glu Asn Trp Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu
130 135 140

Val Ser Pro Val Ala Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu
145 150 155 160

Pro Glu Glu Ala Arg Glu Met Met Gly Pro Met Ser Ser Leu Met Asn
165 170 175

Ser Met Ser Ser Met Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly
180 185 190

Asp Leu Ala Lys Gln Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile
195 200 205

Ser Pro Val Gly Val Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala
210 215 220

Ser Lys Gly Leu Asn Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys
225 230 235 240

Ala Arg Glu Ala Ala Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu
245 250 255

Ser Ser Ala Ser Phe Pro Pro Leu Arg Asn Thr Pro Ser Ala
260 265 270

<210> 635

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> FRXA01459

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Met Asn Ser Asn Gly
1 5

ttt ggt ttc tct ttt ggc aac aac gat gac gac gat gac aaa aac cgc 163
Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp Asp Asp Lys Asn Arg
10 15 20

aac aac gac cca ttc ggc ctt ttc ggt ggc aac ttc gga ttc gga gga 211
Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn Phe Gly Phe Gly Gly
25 30 35

caa ggt ggc gct ggt ggc ccc ggc gga tta ggc gat att tta aac cag 259
Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Asp Ile Leu Asn Gln
40 45 50

ttc ggc cag atg ctg tcc gga atg gga gat tcg atg aac tcc ccc gaa 307

Phe	Gly	Gln	Met	Leu	Ser	Gly	Met	Gly	Asp	Ser	Met	Asn	Ser	Pro	Glu		
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Ala	Ala	Gly	Pro	Val	Asn	Tyr	Asp	Leu	Ala	Ala	Arg	Ile	Ala	Arg	Gln		
70					75				80						85		
cag	att	ggt	cgc	gta	gcg	ccg	gtg	aag	gat	tct	gag	aag	gaa	gca	gtc	403	
Gln	Ile	Gly	Arg	Val	Ala	Pro	Val	Lys	Asp	Ser	Glu	Lys	Glu	Ala	Val		
				90					95					100			
gaa	gag	tcc	ctt	cgc	ctt	gct	gaa	ctc	tgg	ctc	gat	aac	gcc	acc	cag	451	
Glu	Glu	Ser	Leu	Arg	Leu	Ala	Glu	Leu	Trp	Leu	Asp	Asn	Ala	Thr	Gln		
			105					110					115				
ctc	ccc	act	tcc	ggg	cac	cgc	gtc	gaa	gcg	tgg	aat	cca	gaa	aac	tgg	499	
Leu	Pro	Thr	Ser	Gly	His	Arg	Val	Glu	Ala	Trp	Asn	Pro	Glu	Asn	Trp		
		120					125					130					
tta	gaa	aac	acc	ctg	cct	gtg	tgg	aag	cgt	ctt	gtc	tcc	cct	gtt	gcg	547	
Leu	Glu	Asn	Thr	Leu	Pro	Val	Trp	Lys	Arg	Leu	Val	Ser	Pro	Val	Ala		
	135					140					145						
gag	caa	atg	aac	aaa	gcc	caa	tta	gaa	aac	ctc	cct	gaa	gaa	gcc	cgc	595	
Glu	Gln	Met	Asn	Lys	Ala	Gln	Leu	Glu	Asn	Leu	Pro	Glu	Glu	Ala	Arg		
150					155					160					165		
gag	atg	atg	ggc	ccg	atg	tct	tct	ttg	atg	aac	tcc	atg	tct	tcg	atg	643	
Glu	Met	Met	Gly	Pro	Met	Ser	Ser	Leu	Met	Asn	Ser	Met	Ser	Ser	Met		
			170						175					180			
aac	ttc	gga	gtt	caa	tta	gga	aat	gcg	ctg	ggc	gac	ctc	gca	aag	cag	691	
Asn	Phe	Gly	Val	Gln	Leu	Gly	Asn	Ala	Leu	Gly	Asp	Leu	Ala	Lys	Gln		
			185					190					195				
acc	ctc	acc	ggc	tct	gac	ttc	ggt	ttg	cct	atc	tcc	cca	gtc	ggc	gta	739	
Thr	Leu	Thr	Gly	Ser	Asp	Phe	Gly	Leu	Pro	Ile	Ser	Pro	Val	Gly	Val		
		200					205					210					
tct	gcc	gtc	ctg	ccc	ggc	aac	atc	gcc	gaa	gca	tcc	aaa	ggc	ctc	aac	787	
Ser	Ala	Val	Leu	Pro	Gly	Asn	Ile	Ala	Glu	Ala	Ser	Lys	Gly	Leu	Asn		
	215					220					225						
gtg	gca	ccg	caa	gaa	atg	ctc	gtt	tac	atc	tgt	gcc	cgc	gaa	gcc	gcc	835	
Val	Ala	Pro	Gln	Glu	Met	Leu	Val	Tyr	Ile	Cys	Ala	Arg	Glu	Ala	Ala		
230					235					240					245		
gcc	aac	gcc	tct	tca	agc	acg	tgc	cgt	ggc	ttg	tcg	agc	gcc	tcg	ttt	883	
Ala	Asn	Ala	Ser	Ser	Ser	Thr	Cys	Arg	Gly	Leu	Ser	Ser	Ala	Ser	Phe		
			250					255						260			
cct	ccg	ttg	agg	aat	acg	ccg	tcg	gcc	tagaaatcga	cacctcacac						930	
Pro	Pro	Leu	Arg	Asn	Thr	Pro	Ser	Ala									
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att																	933

<210> 636

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 636

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Phe Gly Phe Gly Gly Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly
35 40 45
Asp Ile Leu Asn Gln Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser
50 55 60
Met Asn Ser Pro Glu Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala
65 70 75 80
Arg Ile Ala Arg Gln Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser
85 90 95
Glu Lys Glu Ala Val Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu
100 105 110
Asp Asn Ala Thr Gln Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp
115 120 125
Asn Pro Glu Asn Trp Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu
130 135 140
Val Ser Pro Val Ala Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu
145 150 155 160
Pro Glu Glu Ala Arg Glu Met Met Gly Pro Met Ser Ser Leu Met Asn
165 170 175
Ser Met Ser Ser Met Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly
180 185 190
Asp Leu Ala Lys Gln Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile
195 200 205
Ser Pro Val Gly Val Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala
210 215 220
Ser Lys Gly Leu Asn Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys
225 230 235 240
Ala Arg Glu Ala Ala Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu
245 250 255
Ser Ser Ala Ser Phe Pro Pro Leu Arg Asn Thr Pro Ser Ala
260 265 270

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<211> 417

<212> DNA

<213> Corynebacterium glutamicum

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 <223> RXN01460

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                                   Val Pro Trp Leu Val
                                   1 5
gag cgc ctc gtt tcc tcc gtt gag gaa tac gcc gtc ggc cta gaa atc 163
Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala Val Gly Leu Glu Ile
                                   10 15 20
gac acc tca cac att caa gag gcc atg ggc aac ttc caa atg gac aac 211
Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn Phe Gln Met Asp Asn
                                   25 30 35
cca gat cct gaa cgc ctc cag gaa atg atg aac gaa ctc caa ggt atg 259
Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn Glu Leu Gln Gly Met
                                   40 45 50
gac ctg tcc cca cgc atc gga tcc cgc aac gcc aac gca gta tcc cgc 307
Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala Asn Ala Val Ser Arg
                                   55 60 65
ctg gaa act ctc ctc gca ctc gtc gaa ggc tgg gtc gac atc gta gtt 355
Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp Val Asp Ile Val Val
                                   70 75 80 85
acc caa gcc ctg agc gaa cgc att cca tca ccg acg cca tgaacgaagc 404
Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro Thr Pro
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ctggaagcgc cgc 417

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<210> 638
 <211> 98
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 638

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Val Gly Leu Glu Ile Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn
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Phe Gln Met Asp Asn Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn
  35 40 45
Glu Leu Gln Gly Met Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala
  50 55 60
Asn Ala Val Ser Arg Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp
  65 70 75 80
Val Asp Ile Val Val Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro
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Thr Pro

<210> 639
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 Val Pro Trp Leu Val
 1 5
 gag cgc ctc gtt tcc tcc gtt gag gaa tac gcc gtc ggc cta gaa atc 163
 Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala Val Gly Leu Glu Ile
 10 15 20
 gac acc tca cac att caa gag gcc atg ggc aac ttc caa atg gac aac 211
 Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn Phe Gln Met Asp Asn
 25 30 35
 cca gat cct gaa cgc ctc cag gaa atg atg aac gaa ctc caa ggt atg 259
 Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn Glu Leu Gln Gly Met
 40 45 50
 gac ctg tcc cca cgc atc gga tcc cgc aac gcc aac gca gta tcc cgc 307
 Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala Asn Ala Val Ser Arg
 55 60 65
 ctg gaa act ctc ctc gca ctc gtc gaa ggc tgg gtc gac atc gta gtt 355
 Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp Val Asp Ile Val Val
 70 75 80 85
 acc caa gcc ctg agc gaa cgc att cca tca ccg acg cca tgaacgaagc 404
 Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro Thr Pro
 90 95
 ctggaagcgc cgc 417

<210> 640
 <211> 98
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 640
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 Val Gly Leu Glu Ile Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn
 20 25 30

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 Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu Pro Leu Gly Met Glu
 120 125 130

aac tct gaa cta tgg ggt tct gcg ggc cac gag gcg cgc agc aca gtg 547
 Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu Ala Arg Ser Thr Val
 135 140 145

gct gat ctg acc aag ttc ggc caa gag ctc acc gca cca act ctg atc 595
 Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr Ala Pro Thr Leu Ile
 150 155 160 165

tca cca gaa acc ctt gca gag gct ttc cag gtg caa ttc ccg gaa ctg 643
 Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val Gln Phe Pro Glu Leu
 170 175 180

att ggc acc gtc ccc ggt tat ggc atg cag aag ccg tgt ccg tgg gga 691
 Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys Pro Cys Pro Trp Gly
 185 190 195

ttg ggc ttt gaa att aag gga cag aag tcg ccg cac tgg aca ggt gac 739
 Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro His Trp Thr Gly Asp
 200 205 210

ttg atg ccg gag aac act gct gga cac ttt gga cag tcg gga aca ttc 787
 Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly Gln Ser Gly Thr Phe
 215 220 225

ttt tgg act gtt cca ggc tca ggt caa gtc ggg gtt gtt ttg act gac 835
 Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly Val Val Leu Thr Asp
 230 235 240 245

cga aat ttc ggt cct tgg gct aaa ccg ttg tgg act gcc ttc aat gac 883
 Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp Thr Ala Phe Asn Asp
 250 255 260

gaa gtc tgg gcc gag tta aat tca taaacttttg ccgtaattac ggt 930
 Glu Val Trp Ala Glu Leu Asn Ser
 265

<210> 642

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 642

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Ala Ser Val Ile Ser Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp
 20 25 30

Arg Val Phe Glu Leu Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly
 35 40 45

Phe Leu Val Ala Ile Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met
 50 55 60

Gly Pro Glu Gly Ser Thr Val Arg His Leu Leu Ser His Ala Ser Gly
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<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA01471
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Met Gln Ser Phe Lys
1 5

acg ctt gaa tct tgg cct gtc gac aat gtt tcg gcc agt gtc atc tcc 163
Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser Ala Ser Val Ile Ser
10 15 20

gac ggc gcc gtg cac ttt tac ggc gac gtc gat cgt gtt ttt gaa ctc 211
Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp Arg Val Phe Glu Leu

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25	30	35	
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Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly Phe Leu Val Ala Ile			
40	45	50	
gaa gaa ggt gtt ttt gag ctc gat tca ccg atg ggt cct gaa gga tcc			307
Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met Gly Pro Glu Gly Ser			
55	60	65	
aca gtg agg cat ctg ctc tca cat gct tcc ggc gtg gca ttc gat aag			355
Thr Val Arg His Leu Leu Ser His Ala Ser Gly Val Ala Phe Asp Lys			
70	75	80	85
ccg gta gcg gaa aag gga gtg ggg gag cgc cgc att tac tcc tct gct			403
Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg Ile Tyr Ser Ser Ala			
90	95	100	
ggc atg gac atc ttg gcg gat gct gtt gcc gct gaa gct gaa atg ccg			451
Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala Glu Ala Glu Met Pro			
105	110	115	
ttt gca gag tat ctc cgc gag gct gtg ttc gag cct ttg gga atg gag			499
Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu Pro Leu Gly Met Glu			
120	125	130	
aac tct gaa cta tgg ggt tct gcg ggc cac gag gcg cgc agc aca gtg			547
Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu Ala Arg Ser Thr Val			
135	140	145	
gct gat ctg acc aag ttc ggc caa gag ctc acc gca cca act ctg atc			595
Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr Ala Pro Thr Leu Ile			
150	155	160	165
tca cca gaa acc ctt gca gag gct ttc cag gtg caa ttc ccg gaa ctg			643
Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val Gln Phe Pro Glu Leu			
170	175	180	
att ggc acc gtc ccc ggt tat ggc atg cag aag ccg tgt ccg tgg gga			691
Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys Pro Cys Pro Trp Gly			
185	190	195	
ttg ggc ttt gaa att aag gga cag aag tcg ccg cac tgg aca ggt gac			739
Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro His Trp Thr Gly Asp			
200	205	210	
ttg atg ccg gag aac act gct gga cac ttt gga cag tcg gga aca ttc			787
Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly Gln Ser Gly Thr Phe			
215	220	225	
ttt tgg act gtt cca ggc tca ggt caa gtc ggg gtt gtt ttg act gac			835
Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly Val Val Leu Thr Asp			
230	235	240	245
cga aat ttc ggt cct tgg gct aaa ccg ttg tgg act gcc ttc aat gac			883
Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp Thr Ala Phe Asn Asp			
250	255	260	
gaa gtc tgg gcc gag tta aat tca taaacttttg ccgtaattac ggt			930
Glu Val Trp Ala Glu Leu Asn Ser			
265			

<210> 644

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 644

Met Gln Ser Phe Lys Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser
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Ala Ser Val Ile Ser Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp
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Arg Val Phe Glu Leu Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly
35 40 45

Phe Leu Val Ala Ile Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met
50 55 60

Gly Pro Glu Gly Ser Thr Val Arg His Leu Leu Ser His Ala Ser Gly
65 70 75 80

Val Ala Phe Asp Lys Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg
85 90 95

Ile Tyr Ser Ser Ala Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala
100 105 110

Glu Ala Glu Met Pro Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu
115 120 125

Pro Leu Gly Met Glu Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu
130 135 140

Ala Arg Ser Thr Val Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr
145 150 155 160

Ala Pro Thr Leu Ile Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val
165 170 175

Gln Phe Pro Glu Leu Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys
180 185 190

Pro Cys Pro Trp Gly Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro
195 200 205

His Trp Thr Gly Asp Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly
210 215 220

Gln Ser Gly Thr Phe Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly
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<210> 645

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<223> RXN01479
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<213> Corynebacterium glutamicum
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Ala Ile Asn Ser Pro Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys
      35             40             45

Ala Ile Ala Asn Lys Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys
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Asn Leu Arg Thr Ala Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> FRXA01479

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Val Ile Gly Ala Ala
1 5
gca ggc tac gtg ctt ggc aca aag gcc ggc cgc aag cgt tac cac cag 163
Ala Gly Tyr Val Leu Gly Thr Lys Ala Gly Arg Lys Arg Tyr His Gln
10 15 20
atc aaa aag gga tat gag gca gcg att aac tcc cct gcc acc aaa tct 211
Ile Lys Lys Gly Tyr Glu Ala Ala Ile Asn Ser Pro Ala Thr Lys Ser
25 30 35
gca gta aac gcc gcc cgc aaa gcc att gcc aac aag ctg gat ccg cag 259
Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn Lys Leu Asp Pro Gln
40 45 50
ccc cgc atg aag gaa gta aaa aac ctg cgg act gcg gac ggg cat gaa 307
Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr Ala Asp Gly His Glu
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gtc ctc gag caa gac cag gac taaattaccc tctaaacgcc cgg 351
Val Leu Glu Gln Asp Gln Asp
70 75

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<213> Corynebacterium glutamicum

<400> 648
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20 25 30
Pro Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn
35 40 45
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										Val	Leu	Gly	Thr	Ala	
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Gln	Tyr	Asp	Gly	Val	Pro	Ser	Arg	Gln	Phe	Ala	Ala	Arg	Leu	Arg	His
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Gly	Gly	Lys	Leu	Pro	Gly	Asp	Arg	Phe	Thr	Glu	Ala	Glu	Val	Ala	Arg
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Glu	Tyr	Leu	Ile	Lys	Glu	Gly	Val	Asp	Pro	Asp	Leu	Ile	Phe	Val	Ser
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Ala	Val	Gly	Asn	Asp	Thr	Val	Ser	Ser	Tyr	Glu	Ala	Leu	Asp	Pro	Glu
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aag ctt ggt cgg gtg ctg att gtt act gat ccg aac cat tcg tat cgg															403
Lys	Leu	Gly	Arg	Val	Leu	Ile	Val	Thr	Asp	Pro	Asn	His	Ser	Tyr	Arg
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gcg gtg cgc atc gcg cga cgc atg ggc ttt gac gcg aaa cct tcc ccg															451
Ala	Val	Arg	Ile	Ala	Arg	Arg	Met	Gly	Phe	Asp	Ala	Lys	Pro	Ser	Pro
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aca acc tat agt ccc gcg aag ttt ccg tcg ata gtt tat ttt ctg acc															499
Thr	Thr	Tyr	Ser	Pro	Ala	Lys	Phe	Pro	Ser	Ile	Val	Tyr	Phe	Leu	Thr
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Leu	Ser	His	Glu	Trp	Gly	Gly	Val	Val	Val	Gln	Asp	Val	Ser	Arg	Leu
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Leu	Gly	Glu	Arg	Val	Pro	Asp	Lys	Val	Lys	His	Leu	Cys	Ala	Gln	Ser
	150				155					160				165	
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Lys	Val	Cys	Cys	Ala	Leu	Arg	Gly	Val	His	Ala	Met	Ser	Asn	Phe	Gly
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Gly

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<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 650
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His Val Tyr Thr Val Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu
35 40 45
Ala Glu Val Ala Arg Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp
50 55 60
Leu Ile Phe Val Ser Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu
65 70 75 80
Ala Leu Asp Pro Glu Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro
85 90 95
Asn His Ser Tyr Arg Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp
100 105 110
Ala Lys Pro Ser Pro Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile
115 120 125
Val Tyr Phe Leu Thr Leu Ser His Glu Trp Gly Gly Val Val Val Gln
130 135 140
Asp Val Ser Arg Leu Leu Gly Glu Arg Val Pro Asp Lys Val Lys His
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<210> 651
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(646)
<223> FRXA01484

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Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala Ala Arg Leu Arg His																
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gcc gcg aag ctg tgg cgt ctt cat gaa atc cag cat gta tat act gtc	211															
Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln His Val Tyr Thr Val																
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ggc gga aaa ctt cct ggc gat cgt ttc acc gaa gca gaa gtc gcg cgg	259															
Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu Ala Glu Val Ala Arg																
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gag tat ttg atc aaa gag ggc gtg gat ccg gat ctg att ttt gtc tct	307															
Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp Leu Ile Phe Val Ser																
	55					60					65					
gca gtt ggc aat gac act gtc tcc tcc tat gag gcg ctt gat ccg gaa	355															
Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu Ala Leu Asp Pro Glu																
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aag ctt ggt cgg gtg ctg att gtt act gat ccg aac cat tcg tat cgg	403															
Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro Asn His Ser Tyr Arg																
	90							95						100		
gcg gtg cgc atc gcg cga cgc atg ggc ttt gac gcg aaa cct tcc ccg	451															
Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp Ala Lys Pro Ser Pro																
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aca acc tat agt ccc gcg aag ttt ccg tcg ata gtt tat ttt ctg acc	499															
Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile Val Tyr Phe Leu Thr																
	120						125					130				
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Leu Ser His Glu Trp Gly Gly Val Val Val Gln Asp Val Ser Arg Leu																
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Leu Gly Glu Arg Val Pro Asp Lys Val Lys His Leu Cys Ala Gln Ser																
	150				155				160							165
aag gtc tgc tgc gcc ctt cgc ggc gtg cac gcc atg agc aac ttc gga	643															
Lys Val Cys Cys Ala Leu Arg Gly Val His Ala Met Ser Asn Phe Gly																
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Gly																

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<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 652

Val Leu Gly Thr Ala Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala
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Ala Arg Leu Arg His Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln
 20 25 30

His Val Tyr Thr Val Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu
 35 40 45

Ala Glu Val Ala Arg Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp
 50 55 60

Leu Ile Phe Val Ser Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu
 65 70 75 80

Ala Leu Asp Pro Glu Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro
 85 90 95

Asn His Ser Tyr Arg Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp
 100 105 110

Ala Lys Pro Ser Pro Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile
 115 120 125

Val Tyr Phe Leu Thr Leu Ser His Glu Trp Gly Gly Val Val Val Gln
 130 135 140

Asp Val Ser Arg Leu Leu Gly Glu Arg Val Pro Asp Lys Val Lys His
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Leu Cys Ala Gln Ser Lys Val Cys Cys Ala Leu Arg Gly Val His Ala
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Met Ser Asn Phe Gly Gly
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<210> 653
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 <212> DNA
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<220>
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 <222> (101)..(2152)
 <223> RXN01485

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 Met Asn Phe Ser Leu
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gtg cat ctt cgg gaa aac gtc cgc cgt gta tgc gtc act gtg gca att 163
 Val His Leu Arg Glu Asn Val Arg Arg Val Ser Val Thr Val Ala Ile
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gga gct ggc gcg ctc ctt atc agt gga cca ttt ttt act gct cac act 211
 Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe Phe Thr Ala His Thr
 25 30 35

gca gaa gcc aca gaa aca tat gtc ttg gct gaa tca cca gaa ttt tac 259
 Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu Ser Pro Glu Phe Tyr

40	45	50	
caa gac aat gtc act gac tac acc ggc cag att tcc tcc gat atc Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile Ser Ser Ser Asp Ile 55 60 65			307
acc aac att cag gct gcc atc gat gat gta aag gca tct gaa caa aag Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys Ala Ser Glu Gln Lys 70 75 80 85			355
gtt att ttc gtt gtt ttc cta agc tct ttc gac gga gtt gac cct gaa Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp Gly Val Asp Pro Glu 90 95 100			403
acg tgg acg cag caa gca ctc caa gcc aac ggc ggc gga aac gtc ttg Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly Gly Gly Asn Val Leu 105 110 115			451
att tat gca ctc gct ccc gag gaa cgg cag tac ggc atc caa ggt ggt Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr Gly Ile Gln Gly Gly 120 125 130			499
act caa tgg acc gac gct gaa ctc gac gcc gcc aac aac gct gct ttc Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala Asn Asn Ala Ala Phe 135 140 145			547
cag gca ctt tcc caa gaa gat tgg gca ggc tct gca cta gcg ctg gca Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser Ala Leu Ala Leu Ala 150 155 160 165			595
gaa tca gtt ggt tct agt tct tcc agc tct tcc ggc tcc tcc agc tct Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser 170 175 180			643
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acc aac cgc ctc atg cag ctt ccc atg gaa act ctc gaa cac ctt gcc Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr Leu Glu His Leu Ala 230 235 240 245			835
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gag ctc gct atc gct acc tcc gag ttc gga cca gag cgc acc cgc agc Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro Glu Arg Thr Arg Ser 265 270 275			931
ttc aac cgc gcc atg aac cac tcc acc ggc acc ctg caa aaa gcc ttt Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr Leu Gln Lys Ala Phe 280 285 290			979

gag att cag cag cgc ctc aac gat tct atc cca gaa tcc gaa gcc gaa	1027
Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro Glu Ser Glu Ala Glu	
295 300 305	
cgt caa tcc atg ctg gta gaa atc att tca tcc tgt ggc caa gcc gac	1075
Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser Cys Gly Gln Ala Asp	
310 315 320 325	
gat gcc ctc gac gcc gaa gcc caa aac ttt gcc gat atg cgc aac ctg	1123
Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala Asp Met Arg Asn Leu	
330 335 340	
ctg atc aac gcg ggc agc aaa ttg gat gct ctc acc caa aaa tcc gtc	1171
Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu Thr Gln Lys Ser Val	
345 350 355	
gac ctg cgc acc cgc ctc ccc aag gcc caa gaa aca ctc gct ggc ctg	1219
Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu Thr Leu Ala Gly Leu	
360 365 370	
cgc act cgc tac tca gca gag gtc ctt gaa agc atc gac gac aac gtc	1267
Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser Ile Asp Asp Asn Val	
375 380 385	
gac ctc gcc agc gct tcg ctc gac gaa gca gaa gaa gtc ctg cca cag	1315
Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu Glu Val Leu Pro Gln	
390 395 400 405	
gcg tac gag ata gag tcc atg ccc gca ggc gag cag ggc ggg ctt atc	1363
Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu Gln Gly Gly Leu Ile	
410 415 420	
gac gcg atc cgt cac atc gag cac gcc atc act acc gca gac aaa ctc	1411
Asp Ala Ile Arg His Ile Glu His Ala Ile Thr Thr Ala Asp Lys Leu	
425 430 435	
ctc gcg ggc gtc gag cat gcc gat gaa aac atc tcc aca gcc aaa gca	1459
Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile Ser Thr Ala Lys Ala	
440 445 450	
aac gtt gcc gat ctg atc caa gaa atc tca gac gaa atc aac gaa gcc	1507
Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp Glu Ile Asn Glu Ala	
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Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly Ala Arg Ala Asp Trp	
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Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser Ala Ala Leu Ile Thr	
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Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly Thr Tyr Thr Glu Leu	
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gtc gat gtc gac tcc gcc ctc gac act caa ctt gac aca ctt cgc gcc	1699
Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu Asp Thr Leu Arg Ala	
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acc gca gct gat caa gcc cgc cag cta cgc gta ttc gac caa cag ctg 1747
 Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val Phe Asp Gln Gln Leu
 535 540 545

caa tct gca aga agc caa atc caa aag gcc gaa gac ctc atc tcc acc 1795
 Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu Asp Leu Ile Ser Thr
 550 555 560 565

cgc ggt cgc atc gta aaa tcc gaa gcc cgc acc cac ctg gcc aac gca 1843
 Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr His Leu Ala Asn Ala
 570 575 580

caa aag ctg tac gcc atg gca caa caa aac cgc acc cgc gac acc cgt 1891
 Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg Thr Arg Asp Thr Arg
 585 590 595

gca gga att gat tac gga cgt caa gca gca gtc gca gcc caa cgc gcc 1939
 Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val Ala Ala Gln Arg Ala
 600 605 610

agc aag tca gca caa aac gac atc acc acc tac aac aat cgc cac aat 1987
 Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr Asn Asn Arg His Asn
 615 620 625

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 Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr Gly Met Val Ile Asn
 630 635 640 645

tcg att ctc aac agc ggc cgc ggt ggc ggt ttc tgt gga ggc gga ggc 2083
 Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe Cys Gly Gly Gly Gly
 650 655 660

ttt ggt gga ggc ggt ggc ggc ttc agc ggt ggt ggc ggt ggc gga gga 2131
 Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly Gly Gly
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ggg ttc cgc gga ggc cgc ttc tagcctgaaa cgagcaaaac caa 2175
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<210> 654

<211> 684

<212> PRT

<213> Corynebacterium glutamicum

<400> 654

Met Asn Phe Ser Leu Val His Leu Arg Glu Asn Val Arg Arg Val Ser
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 20 25 30

Phe Thr Ala His Thr Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu
 35 40 45

Ser Pro Glu Phe Tyr Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile
 50 55 60

Ser Ser Ser Asp Ile Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys
 65 70 75 80

Ala	Ser	Glu	Gln	Lys 85	Val	Ile	Phe	Val	Val 90	Phe	Leu	Ser	Ser	Phe 95	Asp
Gly	Val	Asp	Pro 100	Glu	Thr	Trp	Thr	Gln 105	Gln	Ala	Leu	Gln	Ala 110	Asn	Gly
Gly	Gly	Asn 115	Val	Leu	Ile	Tyr	Ala 120	Leu	Ala	Pro	Glu	Glu 125	Arg	Gln	Tyr
Gly	Ile 130	Gln	Gly	Gly	Thr	Gln 135	Trp	Thr	Asp	Ala	Glu 140	Leu	Asp	Ala	Ala
Asn 145	Asn	Ala	Ala	Phe	Gln 150	Ala	Leu	Ser	Gln	Glu 155	Asp	Trp	Ala	Gly	Ser 160
Ala	Leu	Ala	Leu	Ala 165	Glu	Ser	Val	Gly	Ser 170	Ser	Ser	Ser	Ser	Ser 175	Ser
Gly	Ser	Ser	Ser 180	Ser	Ser	Asp	Phe	Ser 185	Gly	Ala	Trp	Leu	Ala 190	Ala	Ala
Gly	Val	Gly 195	Thr	Val	Ala	Ala	Gly 200	Gly	Gly	Ile	Trp	Ala 205	Tyr	Ser	Arg
Ser 210	Arg	Lys	Lys	Lys	Thr	Ser 215	Ala	Ala	Thr	Leu	Glu 220	Asp	Ala	Arg	Glu
Ile 225	Asp	Pro	Arg	Asp	Thr 230	Asn	Arg	Leu	Met	Gln 235	Leu	Pro	Met	Glu	Thr 240
Leu	Glu	His	Leu	Ala 245	Gln	Glu	Glu	Leu	Thr 250	Ser	Thr	Asp	Asp	Ser 255	Ile
Arg	Arg	Gly	Lys 260	Glu	Glu	Leu	Ala	Ile 265	Ala	Thr	Ser	Glu	Phe 270	Gly	Pro
Glu	Arg	Thr 275	Arg	Ser	Phe	Asn	Arg 280	Ala	Met	Asn	His	Ser 285	Thr	Gly	Thr
Leu 290	Gln	Lys	Ala	Phe	Glu	Ile 295	Gln	Gln	Arg	Leu	Asn 300	Asp	Ser	Ile	Pro
Glu 305	Ser	Glu	Ala	Glu	Arg 310	Gln	Ser	Met	Leu	Val 315	Glu	Ile	Ile	Ser	Ser 320
Cys	Gly	Gln	Ala	Asp 325	Asp	Ala	Leu	Asp	Ala 330	Glu	Ala	Gln	Asn	Phe 335	Ala
Asp	Met	Arg	Asn 340	Leu	Leu	Ile	Asn	Ala 345	Gly	Ser	Lys	Leu	Asp 350	Ala	Leu
Thr	Gln	Lys 355	Ser	Val	Asp	Leu	Arg 360	Thr	Arg	Leu	Pro	Lys 365	Ala	Gln	Glu
Thr 370	Leu	Ala	Gly	Leu	Arg	Thr 375	Arg	Tyr	Ser	Ala	Glu 380	Val	Leu	Glu	Ser
Ile 385	Asp	Asp	Asn	Val	Asp 390	Leu	Ala	Ser	Ala	Ser 395	Leu	Asp	Glu	Ala	Glu 400

Glu Val Leu Pro Gln Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu
405 410 415

Gln Gly Gly Leu Ile Asp Ala Ile Arg His Ile Glu His Ala Ile Thr
420 425 430

Thr Ala Asp Lys Leu Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile
435 440 445

Ser Thr Ala Lys Ala Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp
450 455 460

Glu Ile Asn Glu Ala Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly
465 470 475 480

Ala Arg Ala Asp Trp Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser
485 490 495

Ala Ala Leu Ile Thr Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly
500 505 510

Thr Tyr Thr Glu Leu Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu
515 520 525

Asp Thr Leu Arg Ala Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val
530 535 540

Phe Asp Gln Gln Leu Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu
545 550 555 560

Asp Leu Ile Ser Thr Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr
565 570 575

His Leu Ala Asn Ala Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg
580 585 590

Thr Arg Asp Thr Arg Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val
595 600 605

Ala Ala Gln Arg Ala Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr
610 615 620

Asn Asn Arg His Asn Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr
625 630 635 640

Gly Met Val Ile Asn Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe
645 650 655

Cys Gly Gly Gly Gly Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly
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Gly Gly Gly Gly Gly Gly Phe Arg Gly Gly Arg Phe
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<210> 655

<211> 2175

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2152)

<223> FRXA01485

<400> 655

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                                         Met Asn Phe Ser Leu
                                         1 5
gtg cat ctt cgg gaa aac gtc cgc cgt gta tcg gtc act gtg gca att 163
Val His Leu Arg Glu Asn Val Arg Arg Val Ser Val Thr Val Ala Ile
                        10 15 20
gga gct ggc gcg ctc ctt atc agt gga cca ttt ttt act gct cac act 211
Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe Phe Thr Ala His Thr
                        25 30 35
gca gaa gcc aca gaa aca tat gtc ttg gct gaa tca cca gaa ttt tac 259
Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu Ser Pro Glu Phe Tyr
                        40 45 50
caa gac aat gtc act gac tac acc ggc cag att tcc tcg tcc gat atc 307
Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile Ser Ser Ser Asp Ile
                        55 60 65
acc aac att cag gct gcc atc gat gat gta aag gca tct gaa caa aag 355
Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys Ala Ser Glu Gln Lys
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Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp Gly Val Asp Pro Glu
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acg tgg acg cag caa gca ctc caa gcc aac ggc ggc gga aac gtc ttg 451
Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly Gly Gly Asn Val Leu
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att tat gca ctc gct ccc gag gaa cgg cag tac ggc atc caa ggt ggt 499
Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr Gly Ile Gln Gly Gly
                        120 125 130
act caa tgg acc gac gct gaa ctc gac gcc gcc aac aac gct gct ttc 547
Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala Asn Asn Ala Ala Phe
                        135 140 145
cag gca ctt tcc caa gaa gat tgg gca ggc tct gca cta gcg ctg gca 595
Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser Ala Leu Ala Leu Ala
                        150 155 160 165
gaa tca gtt ggt tct agt tct tcc agc tct tcg ggc tcg tcc agc tct 643
Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser
                        170 175 180
tcc gat ttt tcc ggc gct tgg ttg gct gct gcg ggc gtt ggc aca gtg 691
Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala Gly Val Gly Thr Val
                        185 190 195
gcc gct ggt ggc gga att tgg gcc tat tcc cgc agc cgc aag aag aaa 739
Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg Ser Arg Lys Lys Lys

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200	205	210	
aca agt gct gca acc ttg gaa gat gca cgc gaa atc gac ccg cgc gat Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu Ile Asp Pro Arg Asp 215 220 225			787
acc aac cgc ctc atg cag ctt ccc atg gaa act ctc gaa cac ctt gcc Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr Leu Glu His Leu Ala 230 235 240 245			835
caa gaa gag ctc acc tcc act gat gac tcc atc cgt cgc gga aaa gaa Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile Arg Arg Gly Lys Glu 250 255 260			883
gag ctc gct atc gct acc tcc gag ttc gga cca gag cgc acc cgc agc Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro Glu Arg Thr Arg Ser 265 270 275			931
ttc aac cgc gcc atg aac cac tcc acc ggc acc ctg caa aaa gcc ttt Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr Leu Gln Lys Ala Phe 280 285 290			979
gag att cag cag cgc ctc aac gat tct atc cca gaa tcc gaa gcc gaa Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro Glu Ser Glu Ala Glu 295 300 305			1027
cgt caa tcc atg ctg gta gaa atc att tca tcc tgt ggc caa gcc gac Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser Cys Gly Gln Ala Asp 310 315 320 325			1075
gat gcc ctc gac gcc gaa gcc caa aac ttt gcc gat atg cgc aac ctg Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala Asp Met Arg Asn Leu 330 335 340			1123
ctg atc aac gcg ggc agc aaa ttg gat gct ctc acc caa aaa tcc gtc Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu Thr Gln Lys Ser Val 345 350 355			1171
gac ctg cgc acc cgc ctc ccc aag gcc caa gaa aca ctc gct ggc ctg Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu Thr Leu Ala Gly Leu 360 365 370			1219
cgc act cgc tac tca gca gag gtc ctt gaa agc atc gac gac aac gtc Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser Ile Asp Asp Asn Val 375 380 385			1267
gac ctc gcc agc gct tcg ctc gac gaa gca gaa gaa gtc ctg cca cag Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu Glu Val Leu Pro Gln 390 395 400 405			1315
gcg tac gag ata gag tcc atg ccc gca ggc gag cag ggc ggg ctt atc Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu Gln Gly Gly Leu Ile 410 415 420			1363
gac gcg atc cgt cac atc gag cac gcc atc act acc gca gac aaa ctc Asp Ala Ile Arg His Ile Glu His Ala Ile Thr Thr Ala Asp Lys Leu 425 430 435			1411
ctc gcg ggc gtc gag cat gcc gat gaa aac atc tcc aca gcc aaa gca Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile Ser Thr Ala Lys Ala 440 445 450			1459

aac gtt gcc gat ctg atc caa gaa atc tca gac gaa atc aac gaa gcc Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp Glu Ile Asn Glu Ala 455 460 465	1507
ggc caa ctc aaa caa agc gca gga gcc gac ggt gcc cgt gcc gac tgg Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly Ala Arg Ala Asp Trp 470 475 480 485	1555
gcc tcc ctc gac gat gct gtc cgc gca gcc agc gca gca cta atc acc Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser Ala Ala Leu Ile Thr 490 495 500	1603
gca tca gca gac gcc gaa aag gat ccg ctc gga acc tac aca gaa ctt Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly Thr Tyr Thr Glu Leu 505 510 515	1651
gtc gat gtc gac tcc gcc ctc gac act caa ctt gac aca ctt cgc gcc Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu Asp Thr Leu Arg Ala 520 525 530	1699
acc gca gct gat caa gcc cgc cag cta cgc gta ttc gac caa cag ctg Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val Phe Asp Gln Gln Leu 535 540 545	1747
caa tct gca aga agc caa atc caa aag gcc gaa gac ctc atc tcc acc Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu Asp Leu Ile Ser Thr 550 555 560 565	1795
cgc ggt cgc atc gta aaa tcc gaa gcc cgc acc cac ctg gcc aac gca Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr His Leu Ala Asn Ala 570 575 580	1843
caa aag ctg tac gcc atg gca caa caa aac cgc acc cgc gac acc cgt Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg Thr Arg Asp Thr Arg 585 590 595	1891
gca gga att gat tac gga cgt caa gca gca gtc gca gcc caa cgc gcc Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val Ala Ala Gln Arg Ala 600 605 610	1939
agc aag tca gca caa aac gac atc acc acc tac aac aat cgc cac aat Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr Asn Asn Arg His Asn 615 620 625	1987
tcc ggt ggc gga acc acc ggt gcg att gtc acc ggc atg gtg atc aac Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr Gly Met Val Ile Asn 630 635 640 645	2035
tcg att ctc aac agc ggc cgc ggt ggc ggt ttc tgt gga ggc gga ggc Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe Cys Gly Gly Gly Gly 650 655 660	2083
ttt ggt gga ggc ggt ggc ggc ttc agc ggt ggt ggc ggt ggc gga gga Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly Gly Gly 665 670 675	2131
ggg ttc cgc gga ggc cgc ttc tagcctgaaa cgagcaaaac caa Gly Phe Arg Gly Gly Arg Phe 680	2175

<210> 656

<211> 684

<212> PRT

<213> Corynebacterium glutamicum

<400> 656

Met Asn Phe Ser Leu Val His Leu Arg Glu Asn Val Arg Arg Val Ser
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Val Thr Val Ala Ile Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe
 20 25 30

Phe Thr Ala His Thr Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu
 35 40 45

Ser Pro Glu Phe Tyr Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile
 50 55 60

Ser Ser Ser Asp Ile Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys
 65 70 75 80

Ala Ser Glu Gln Lys Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp
 85 90 95

Gly Val Asp Pro Glu Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly
 100 105 110

Gly Gly Asn Val Leu Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr
 115 120 125

Gly Ile Gln Gly Gly Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala
 130 135 140

Asn Asn Ala Ala Phe Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser
 145 150 155 160

Ala Leu Ala Leu Ala Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser
 165 170 175

Gly Ser Ser Ser Ser Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala
 180 185 190

Gly Val Gly Thr Val Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg
 195 200 205

Ser Arg Lys Lys Lys Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu
 210 215 220

Ile Asp Pro Arg Asp Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr
 225 230 235 240

Leu Glu His Leu Ala Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile
 245 250 255

Arg Arg Gly Lys Glu Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro
 260 265 270

Glu Arg Thr Arg Ser Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr
 275 280 285

Leu Gln Lys Ala Phe Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro
290 295 300

Glu Ser Glu Ala Glu Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser
305 310 315 320

Cys Gly Gln Ala Asp Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala
325 330 335

Asp Met Arg Asn Leu Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu
340 345 350

Thr Gln Lys Ser Val Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu
355 360 365

Thr Leu Ala Gly Leu Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser
370 375 380

Ile Asp Asp Asn Val Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu
385 390 395 400

Glu Val Leu Pro Gln Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu
405 410 415

Gln Gly Gly Leu Ile Asp Ala Ile Arg His Ile Glu His Ala Ile Thr
420 425 430

Thr Ala Asp Lys Leu Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile
435 440 445

Ser Thr Ala Lys Ala Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp
450 455 460

Glu Ile Asn Glu Ala Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly
465 470 475 480

Ala Arg Ala Asp Trp Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser
485 490 495

Ala Ala Leu Ile Thr Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly
500 505 510

Thr Tyr Thr Glu Leu Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu
515 520 525

Asp Thr Leu Arg Ala Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val
530 535 540

Phe Asp Gln Gln Leu Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu
545 550 555 560

Asp Leu Ile Ser Thr Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr
565 570 575

His Leu Ala Asn Ala Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg
580 585 590

Thr Arg Asp Thr Arg Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val
595 600 605

Ala Ala Gln Arg Ala Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr

610	615	620
Asn Asn Arg His Asn Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr		
625	630	635
Gly Met Val Ile Asn Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe		
	645	650
Cys Gly Gly Gly Gly Phe Gly Gly Gly Gly Gly Phe Ser Gly Gly		
	660	665
Gly Gly Gly Gly Gly Gly Phe Arg Gly Gly Arg Phe		
	675	680

<210> 657

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXN01492

<400> 657

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tggacaaaga ctttttagcaa caactatgtg gaggtgacag	gtg acc aca act ctg	115
	Val Thr Thr Thr Leu	
	1 5	

tgg gcg gtt tct gac ctc cat gca gcg gtg aaa gct aac gct gat cca	163
Trp Ala Val Ser Asp Leu His Ala Ala Val Lys Ala Asn Ala Asp Pro	
	10 15 20

att gag aat att cag cct aag gat ccg tct gac tgg ttg att gtt gca	211
Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp Trp Leu Ile Val Ala	
	25 30 35

ggt gac gtg gcg gaa cgt acc gaa ttg gtg ctg gaa att ttg gca cgt	259
Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu Glu Ile Leu Ala Arg	
	40 45 50

ttg cgc agg cgc ttt gcc aag gtg atc tgg gtt ccg ggt aac cat gag	307
Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val Pro Gly Asn His Glu	
	55 60 65

ttg ttt tct cgc tcc gcg gac cgc tat cag ggg cgc gat aag tac tct	355
Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly Arg Asp Lys Tyr Ser	
	70 75 80 85

gaa ctc gtt gaa ggc tgc cgc aag att gat gtg ttg act ccg gag gac	403
Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val Leu Thr Pro Glu Asp	
	90 95 100

cct tac tta acc ttt ggt ggg gtt act atc gtt ccg ttg ttt aca ctc	451
Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val Pro Leu Phe Thr Leu	
	105 110 115

tat gac tac tcg ttc cgt cga cct ggt ttc acc gtg gag cag gct gtg	499
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Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr Val Glu Gln Ala Val
 120 125 130
 caa gcg gcg cgg gat cgt caa gtg atg atg act gat gag ttt tct att 547
 Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr Asp Glu Phe Ser Ile
 135 140 145
 gcg cct ttt gtt gat atc cga gcg tgg tgc tgg gat cgc tta gcc tat 595
 Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp Asp Arg Leu Ala Tyr
 150 155 160 165
 tcc att aag cgt ttg agc aag atc aac ggg cca aca att ttg att aac 643
 Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro Thr Ile Leu Ile Asn
 170 175 180
 cac tgg ccg ctg gtg gtg gaa ccg act tat cag atg cgc tgg cag gaa 691
 His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln Met Arg Trp Gln Glu
 185 190 195
 ctt gca ttg tgg tgc ggt act cgc cac acc agg gga tgg gcc gaa cgc 739
 Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg Gly Trp Ala Glu Arg
 200 205 210
 tac aac gcg gaa gcc gtt att tac ggt cat ctg cat atg ccc gga ata 787
 Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu His Met Pro Gly Ile
 215 220 225
 acc aac gtc aac ggt gtg aaa cac att gaa gtg tcg ttg ggt tat ccg 835
 Thr Asn Val Asn Gly Val Lys His Ile Glu Val Ser Leu Gly Tyr Pro
 230 235 240 245
 cgc gaa tgg gag cat tgg tct ggg cag cat gtg tgg cca tat cca gtg 883
 Arg Glu Trp Glu His Trp Ser Gly Gln His Val Trp Pro Tyr Pro Val
 250 255 260
 atg gag gtg gac aat gct gga tgagtctttg tttccaaatt cgg 927
 Met Glu Val Asp Asn Ala Gly
 265

<210> 658

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 658

Val Thr Thr Thr Leu Trp Ala Val Ser Asp Leu His Ala Ala Val Lys
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 Ala Asn Ala Asp Pro Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp
 20 25 30
 Trp Leu Ile Val Ala Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu
 35 40 45
 Glu Ile Leu Ala Arg Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val
 50 55 60
 Pro Gly Asn His Glu Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly
 65 70 75 80

ggt gac gtg gcg gaa cgt acc gaa ttg gtg ctg gaa att ttg gca cgt Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu Glu Ile Leu Ala Arg 40 45 50	259
ttg cgc agg cgc ttt gcc aag gtg atc tgg gtt ccg ggt aac cat gag Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val Pro Gly Asn His Glu 55 60 65	307
ttg ttt tct cgc tcc gcg gac cgc tat cag ggg cgc gat aag tac tct Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly Arg Asp Lys Tyr Ser 70 75 80 85	355
gaa ctc gtt gaa ggc tgc cgc aag att gat gtg ttg act ccg gag gac Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val Leu Thr Pro Glu Asp 90 95 100	403
cct tac tta acc ttt ggt ggg gtt act atc gtt ccg ttg ttt aca ctc Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val Pro Leu Phe Thr Leu 105 110 115	451
tat gac tac tcg ttc cgt cga cct ggt ttc acc gtg gag cag gct gtg Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr Val Glu Gln Ala Val 120 125 130	499
caa gcg gcg cgg gat cgt caa gtg atg atg act gat gag ttt tct att Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr Asp Glu Phe Ser Ile 135 140 145	547
gcg cct ttt gtt gat atc cga gcg tgg tgc tgg gat cgc tta gcc tat Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp Asp Arg Leu Ala Tyr 150 155 160 165	595
tcc att aag cgt ttg agc aag atc aac ggg cca aca att ttg att aac Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro Thr Ile Leu Ile Asn 170 175 180	643
cac tgg ccg ctg gtg gtg gaa ccg act tat cag atg cgc tgg cag gaa His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln Met Arg Trp Gln Glu 185 190 195	691
ctt gca ttg tgg tgc ggt act cgc cac acc agg gga tgg gcc gaa cgc Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg Gly Trp Ala Glu Arg 200 205 210	739
tac aac gcg gaa gcc gtt att tac ggt cat ctg cat atg ccc gga ata Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu His Met Pro Gly Ile 215 220 225	787
acc aac gtc aac ggt gtg aaa cac att gaa gtg tcg ttg ggt tat ccg Thr Asn Val Asn Gly Val Lys His Ile Glu Val Ser Leu Gly Tyr Pro 230 235 240 245	835
cgc gaa tgg gag cat tgg tct ggg cag cat gtg tgg cca tat cca gtg Arg Glu Trp Glu His Trp Ser Gly Gln His Val Trp Pro Tyr Pro Val 250 255 260	883
atg gag gtg gac aat gct gga tgagtccttg tttccaaatt cg Met Glu Val Asp Asn Ala Gly 265	927

<210> 660

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

Val Thr Thr Thr Leu Trp Ala Val Ser Asp Leu His Ala Ala Val Lys
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20 25 30
Trp Leu Ile Val Ala Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu
35 40 45
Glu Ile Leu Ala Arg Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val
50 55 60
Pro Gly Asn His Glu Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly
65 70 75 80
Arg Asp Lys Tyr Ser Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val
85 90 95
Leu Thr Pro Glu Asp Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val
100 105 110
Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr
115 120 125
Val Glu Gln Ala Val Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr
130 135 140
Asp Glu Phe Ser Ile Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp
145 150 155 160
Asp Arg Leu Ala Tyr Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro
165 170 175
Thr Ile Leu Ile Asn His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln
180 185 190
Met Arg Trp Gln Glu Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg
195 200 205
Gly Trp Ala Glu Arg Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu
210 215 220
His Met Pro Gly Ile Thr Asn Val Asn Gly Val Lys His Ile Glu Val
225 230 235 240
Ser Leu Gly Tyr Pro Arg Glu Trp Glu His Trp Ser Gly Gln His Val
245 250 255
Trp Pro Tyr Pro Val Met Glu Val Asp Asn Ala Gly
260 265

<210> 661

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXN01518

<400> 661

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tcccacagac attgaagggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
                                         Val Ala Phe Met Gln
                                         1 5
aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
                        10 15 20
gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211
Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
                        25 30 35
tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
                        40 45 50
ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
                        55 60 65
cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
                        70 75 80 85
ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
                        90 95 100
gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
                        105 110 115
gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
                        120 125 130
gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
                        135 140 145
cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcattgaatc 594
Pro Pro Gln Ser Gly Glu Ala Ile Ser
150 155
aag 597

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<210> 662

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
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Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
 20 25 30

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
 35 40 45

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
 50 55 60

Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
 65 70 75 80

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
 85 90 95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
 100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
 115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
 130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
 145 150 155

<210> 663

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> FRXA01518

<400> 663

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tccacagac attgaagggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
 Val Ala Phe Met Gln
 1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
 10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211
 Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
 25 30 35

tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly

40	45	50	
ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc			307
Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly			
55	60	65	
cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg			355
Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met			
70	75	80	85
ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat			403
Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr			
90	95	100	
gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca			451
Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala			
105	110	115	
gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc			499
Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile			
120	125	130	
gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg			547
Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro			
135	140	145	
cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatgaatc			594
Pro Pro Gln Ser Gly Glu Ala Ile Ser			
150	155		
aag			597
<210> 664			
<211> 158			
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<213> Corynebacterium glutamicum			
<400> 664			
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Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly			
20	25	30	
Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu			
35	40	45	
Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp			
50	55	60	
Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile			
65	70	75	80
Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile			
85	90	95	
Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala			
100	105	110	
Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys			

115 120 125
 Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
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Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
 145 150 155

<210> 665
 <211> 1727
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (46)..(1704)
 <223> RXN01549

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 Val Ala Asn Asp
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ttt ata gaa cca aat gat gcc ccc gat gca cct gat aat ggt gac tcg 105
 Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp Asn Gly Asp Ser
 5 10 15 20

gga agc tcg ggg ttt gtt gat gaa gca aaa gat aag acc cgc tca gct 153
 Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys Thr Arg Ser Ala
 25 30 35

gca caa ggc tta ggt tat ggc gca cta cgt gta ggt ttt ggt act gca 201
 Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly Phe Gly Thr Ala
 40 45 50

gca ctt gca gcc aat ggt gct cgc tct atg ggt aat ttg gct aaa aac 249
 Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn Leu Ala Lys Asn
 55 60 65

ctg tgg aca cga atg atg ggg ctt gcc ctg tct gcc ggt act ggt atc 297
 Leu Trp Thr Arg Met Met Gly Leu Ala Leu Ser Ala Gly Thr Gly Ile
 70 75 80

tct gct gcc aca ggt ggc atg atc act gca cgt gta ggc gca atg ctg 345
 Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val Gly Ala Met Leu
 85 90 95 100

gca ggt aca ggc tcg gtg ttg tcg tcg gtg acg act att gcg ttg att 393
 Ala Gly Thr Gly Ser Val Leu Ser Ser Val Thr Thr Ile Ala Leu Ile
 105 110 115

gtg tcg atg att gtg gtg ccg gca ggt cga aaa gac ggc att atc gag 441
 Val Ser Met Ile Val Val Pro Ala Gly Arg Lys Asp Gly Ile Ile Glu
 120 125 130

ttg tgt gag ccg cca gta acg gcc aac ccg ttt acc att gac gca ggt 489
 Leu Cys Glu Pro Pro Val Thr Ala Asn Pro Phe Thr Ile Asp Ala Gly
 135 140 145

gat atg act gag aac gcg aag ttg gtg tac ggt gcg ctg tcg tat ctt 537

Asp	Met	Thr	Glu	Asn	Ala	Lys	Leu	Val	Tyr	Gly	Ala	Leu	Ser	Tyr	Leu		
150						155					160						
ggg	atg	aat	gat	caa	aat	atc	gcc	ggt	gtc	ttg	ggc	aac	ttt	gag	aca	585	
Gly	Met	Asn	Asp	Gln	Asn	Ile	Ala	Gly	Val	Leu	Gly	Asn	Phe	Glu	Thr		
165					170				175						180		
gaa	tca	ggt	atc	gac	ccg	act	gcg	gtg	gag	ggt	att	ttt	gat	gaa	cca	633	
Glu	Ser	Gly	Ile	Asp	Pro	Thr	Ala	Val	Glu	Gly	Ile	Phe	Asp	Glu	Pro		
				185					190					195			
aat	acc	atc	ggt	cct	cgg	aag	aga	gct	gcg	tgg	gat	aag	aac	ttt	gaa	681	
Asn	Thr	Ile	Gly	Pro	Arg	Lys	Arg	Ala	Ala	Trp	Asp	Lys	Asn	Phe	Glu		
			200					205						210			
cct	cag	ccg	atg	ggt	att	ggg	ctt	ggg	cag	tgg	aca	gca	ggg	cgc	aca	729	
Pro	Gln	Pro	Met	Gly	Ile	Gly	Leu	Gly	Gln	Trp	Thr	Ala	Gly	Arg	Thr		
			215				220						225				
cag	atg	ttg	cta	gat	ttt	gcc	gcc	gat	aga	aac	cga	gac	tgg	cat	tac	777	
Gln	Met	Leu	Leu	Asp	Phe	Ala	Ala	Asp	Arg	Asn	Arg	Asp	Trp	His	Tyr		
	230					235					240						
atc	gac	gtg	cag	ctt	gca	ttt	gct	att	agt	ggc	gat	aat	gaa	agc	gat	825	
Ile	Asp	Val	Gln	Leu	Ala	Phe	Ala	Ile	Ser	Gly	Asp	Asn	Glu	Ser	Asp		
245					250					255					260		
cgc	aag	gtt	ttt	ctg	gaa	atg	gtt	gat	aat	aaa	aac	tcc	agt	agc	aat	873	
Arg	Lys	Val	Phe	Leu	Glu	Met	Val	Asp	Asn	Lys	Asn	Ser	Ser	Ser	Asn		
				265					270					275			
agc	ccc	acc	gca	gcg	tcc	gag	tac	ttc	ctg	cgt	gag	tgg	gag	cgc	ccg	921	
Ser	Pro	Thr	Ala	Ala	Ser	Glu	Tyr	Phe	Leu	Arg	Glu	Trp	Glu	Arg	Pro		
			280					285					290				
gca	gat	gtc	gca	ggt	aat	gca	ccc	att	cgt	gca	gag	caa	gca	tct	aag	969	
Ala	Asp	Val	Ala	Gly	Asn	Ala	Pro	Ile	Arg	Ala	Glu	Gln	Ala	Ser	Lys		
		295					300					305					
tgg	tac	gcg	cag	atg	ggt	ggt	tgg	caa	aag	aac	tca	acc	ttg	ggt	gag	1017	
Trp	Tyr	Ala	Gln	Met	Gly	Gly	Trp	Gln	Lys	Asn	Ser	Thr	Leu	Gly	Glu		
	310					315					320						
tct	gtg	atc	gct	atg	gct	gat	ggt	gca	gca	gca	aaa	tcc	acg	gcg	cgt	1065	
Ser	Val	Ile	Ala	Met	Ala	Asp	Gly	Ala	Ala	Ala	Lys	Ser	Thr	Ala	Arg		
325					330					335					340		
gat	gag	cag	gat	gct	ctt	aat	gat	tgt	cct	gaa	gag	gac	cgc	acc	tca	1113	
Asp	Glu	Gln	Asp	Ala	Leu	Asn	Asp	Cys	Pro	Glu	Glu	Asp	Arg	Thr	Ser		
				345					350					355			
ggt	gga	aat	acg	tcc	gct	gca	gaa	gca	atg	gtg	act	att	tca	cat	cct	1161	
Gly	Gly	Asn	Thr	Ser	Ala	Ala	Glu	Ala	Met	Val	Thr	Ile	Ser	His	Pro		
			360					365					370				
tat	ctg	gct	gat	tct	cgt	ggc	aat	gac	ggt	act	gat	att	tac	cgc	tat	1209	
Tyr	Leu	Ala	Asp	Ser	Arg	Gly	Asn	Asp	Gly	Thr	Asp	Ile	Tyr	Arg	Tyr		
		375				380						385					
atc	cat	gat	gaa	gtg	ctc	acc	ggt	gat	ccg	tat	tac	gca	tcc	tgt	gac	1257	
Ile	His	Asp	Glu	Val	Leu	Thr	Gly	Asp	Pro	Tyr	Tyr	Ala	Ser	Cys	Asp		

390	395	400	
cgt ggc gtt gct acc gct att cgc tgg tcg ggc acg gat gat acg ttc			1305
Arg Gly Val Ala Thr Ala Ile Arg Trp Ser Gly Thr Asp Asp Thr Phe			
405	410	415	420
cca gca ggt cca aca gca gca cag tat gaa tac gtt gtg ggc aca gga			1353
Pro Ala Gly Pro Thr Ala Ala Gln Tyr Glu Tyr Val Val Gly Thr Gly			
	425	430	435
tcg ggc cgt tgg gag gaa atc ggc aat ctt gcc acc atg tca gag aac			1401
Ser Gly Arg Trp Glu Glu Ile Gly Asn Leu Ala Thr Met Ser Glu Asn			
	440	445	450
gat ttg tta cct ggc gat gtg ctt ctt ggt gca ccg aat cac gtt gcg			1449
Asp Leu Leu Pro Gly Asp Val Leu Leu Gly Ala Pro Asn His Val Ala			
	455	460	465
atg tat gtc agc aat gag gtt gtt gtg gac atg ttg ggc cct ggt aat			1497
Met Tyr Val Ser Asn Glu Val Val Val Asp Met Leu Gly Pro Gly Asn			
	470	475	480
gca gag cct aat gca gct att ggt cat gca tcg ttg aat gac cgc tca			1545
Ala Glu Pro Asn Ala Ala Ile Gly His Ala Ser Leu Asn Asp Arg Ser			
485	490	495	500
cct ggt ctg gat acc ttg agt ctg gat gga tgg ggc gtg aac ttc aag			1593
Pro Gly Leu Asp Thr Leu Ser Leu Asp Gly Trp Gly Val Asn Phe Lys			
	505	510	515
gtg ttc cgc aac acc cag gct gag aca aac tca gtg ttc tct ggt gta			1641
Val Phe Arg Asn Thr Gln Ala Glu Thr Asn Ser Val Phe Ser Gly Val			
	520	525	530
cag att ccg gct ggt aaa gaa att ggc gaa atg act aac cca act cga			1689
Gln Ile Pro Ala Gly Lys Glu Ile Gly Glu Met Thr Asn Pro Thr Arg			
	535	540	545
act act cct gca gga taagtttttt tcatcgctgg gtt			1727
Thr Thr Pro Ala Gly			
550			

<210> 666

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

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Asn	Gly	Asp	Ser	Gly	Ser	Ser	Gly	Phe	Val	Asp	Glu	Ala	Lys	Asp	Lys
		20						25					30		

Thr	Arg	Ser	Ala	Ala	Gln	Gly	Leu	Gly	Tyr	Gly	Ala	Leu	Arg	Val	Gly
		35					40					45			

Phe	Gly	Thr	Ala	Ala	Leu	Ala	Ala	Asn	Gly	Ala	Arg	Ser	Met	Gly	Asn
	50					55					60				

Leu Ala Lys Asn Leu Trp Thr Arg Met Met Gly Leu Ala Leu Ser Ala
 65 70 75 80
 Gly Thr Gly Ile Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val
 85 90 95
 Gly Ala Met Leu Ala Gly Thr Gly Ser Val Leu Ser Ser Val Thr Thr
 100 105 110
 Ile Ala Leu Ile Val Ser Met Ile Val Val Pro Ala Gly Arg Lys Asp
 115 120 125
 Gly Ile Ile Glu Leu Cys Glu Pro Pro Val Thr Ala Asn Pro Phe Thr
 130 135 140
 Ile Asp Ala Gly Asp Met Thr Glu Asn Ala Lys Leu Val Tyr Gly Ala
 145 150 155 160
 Leu Ser Tyr Leu Gly Met Asn Asp Gln Asn Ile Ala Gly Val Leu Gly
 165 170 175
 Asn Phe Glu Thr Glu Ser Gly Ile Asp Pro Thr Ala Val Glu Gly Ile
 180 185 190
 Phe Asp Glu Pro Asn Thr Ile Gly Pro Arg Lys Arg Ala Ala Trp Asp
 195 200 205
 Lys Asn Phe Glu Pro Gln Pro Met Gly Ile Gly Leu Gly Gln Trp Thr
 210 215 220
 Ala Gly Arg Thr Gln Met Leu Leu Asp Phe Ala Ala Asp Arg Asn Arg
 225 230 235 240
 Asp Trp His Tyr Ile Asp Val Gln Leu Ala Phe Ala Ile Ser Gly Asp
 245 250 255
 Asn Glu Ser Asp Arg Lys Val Phe Leu Glu Met Val Asp Asn Lys Asn
 260 265 270
 Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser Glu Tyr Phe Leu Arg Glu
 275 280 285
 Trp Glu Arg Pro Ala Asp Val Ala Gly Asn Ala Pro Ile Arg Ala Glu
 290 295 300
 Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly Gly Trp Gln Lys Asn Ser
 305 310 315 320
 Thr Leu Gly Glu Ser Val Ile Ala Met Ala Asp Gly Ala Ala Ala Lys
 325 330 335
 Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu Asn Asp Cys Pro Glu Glu
 340 345 350
 Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala Ala Glu Ala Met Val Thr
 355 360 365
 Ile Ser His Pro Tyr Leu Ala Asp Ser Arg Gly Asn Asp Gly Thr Asp
 370 375 380
 Ile Tyr Arg Tyr Ile His Asp Glu Val Leu Thr Gly Asp Pro Tyr Tyr

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<210> 667
<211> 942
<212> DNA
<213> Corynebacterium glutamicum
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<222> (59) .. (919)
<223> FRXA01549
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gtt gat aat aaa aac tcc agt agc aat agc ccc acc gca gcg tcc gag 109
Val Asp Asn Lys Asn Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser Glu
5 10 15

tac ttc ctg cgt gag tgg gag cgc ccg gca gat gtc gca ggt aat gca 157
 Tyr Phe Leu Arg Glu Trp Glu Arg Pro Ala Asp Val Ala Gly Asn Ala
 20 25 30

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ccc att cgt gca gag caa gca tct aag tgg tac gcg cag atg ggt ggt    205
Pro Ile Arg Ala Glu Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly Gly
      35                      40                      45

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<210> 668

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 668

Met Val Asp Asn Lys Asn Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser
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Glu Tyr Phe Leu Arg Glu Trp Glu Arg Pro Ala Asp Val Ala Gly Asn
20 25 30

Ala Pro Ile Arg Ala Glu Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly
35 40 45

Gly Trp Gln Lys Asn Ser Thr Leu Gly Glu Ser Val Ile Ala Met Ala
50 55 60

Asp Gly Ala Ala Ala Lys Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu
65 70 75 80

Asn Asp Cys Pro Glu Glu Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala
85 90 95

Ala Glu Ala Met Val Thr Ile Ser His Pro Tyr Leu Ala Asp Ser Arg
100 105 110

Gly Asn Asp Gly Thr Asp Ile Tyr Arg Tyr Ile His Asp Glu Val Leu
115 120 125

Thr Gly Asp Pro Tyr Tyr Ala Ser Cys Asp Arg Gly Val Ala Thr Ala
130 135 140

Ile Arg Trp Ser Gly Thr Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala
145 150 155 160

Ala Gln Tyr Glu Tyr Val Val Gly Thr Gly Ser Gly Arg Trp Glu Glu
165 170 175

Ile Gly Asn Leu Ala Thr Met Ser Glu Asn Asp Leu Leu Pro Gly Asp
180 185 190

Val Leu Leu Gly Ala Pro Asn His Val Ala Met Tyr Val Ser Asn Glu
195 200 205

Val Val Val Asp Met Leu Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala
210 215 220

Ile Gly His Ala Ser Leu Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu
225 230 235 240

Ser Leu Asp Gly Trp Gly Val Asn Phe Lys Val Phe Arg Asn Thr Gln
245 250 255

Ala Glu Thr Asn Ser Val Phe Ser Gly Val Gln Ile Pro Ala Gly Lys
260 265 270

Glu Ile Gly Glu Met Thr Asn Pro Thr Arg Thr Thr Pro Ala Gly
275 280 285

<210> 669

<211> 363

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (46)..(363)

<223> FRXA02011

<400> 669

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 Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp Asn Gly Asp Ser
 5 10 15 20

gga agc tcg ggg ttt gtt gat gaa gca aaa gat aag acc cgc tca gct 153
 Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys Thr Arg Ser Ala
 25 30 35

gca caa ggc tta ggt tat ggc gca cta cgt gta ggt ttt ggt act gca 201
 Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly Phe Gly Thr Ala
 40 45 50

gca ctt gca gcc aat ggt gct cgc tct atg ggt aat ttg gct aaa aac 249
 Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn Leu Ala Lys Asn
 55 60 65

ctg tgg aca cca atg atg ggg ctt gcc ctg tct gcc ggt act ggt atc 297
 Leu Trp Thr Pro Met Met Gly Leu Ala Leu Ser Ala Gly Thr Gly Ile
 70 75 80

tct gct gcc aca ggt ggc atg atc act gca cgt gta ggc gca atg ctg 345
 Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val Gly Ala Met Leu
 85 90 95 100

gca ggt aca ggc tcg gcg 363
 Ala Gly Thr Gly Ser Ala
 105

<210> 670

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

Val Ala Asn Asp Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp
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Asn Gly Asp Ser Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys
 20 25 30

Thr Arg Ser Ala Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly
 35 40 45

Phe Gly Thr Ala Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn

ggt aac gcc aac gca ggt ggc ctc att ggc cag gca gtc ctt ggc acc 547
 Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln Ala Val Leu Gly Thr
 135 140 145

 atc ggt gta ttc att ggc atg ctg ttt gta tac aag act ggc gct atc 595
 Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr Lys Thr Gly Ala Ile
 150 155 160 165

 aag gtc act cct aag ttc aac cgc atc ctc acc ggc atg atg gtt ggc 643
 Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr Gly Met Met Val Gly
 170 175 180

 gtc ctg gtt ctt gtc ctg ggc aac gtt gta tgg gca ctg ttc act ggt 691
 Val Leu Val Leu Val Leu Gly Asn Val Val Trp Ala Leu Phe Thr Gly
 185 190 195

 ggc gca agc cca ctg cgt gac ggt gga atc atc gcg att atc ttc tcc 739
 Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile Ala Ile Ile Phe Ser
 200 205 210

 ctc ttc tgc atc ggc ctg gca gca ttc agc ttc ctc tcc gac ttc gat 787
 Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe Leu Ser Asp Phe Asp
 215 220 225

 gca gct gac cgc ctc gtc cgc gaa ggt gca cct tcc aag atg gca tgg 835
 Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro Ser Lys Met Ala Trp
 230 235 240 245

 ggc gtt gcg ctt ggt ctt gca gtg acc ttg gtc tgg ctc tac acc gaa 883
 Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val Trp Leu Tyr Thr Glu
 250 255 260

 atc cta cgt ctg ctt agc tac ttc caa aac cgc tagttttacgc agcacaagac 936
 Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
 265 270

 ccc 939

<210> 672
 <211> 272
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 672
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 Pro Gln Gly Gln Asn Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val
 20 25 30

 Tyr Gln Gln Asn Val Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val
 35 40 45

 Asp Asp Val Ile Thr Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val
 50 55 60

 Phe Ala Leu Val Thr Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly
 65 70 75 80

 Met Ile Leu Thr Leu Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu

85										90					95				
Val	Ser	Thr	Phe	Gly	Lys	Lys	Tyr	Gly	Ser	Ala	Ala	Val	Thr	Leu	Ile				
			100					105					110						
Tyr	Ala	Val	Phe	Glu	Gly	Leu	Phe	Val	Gly	Gly	Ile	Ser	Leu	Leu	Leu				
		115					120					125							
Ser	Gly	Phe	Thr	Val	Gly	Asn	Ala	Asn	Ala	Gly	Gly	Leu	Ile	Gly	Gln				
	130					135					140								
Ala	Val	Leu	Gly	Thr	Ile	Gly	Val	Phe	Ile	Gly	Met	Leu	Phe	Val	Tyr				
145					150					155					160				
Lys	Thr	Gly	Ala	Ile	Lys	Val	Thr	Pro	Lys	Phe	Asn	Arg	Ile	Leu	Thr				
			165						170					175					
Gly	Met	Met	Val	Gly	Val	Leu	Val	Leu	Val	Leu	Gly	Asn	Val	Val	Trp				
			180					185					190						
Ala	Leu	Phe	Thr	Gly	Gly	Ala	Ser	Pro	Leu	Arg	Asp	Gly	Gly	Ile	Ile				
		195					200					205							
Ala	Ile	Ile	Phe	Ser	Leu	Phe	Cys	Ile	Gly	Leu	Ala	Ala	Phe	Ser	Phe				
	210					215					220								
Leu	Ser	Asp	Phe	Asp	Ala	Ala	Asp	Arg	Leu	Val	Arg	Glu	Gly	Ala	Pro				
225					230				235						240				
Ser	Lys	Met	Ala	Trp	Gly	Val	Ala	Leu	Gly	Leu	Ala	Val	Thr	Leu	Val				
			245						250					255					
Trp	Leu	Tyr	Thr	Glu	Ile	Leu	Arg	Leu	Leu	Ser	Tyr	Phe	Gln	Asn	Arg				
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<210> 673

<211> 939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(916)

<223> FRXA01557

<400> 673

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				Val	Arg	Ser	Ser	Asn	
				1				5	

ccc	gtt	ttt	agt	tcc	ctt	aag	gaa	act	caa	cgt	cca	caa	ggc	cag	aac	163
Pro	Val	Phe	Ser	Ser	Leu	Lys	Glu	Thr	Gln	Arg	Pro	Gln	Gly	Gln	Asn	
			10					15						20		

cca	tac	ggt	ggt	tac	gac	aac	ttc	ggt	ggt	gtc	tac	cag	caa	aac	gta	211
Pro	Tyr	Gly	Gly	Tyr	Asp	Asn	Phe	Gly	Gly	Val	Tyr	Gln	Gln	Asn	Val	
		25						30					35			

gct cca cag aag gcg gag cgc cca atg act gtg gat gat gtg atc acc 259
Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val Asp Asp Val Ile Thr
40 45 50

aag act ggt atc act ctc gcg gtt att atc gtt ttt gca ttg gtc acc 307
Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val Phe Ala Leu Val Thr
55 60 65

ttt ggc gtg tgg ttg gtt agc ccc ggc ctc gga atg atc ttg acc ctt 355
Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly Met Ile Leu Thr Leu
70 75 80 85

gtt ggt gcc atc ggt ggt ttc atc acc gtt ctg gtc agc acc ttc ggc 403
Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu Val Ser Thr Phe Gly
90 95 100

aag aag tac gga tct gcg gca gtc act ttg att tac gca gta ttc gaa 451
Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile Tyr Ala Val Phe Glu
105 110 115

ggc ctc ttc gtc ggc gga att tcc ctt ctg ctg tcc ggc ttc aca gtt 499
Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu Ser Gly Phe Thr Val
120 125 130

ggt aac gcc aac gca ggt ggc ctc att ggc cag gca gtc ctt ggc acc 547
Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln Ala Val Leu Gly Thr
135 140 145

atc ggt gta ttc att ggc atg ctg ttt gta tac aag act ggc gct atc 595
Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr Lys Thr Gly Ala Ile
150 155 160 165

aag gtc act cct aag ttc aac cgc atc ctc acc ggc atg atg gtt ggc 643
Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr Gly Met Met Val Gly
170 175 180

gtc ctg gtt ctt gtc ctg ggc aac gtt gta tgg gca ctg ttc act ggt 691
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185 190 195

ggc gca agc cca ctg cgt gac ggt gga atc atc gcg att atc ttc tcc 739
Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile Ala Ile Ile Phe Ser
200 205 210

ctc ttc tgc atc ggc ctg gca gca ttc agc ttc ctc tcc gac ttc gat 787
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215 220 225

gca gct gac cgc ctc gtc cgc gaa ggt gca cct tcc aag atg gca tgg 835
Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro Ser Lys Met Ala Trp
230 235 240 245

ggc gtt gcg ctt ggt ctt gca gtg acc ttg gtc tgg ctc tac acc gaa 883
Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val Trp Leu Tyr Thr Glu
250 255 260

atc cta cgt ctg ctt agc tac ttc caa aac cgc tagttttacgc agcacaagac 936
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939

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<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 674

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Phe	Ala	Leu	Val	Thr	Phe	Gly	Val	Trp	Leu	Val	Ser	Pro	Gly	Leu	Gly
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Met	Ile	Leu	Thr	Leu	Val	Gly	Ala	Ile	Gly	Gly	Phe	Ile	Thr	Val	Leu
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Val	Ser	Thr	Phe	Gly	Lys	Lys	Tyr	Gly	Ser	Ala	Ala	Val	Thr	Leu	Ile
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Tyr	Ala	Val	Phe	Glu	Gly	Leu	Phe	Val	Gly	Gly	Ile	Ser	Leu	Leu	Leu
		115					120					125			
Ser	Gly	Phe	Thr	Val	Gly	Asn	Ala	Asn	Ala	Gly	Gly	Leu	Ile	Gly	Gln
	130					135					140				
Ala	Val	Leu	Gly	Thr	Ile	Gly	Val	Phe	Ile	Gly	Met	Leu	Phe	Val	Tyr
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Lys	Thr	Gly	Ala	Ile	Lys	Val	Thr	Pro	Lys	Phe	Asn	Arg	Ile	Leu	Thr
			165						170					175	
Gly	Met	Met	Val	Gly	Val	Leu	Val	Leu	Val	Leu	Gly	Asn	Val	Val	Trp
			180					185					190		
Ala	Leu	Phe	Thr	Gly	Gly	Ala	Ser	Pro	Leu	Arg	Asp	Gly	Gly	Ile	Ile
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Ala	Ile	Ile	Phe	Ser	Leu	Phe	Cys	Ile	Gly	Leu	Ala	Ala	Phe	Ser	Phe
	210						215				220				
Leu	Ser	Asp	Phe	Asp	Ala	Ala	Asp	Arg	Leu	Val	Arg	Glu	Gly	Ala	Pro
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Ser	Lys	Met	Ala	Trp	Gly	Val	Ala	Leu	Gly	Leu	Ala	Val	Thr	Leu	Val
			245						250					255	
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<211> 1158
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 <222> (101)..(1135)
 <223> RXN01574

<400> 675

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                                         Met Ser Asn Lys Arg
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Ile Gly Val Val Ile Val Ser Tyr Gly His Glu Gln Asp Val Ala Asn
                        10 15 20
ctg gta gac aca ttt gca gat cag ctg aaa act ggt gac cgc gta gtt 211
Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr Gly Asp Arg Val Val
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Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys Asp Ala Val Gly Glu
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cgc ctg gaa aaa cac ggc gca gag atc atc aac cac gac aac ggt ggt 307
Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn His Asp Asn Gly Gly
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Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His Ile Val Asp Asp Val
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Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg Leu Gly Gly Met Glu
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Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp Phe Ser Ala Arg Leu
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 ctg ctg gcc ggc ggt cga att ggt ctc ctg cat tcc gcg tat gtc acc 739
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 200 205 210
 cac cat tac gac tac gcc aag ggt gac tac aag tgg att tac atc gaa 787
 His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys Trp Ile Tyr Ile Glu
 215 220 225
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 Arg Asn Arg His Val Leu Leu Leu Ser Val Leu Pro Leu Pro Leu Leu
 230 235 240 245
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 Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn Leu Gly Leu Trp Ala
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 Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys Val Lys Ser Leu Arg
 265 270 275
 ctc ctg atc cgc gat cta cca gcg att ttc aaa ctg cgt agg agc acg 979
 Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys Leu Arg Arg Ser Thr
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 cag gag ctt gcc gaa ctc aca cca tcg caa tat ctg gca aaa atg gaa 1027
 Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr Leu Ala Lys Met Glu
 295 300 305
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 Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile Gly Ser Asn Lys Ile
 310 315 320 325
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 Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu Cys Met Ser Ile Leu
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 Lys Leu Leu Ala
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<210> 676

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 676

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 Gly Asp Arg Val Val Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys
 35 40 45
 Asp Ala Val Gly Glu Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn
 50 55 60

His Asp Asn Gly Gly Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His
 65 70 75 80
 Ile Val Asp Asp Val Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val
 85 90 95
 Ile Asp Asp Pro Thr Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln
 100 105 110
 Trp Ala Ala Phe Met Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn
 115 120 125
 Ser Ala Gly Asn Ala Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly
 130 135 140
 Leu Asp Glu Lys Pro Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser
 145 150 155 160
 Ile Ala Ser Gly Ala Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg
 165 170 175
 Leu Gly Gly Met Glu Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp
 180 185 190
 Phe Ser Ala Arg Leu Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His
 195 200 205
 Ser Ala Tyr Val Thr His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys
 210 215 220
 Trp Ile Tyr Ile Glu Arg Asn Arg His Val Leu Leu Leu Ser Val Leu
 225 230 235 240
 Pro Leu Pro Leu Leu Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn
 245 250 255
 Leu Gly Leu Trp Ala Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys
 260 265 270
 Val Lys Ser Leu Arg Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys
 275 280 285
 Leu Arg Arg Ser Thr Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr
 290 295 300
 Leu Ala Lys Met Glu Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile
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 325 330 335
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 340 345

<210> 677

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1135)

<223> FRXA01574

<400> 677

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Ile Gly Val Val Ile Val Ser Tyr Gly His Glu Gln Asp Val Ala Asn
                        10                        15                        20

ctg gta gac aca ttt gca gat cag ctg aaa act ggt gac cgc gta gtt 211
Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr Gly Asp Arg Val Val
                        25                        30                        35

gtc gtg gac aac cgc aaa cct tgg gtg tta aaa gac gcc gtg ggg gag 259
Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys Asp Ala Val Gly Glu
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cgc ctg gaa aaa cac ggc gca gag atc atc aac cac gac aac ggt ggt 307
Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn His Asp Asn Gly Gly
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ttc gcc gct ggc tgc aac gtg ggc gca gcg cac atc gtg gat gac gtt 355
Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His Ile Val Asp Asp Val
                        70                        75                        80                        85

gac ctg ctg ttc ttc ctc aac ccc gac aca gtg atc gac gat ccc acc 403
Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val Ile Asp Asp Pro Thr
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Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln Trp Ala Ala Phe Met
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ccg tac ctg ctg ctt cct gac agc acc att aac tcc gca ggc aac gcc 499
Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn Ser Ala Gly Asn Ala
                        120                        125                        130

ctg cat att tcc gga ctg tcg tgg gtg act ggt ctg gat gaa aaa cca 547
Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly Leu Asp Glu Lys Pro
                        135                        140                        145

gtt gaa ggc tca tct gaa gtt acc gat att tcc att gcc tct ggc gcc 595
Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser Ile Ala Ser Gly Ala
                        150                        155                        160                        165

tgc ctt gcc gtg cgc gtg gac tgg tgg aaa cgc ctc ggt ggc atg gaa 643
Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg Leu Gly Gly Met Glu
                        170                        175                        180

gaa ctg tat ttc atg tac cac gaa gac act gac ttc tcc gcc cgc ttg 691
Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp Phe Ser Ala Arg Leu
                        185                        190                        195

ctg ctg gcc ggc ggt cga att ggt ctc ctg cat tcc gcg tat gtc acc 739

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Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His Ser Ala Tyr Val Thr
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 His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys Trp Ile Tyr Ile Glu
 215 220 225
 cga aac cga cac gtt ttg ctg ctc agc gtg ctg ccg ctt cca ttg ctg 835
 Arg Asn Arg His Val Leu Leu Leu Ser Val Leu Pro Leu Pro Leu Leu
 230 235 240 245
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 Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn Leu Gly Leu Trp Ala
 250 255 260
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 Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys Val Lys Ser Leu Arg
 265 270 275
 ctc ctg atc cgc gat cta cca gcg att ttc aaa ctg cgt agg agc acg 979
 Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys Leu Arg Arg Ser Thr
 280 285 290
 cag gag ctt gcc gaa ctc aca cca tcg caa tat ctg gca aaa atg gaa 1027
 Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr Leu Ala Lys Met Glu
 295 300 305
 tgg cgc cta gac aat ccc aac cta ggc aac att gga tcc aac aag att 1075
 Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile Gly Ser Asn Lys Ile
 310 315 320 325
 gtt gcg act gga tat aag acc tat tac aag ttg tgt atg agt atc ctg 1123
 Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu Cys Met Ser Ile Leu
 330 335 340
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 Lys Leu Leu Ala
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<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

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 Gly Asp Arg Val Val Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys
 35 40 45
 Asp Ala Val Gly Glu Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn
 50 55 60
 His Asp Asn Gly Gly Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His
 65 70 75 80

Ile Val Asp Asp Val Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val
85 90 95
Ile Asp Asp Pro Thr Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln
100 105 110
Trp Ala Ala Phe Met Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn
115 120 125
Ser Ala Gly Asn Ala Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly
130 135 140
Leu Asp Glu Lys Pro Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser
145 150 155 160
Ile Ala Ser Gly Ala Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg
165 170 175
Leu Gly Gly Met Glu Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp
180 185 190
Phe Ser Ala Arg Leu Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His
195 200 205
Ser Ala Tyr Val Thr His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys
210 215 220
Trp Ile Tyr Ile Glu Arg Asn Arg His Val Leu Leu Leu Ser Val Leu
225 230 235 240
Pro Leu Pro Leu Leu Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn
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Leu Gly Leu Trp Ala Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys
260 265 270
Val Lys Ser Leu Arg Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys
275 280 285
Leu Arg Arg Ser Thr Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr
290 295 300
Leu Ala Lys Met Glu Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile
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<400> 679

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aaa gat aaa cta gga cgt ccc atc cgt gac tta cgg tta tct gtg aca 163
Lys Asp Lys Leu Gly Arg Pro Ile Arg Asp Leu Arg Leu Ser Val Thr
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gat cgg tgt aac ttt agg tgt gat tat tgc atg cct aaa gag gta ttt 211
Asp Arg Cys Asn Phe Arg Cys Asp Tyr Cys Met Pro Lys Glu Val Phe
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Gly Asp Asp Phe Val Phe Leu Pro Lys Asn Glu Leu Leu Thr Phe Asp
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Glu Met Ala Arg Ile Ala Lys Val Tyr Ala Glu Leu Gly Val Lys Lys
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Ile Arg Ile Thr Gly Glu Pro Leu Met Arg Arg Asp Leu Asp Val
                        70 75 80 85

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Ala Gly Leu Arg Arg Ile Asn Val Ser Leu Asp Ala Ile Asp Asp Thr
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Leu Phe Gln Ser Ile Asn Asn Arg Asn Ile Lys Ala Thr Thr Ile Leu
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gaa caa att gat tac gcg acg tct att ggt ttg aat gta aaa gta aat 595
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Val Val Ile Gln Lys Gly Ile Asn Asp Asp Gln Ile Ile Pro Met Leu
                        170 175 180

gaa tat ttt aaa gat aaa cat ata gag att cga ttt ata gaa ttt atg 691
Glu Tyr Phe Lys Asp Lys His Ile Glu Ile Arg Phe Ile Glu Phe Met
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gat gtt ggt aat gat aat gga tgg gat ttc agt aaa gtt gta act aaa 739
Asp Val Gly Asn Asp Asn Gly Trp Asp Phe Ser Lys Val Val Thr Lys
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gat gaa atg ctt aca atg ata gag cag cac ttt gaa atc gat cct gta 787

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 Glu Pro Lys Tyr Phe Gly Glu Val Ala Lys Tyr Tyr Arg His Lys Asp
 230 235 240 245
 aat ggt gtt caa ttt ggt ttg att aca agt gtt tca caa tca ttt tgt 883
 Asn Gly Val Gln Phe Gly Leu Ile Thr Ser Val Ser Gln Ser Phe Cys
 250 255 260
 tct aca tgt aca cgc gca agg ctg tca tca gat ggg aag ttt tac gga 931
 Ser Thr Cys Thr Arg Ala Arg Leu Ser Ser Asp Gly Lys Phe Tyr Gly
 265 270 275
 tgt tta ttt gca act gtc gat gga ttt aac gtt aaa gcg ttt att cgt 979
 Cys Leu Phe Ala Thr Val Asp Gly Phe Asn Val Lys Ala Phe Ile Arg
 280 285 290
 tct ggc gtg acc gac gaa gaa tta aaa gaa caa ttt aaa gct tta tgg 1027
 Ser Gly Val Thr Asp Glu Glu Leu Lys Glu Gln Phe Lys Ala Leu Trp
 295 300 305
 caa ata aga gat gat cga tat tca gat gag aga act gct caa aca gtt 1075
 Gln Ile Arg Asp Asp Arg Tyr Ser Asp Glu Arg Thr Ala Gln Thr Val
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<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

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 35 40 45
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 Leu Gly Val Lys Lys Ile Arg Ile Thr Gly Gly Glu Pro Leu Met Arg
 65 70 75 80
 Arg Asp Leu Asp Val Leu Ile Ala Lys Leu Asn Gln Ile Asp Gly Ile
 85 90 95
 Glu Asp Ile Gly Leu Thr Thr Asn Gly Leu Leu Leu Lys Lys His Gly
 100 105 110

Gln Lys Leu Tyr Asp Ala Gly Leu Arg Arg Ile Asn Val Ser Leu Asp
115 120 125

Ala Ile Asp Asp Thr Leu Phe Gln Ser Ile Asn Asn Arg Asn Ile Lys
130 135 140

Ala Thr Thr Ile Leu Glu Gln Ile Asp Tyr Ala Thr Ser Ile Gly Leu
145 150 155 160

Asn Val Lys Val Asn Val Val Ile Gln Lys Gly Ile Asn Asp Asp Gln
165 170 175

Ile Ile Pro Met Leu Glu Tyr Phe Lys Asp Lys His Ile Glu Ile Arg
180 185 190

Phe Ile Glu Phe Met Asp Val Gly Asn Asp Asn Gly Trp Asp Phe Ser
195 200 205

Lys Val Val Thr Lys Asp Glu Met Leu Thr Met Ile Glu Gln His Phe
210 215 220

Glu Ile Asp Pro Val Glu Pro Lys Tyr Phe Gly Glu Val Ala Lys Tyr
225 230 235 240

Tyr Arg His Lys Asp Asn Gly Val Gln Phe Gly Leu Ile Thr Ser Val
245 250 255

Ser Gln Ser Phe Cys Ser Thr Cys Thr Arg Ala Arg Leu Ser Ser Asp
260 265 270

Gly Lys Phe Tyr Gly Cys Leu Phe Ala Thr Val Asp Gly Phe Asn Val
275 280 285

Lys Ala Phe Ile Arg Ser Gly Val Thr Asp Glu Glu Leu Lys Glu Gln
290 295 300

Phe Lys Ala Leu Trp Gln Ile Arg Asp Asp Arg Tyr Ser Asp Glu Arg
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<222> (101)..(1402)
<223> RXN01592

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Met Ala Asp Asn Phe

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Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Arg Gly Asn Asp Asp	
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cgc gga aac tac cgt caa aac cga gat ggt gaa tca cga gat cgc ggc	259
Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp Arg Gly	
40 45 50	
gga tac ctc ggt gac cgt cgc gac aac cgc tca ggt gaa tat cgt caa	307
Gly Tyr Leu Gly Asp Arg Arg Asn Arg Ser Gly Glu Tyr Arg Gln	
55 60 65	
cgt gac gat agg cgt gac gat cgt agg gac aac cga agc gat gac cgc	355
Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp Asp Arg	
70 75 80 85	
cgc ggt ggt tac cgc tcc gat cgc aac ttt gac gat cgc aac agc aac	403
Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn Ser Asn	
90 95 100	
atg cgt gat gat cgt cgc ggc ggc gac cgt tca tac agc cgt aat gat	451
Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg Asn Asp	
105 110 115	
cgc tcc gat cgt ggc tat cgt agc aat gac cgc tac gac cgt aat gat	499
Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg Asn Asp	
120 125 130	
cgt cgc gat gac aac agg gac acc agg ggt ggc gat cgc gga gac cgt	547
Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly Asp Arg	
135 140 145	
cgc tac gac agg cgc gat gac cga cgt gat gat cgt cgc gat gat cgt	595
Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Arg Arg Asp Asp Arg	
150 155 160 165	
cgt ggc gga cag ggc cag ggg cgt cca ggt gga gat cgt cga cat gcg	643
Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg His Ala	
170 175 180	
aac cgt gca ggt gca ggt cgc gat cag cag cgt gat tcg ctg cat cca	691
Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu His Pro	
185 190 195	
cag cgc gct ggt ttc cgt gaa gag cgc ttg aac act cgt ctc aat gag	739
Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu Asn Glu	
200 205 210	
cct gat ttg ccg ggc gat att gat atc aag gac ttg gat cct ttg gtc	787
Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro Leu Val	
215 220 225	
ctg cag gat ttg aag gtt ttg tct aag gac aac gca gat gcc gtc gca	835
Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala Val Ala	
230 235 240 245	


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aag cat atg atc atg gct gcg acc tgg ctg gcc gac gat cct caa ttg      883
Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro Gln Leu
                250                      255                      260

gca ctg cgc cac gcc cgt gct gcg aag gat cgc gcg gga cgc gtg tcc      931
Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg Val Ser
                265                      270                      275

gtc gtg cgt gag acg aac ggc att gct gct tac cat gct ggt gag tgg      979
Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly Glu Trp
                280                      285                      290

aag gaa gct ctt tcg gag ctt cgt gct gcg cgc cgc atg tcg ggt ggt     1027
Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser Gly Gly
                295                      300                      305

cct ggt ttg att gct gtg atg gct gac tgt gag cgt ggc ttg ggt cgt     1075
Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu Gly Arg
310                      315                      320                      325

cct gag aag gcg att gag ctg gct cga gaa gag gat ttg agc tct ttg     1123
Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser Ser Leu
                330                      335                      340

gat cag gat aac ctg atc gag tta gcg att gtt gtt gct gga gca cgc     1171
Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly Ala Arg
                345                      350                      355

cat gat ttg ggt cag cat gac tct gcg att gtg gaa ttg cag aag gtt     1219
His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln Lys Val
                360                      365                      370

aat cca agc ttg aag agc acc ggt ttc acc cat tct cgt ttg tct tac     1267
Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu Ser Tyr
                375                      380                      385

gct tac gcc gat gcg ctt gtt ttg gct ggt cgt ggc gat gaa gca cgt     1315
Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu Ala Arg
390                      395                      400                      405

gag tgg ttc cag cac gct gcc acc ttg gat gag gac ggc tac ctc gat     1363
Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr Leu Asp
                410                      415                      420

gca gag gag cgt atc gag cag ctc gat aat ggg aac aac tagactattg     1412
Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
                425                      430

gtctagagtg taa                                                         1425

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<210> 682

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 682

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  1              5              10              15

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Arg Gly Asn Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu
35 40 45

Ser Arg Asp Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser
50 55 60

Gly Glu Tyr Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn
65 70 75 80

Arg Ser Asp Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp
85 90 95

Asp Arg Asn Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser
100 105 110

Tyr Ser Arg Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg
115 120 125

Tyr Asp Arg Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly
130 135 140

Asp Arg Gly Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp
145 150 155 160

Arg Arg Asp Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly
165 170 175

Asp Arg Arg His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg
180 185 190

Asp Ser Leu His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn
195 200 205

Thr Arg Leu Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp
210 215 220

Leu Asp Pro Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn
225 230 235 240

Ala Asp Ala Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala
245 250 255

Asp Asp Pro Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg
260 265 270

Ala Gly Arg Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr
275 280 285

His Ala Gly Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg
290 295 300

Arg Met Ser Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu
305 310 315 320

Arg Gly Leu Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu
325 330 335

Asp Leu Ser Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val

340 345 350
 Val Ala Gly Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val
 355 360 365
 Glu Leu Gln Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His
 370 375 380
 Ser Arg Leu Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg
 385 390 395 400
 Gly Asp Glu Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu
 405 410 415
 Asp Gly Tyr Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly
 420 425 430
 Asn Asn

<210> 683
 <211> 1316
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1293)
 <223> FRXA01592

<400> 683
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 cgt gga gac cgc ggc gat cgc ggt ggc tac cga aac tcc cgc ggc aac 96
 Arg Gly Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Arg Gly Asn
 20 25 30
 gat gac cgc gga aac tac cgt caa aac cga gat ggt gaa tca cga gat 144
 Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp
 35 40 45
 cgc ggc gga tac ctc ggt gac cgt cgc gac aac cgc tca ggt gaa tat 192
 Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr
 50 55 60
 cgt caa cgt gac gat agg cgt gac gat cgt agg gac aac cga agc gat 240
 Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp
 65 70 75 80
 gac cgc cgc ggt ggt tac cgc tcc gat cgc aac ttt gac gat cgc aac 288
 Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn
 85 90 95
 agc aac atg cgt gat gat cgt cgc ggc ggc gac cgt tca tac agc cgt 336
 Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg
 100 105 110
 aat gat cgc tcc gat cgt ggc tat cgt agc aat gac cgc tac gac cgt 384

Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg	
115 120 125	
aat gat cgt cgc gat gac aac agg gac acc agg ggt ggc gat cgc gga	432
Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly	
130 135 140	
gac cgt cgc tac gac agg cgc gat gac cga cgt gat gat cgt cgc gat	480
Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Asp Arg Arg Asp	
145 150 155 160	
gat cgt cgt ggc gga cag ggc cag ggg cgt cca ggt gga gat cgt cga	528
Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg	
165 170 175	
cat gcg aac cgt gca ggt gca ggt cgc gat cag cag cgt gat tcg ctg	576
His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu	
180 185 190	
cat cca cag cgc gct ggt ttc cgt gaa gag cgc ttg aac act cgt ctc	624
His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu	
195 200 205	
aat gag cct gat ttg ccg ggc gat att gat atc aag gac ttg gat cct	672
Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro	
210 215 220	
ttg gtc ctg cag gat ttg aag gtt ttg tct aag gac aac gca gat gcc	720
Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala	
225 230 235 240	
gtc gca aag cat atg atc atg gct gcg acc tgg ctg gcc gac gat cct	768
Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro	
245 250 255	
caa ttg gca ctg cgc cac gcc cgt gct gcg aag gat cgc gcg gga cgc	816
Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg	
260 265 270	
gtg tcc gtc gtg cgt gag acg aac ggc att gct gct tac cat gct ggt	864
Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly	
275 280 285	
gag tgg aag gaa gct ctt tcg gag ctt cgt gct gcg cgc cgc atg tcg	912
Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser	
290 295 300	
ggt ggt cct ggt ttg att gct gtg atg gct gac tgt gag cgt ggc ttg	960
Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu	
305 310 315 320	
ggt cgt cct gag aag gcg att gag ctg gct cga gaa gag gat ttg agc	1008
Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser	
325 330 335	
tct ttg gat cag gat aac ctg atc gag tta gcg att gtt gtt gct gga	1056
Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly	
340 345 350	
gca cgc cat gat ttg ggt cag cat gac tct gcg att gtg gaa ttg cag	1104
Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln	

355	360	365	
aag gtt aat cca agc ttg	aag agc acc ggt ttc acc cat tct cgt ttg		1152
Lys Val Asn Pro Ser Leu	Lys Ser Thr Gly Phe Thr His Ser Arg Leu		
370	375	380	
tct tac gct tac gcc gat gcg ctt gtt ttg gct ggt cgt ggc gat gaa			1200
Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu			
385	390	395	400
gca cgt gag tgg ttc cag cac gct gcc acc ttg gat gag gac ggc tac			1248
Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr			
405	410	415	
ctc gat gca gag gag cgt atc gag cag ctc gat aat ggg aac aac			1293
Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn			
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tagactattg gtctagagtg taa			1316

<210> 684

<211> 431

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

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Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp			
35	40	45	
Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr			
50	55	60	
Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp			
65	70	75	80
Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn			
85	90	95	
Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg			
100	105	110	
Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg			
115	120	125	
Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly			
130	135	140	
Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp			
145	150	155	160
Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg			
165	170	175	
His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu			

180					185					190						
His	Pro	Gln	Arg	Ala	Gly	Phe	Arg	Glu	Glu	Arg	Leu	Asn	Thr	Arg	Leu	
195					200					205						
Asn	Glu	Pro	Asp	Leu	Pro	Gly	Asp	Ile	Asp	Ile	Lys	Asp	Leu	Asp	Pro	
210					215					220						
Leu	Val	Leu	Gln	Asp	Leu	Lys	Val	Leu	Ser	Lys	Asp	Asn	Ala	Asp	Ala	
225					230					235					240	
Val	Ala	Lys	His	Met	Ile	Met	Ala	Ala	Thr	Trp	Leu	Ala	Asp	Asp	Pro	
245					250					255						
Gln	Leu	Ala	Leu	Arg	His	Ala	Arg	Ala	Ala	Lys	Asp	Arg	Ala	Gly	Arg	
260					265					270						
Val	Ser	Val	Val	Arg	Glu	Thr	Asn	Gly	Ile	Ala	Ala	Tyr	His	Ala	Gly	
275					280					285						
Glu	Trp	Lys	Glu	Ala	Leu	Ser	Glu	Leu	Arg	Ala	Ala	Arg	Arg	Met	Ser	
290					295					300						
Gly	Gly	Pro	Gly	Leu	Ile	Ala	Val	Met	Ala	Asp	Cys	Glu	Arg	Gly	Leu	
305					310					315					320	
Gly	Arg	Pro	Glu	Lys	Ala	Ile	Glu	Leu	Ala	Arg	Glu	Glu	Asp	Leu	Ser	
325					330					335						
Ser	Leu	Asp	Gln	Asp	Asn	Leu	Ile	Glu	Leu	Ala	Ile	Val	Val	Ala	Gly	
340					345					350						
Ala	Arg	His	Asp	Leu	Gly	Gln	His	Asp	Ser	Ala	Ile	Val	Glu	Leu	Gln	
355					360					365						
Lys	Val	Asn	Pro	Ser	Leu	Lys	Ser	Thr	Gly	Phe	Thr	His	Ser	Arg	Leu	
370					375					380						
Ser	Tyr	Ala	Tyr	Ala	Asp	Ala	Leu	Val	Leu	Ala	Gly	Arg	Gly	Asp	Glu	
385					390					395					400	
Ala	Arg	Glu	Trp	Phe	Gln	His	Ala	Ala	Thr	Leu	Asp	Glu	Asp	Gly	Tyr	
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Leu	Asp	Ala	Glu	Glu	Arg	Ile	Glu	Gln	Leu	Asp	Asn	Gly	Asn	Asn		
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<210> 685

<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1282)

<223> RXN01597

<400> 685

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	Met Ser Leu Phe Asn	
	1 5	
cgc aaa gcc gac ctg ccc ggc ctg caa ggt gcc acc cga atc tgc acc	163	
Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala Thr Arg Ile Cys Thr		
10 15 20		
ccg cag ggc aaa ggg cta aag cgc ctg tcc gaa ggc gat ctc gca atc	211	
Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu Gly Asp Leu Ala Ile		
25 30 35		
att gat gca cca gat cta tcc agg acc ttc gcc caa cga ttg cta gca	259	
Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala Gln Arg Leu Leu Ala		
40 45 50		
gca aaa ccc gcc gca gtc ctc aac gtt tcc cgg ttc acc acc gga tcg	307	
Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg Phe Thr Thr Gly Ser		
55 60 65		
gtg ccc aac ttt gga ccg caa atg ctt atc gac ggc ggc atc cag ctc	355	
Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp Gly Gly Ile Gln Leu		
70 75 80 85		
gtg gaa ggc ttt ggc cag gag ctg ctc gac ggc acc aac gac ggt aag	403	
Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly Thr Lys Asp Gly Lys		
90 95 100		
aaa ggt cgc ctg aca gaa gat gga cag ctc ttc tac ggc gaa cga ctg	451	
Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe Tyr Gly Glu Arg Leu		
105 110 115		
atc tct aac ggc agt gtt ctc agt gga cct gcg gct gaa aat gca ttt	499	
Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala Ala Glu Asn Ala Phe		
120 125 130		
gca gac gcc cag caa tca ctg ctg gac cgc atg gaa gcc tat ttc ggc	547	
Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met Glu Ala Tyr Phe Gly		
135 140 145		
aac acc att cag ttc att cac tca gaa gca ccg ctc ctg atc gat ggc	595	
Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro Leu Leu Ile Asp Gly		
150 155 160 165		
ctc ggc att ccc gat acc gga aat gcc att gaa ggc cgc aaa gtt ctc	643	
Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu Gly Arg Lys Val Leu		
170 175 180		
att gcc tca cca ggg gat aac cac cgc agc agg ctc aaa gaa ctc cgc	691	
Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg Leu Lys Glu Leu Arg		
185 190 195		
agc ttc atc cgc gaa tac gat cca gta ctc atc ggt gtc gat ggg gca	739	
Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile Gly Val Asp Gly Ala		
200 205 210		
gca gac acc ttg gtg gaa ttg ggg tac aag ccc gcg ctg atc gtc ggc	787	
Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro Ala Leu Ile Val Gly		
215 220 225		
aat ccc act ggt atc ggc gca gat gcg ctg cgc agt ggc gcc aac gta	835	

Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg Ser Gly Ala Asn Val
 230 235 240 245
 att ttg cca gct gat cca gac ggc cac gct gtt ggt ctg gag cgc atc 883
 Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val Gly Leu Glu Arg Ile
 250 255 260
 cag gat ctt ggc atc ggt gcg atg acc ttc cca tcc tca gta aat tcc 931
 Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro Ser Ser Val Asn Ser
 265 270 275
 tcc acg gat ctg gcg ctc ctg ctt gcg gat ttc cac aac ccg cag atg 979
 Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe His Asn Pro Gln Met
 280 285 290
 atc gtc aac gtc ggc ggt cct gtc acc ctt gat ggt gtt ttt gaa aac 1027
 Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp Gly Val Phe Glu Asn
 295 300 305
 cga gaa gat tcc gat ccc gcg gcg ctt ttg acg cgc gcc aag cta ggc 1075
 Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr Arg Ala Lys Leu Gly
 310 315 320 325
 acc aag ctt gtc gac gga tcc gtc atc gca agt ctt tac aca gtg cgc 1123
 Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser Leu Tyr Thr Val Arg
 330 335 340
 agc tcc agc aac ctt gga tgg atg tgg gca ctg tta gcc att ttg gtg 1171
 Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu Leu Ala Ile Leu Val
 345 350 355
 gtt ctt gca gtc gtg att gtt atc gct ggc acc gca gga tca ggc tct 1219
 Val Leu Ala Val Val Ile Val Ile Ala Gly Thr Ala Gly Ser Gly Ser
 360 365 370
 ttt acc gac aac ctc att gac acc tgg aac agc ttc gcg ctg aca gtg 1267
 Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser Phe Ala Leu Thr Val
 375 380 385
 cag ggt tgg ttc aaa taggaaggca acatggctaa acg 1305
 Gln Gly Trp Phe Lys
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<210> 686

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

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 20 25 30

Gly Asp Leu Ala Ile Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala
 35 40 45

Gln Arg Leu Leu Ala Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg
 50 55 60

Phe Thr Thr Gly Ser Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp
 65 70 75 80
 Gly Gly Ile Gln Leu Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly
 85 90 95
 Thr Lys Asp Gly Lys Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe
 100 105 110
 Tyr Gly Glu Arg Leu Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala
 115 120 125
 Ala Glu Asn Ala Phe Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met
 130 135 140
 Glu Ala Tyr Phe Gly Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro
 145 150 155 160
 Leu Leu Ile Asp Gly Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu
 165 170 175
 Gly Arg Lys Val Leu Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg
 180 185 190
 Leu Lys Glu Leu Arg Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile
 195 200 205
 Gly Val Asp Gly Ala Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro
 210 215 220
 Ala Leu Ile Val Gly Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg
 225 230 235 240
 Ser Gly Ala Asn Val Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val
 245 250 255
 Gly Leu Glu Arg Ile Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro
 260 265 270
 Ser Ser Val Asn Ser Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe
 275 280 285
 His Asn Pro Gln Met Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp
 290 295 300
 Gly Val Phe Glu Asn Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr
 305 310 315 320
 Arg Ala Lys Leu Gly Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser
 325 330 335
 Leu Tyr Thr Val Arg Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu
 340 345 350
 Leu Ala Ile Leu Val Val Leu Ala Val Val Ile Val Ile Ala Gly Thr
 355 360 365
 Ala Gly Ser Gly Ser Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser
 370 375 380

Phe Ala Leu Thr Val Gln Gly Trp Phe Lys
 385 390

<210> 687
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1282)
 <223> FRXA01597

<400> 687
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 Met Ser Leu Phe Asn
 1 5
 cgc aaa gcc gac ctg ccc ggc ctg caa ggt gcc acc cga atc tgc acc 163
 Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala Thr Arg Ile Cys Thr
 10 15 20
 ccg cag ggc aaa ggg cta aag cgc ctg tcc gaa ggc gat ctc gca atc 211
 Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu Gly Asp Leu Ala Ile
 25 30 35
 att gat gca cca gat cta tcc agg acc ttc gcc caa cga ttg cta gca 259
 Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala Gln Arg Leu Leu Ala
 40 45 50
 gca aaa ccc gcc gca gtc ctc aac gtt tcc cgg ttc acc acc gga tcg 307
 Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg Phe Thr Thr Gly Ser
 55 60 65
 gtg ccc aac ttt gga ccg caa atg ctt atc gac ggc ggc atc cag ctc 355
 Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp Gly Gly Ile Gln Leu
 70 75 80 85
 gtg gaa ggc ttt ggc cag gag ctg ctc gac ggc acc aaa gac ggt aag 403
 Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly Thr Lys Asp Gly Lys
 90 95 100
 aaa ggt cgc ctg aca gaa gat gga cag ctc ttc tac ggc gaa cga ctg 451
 Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe Tyr Gly Glu Arg Leu
 105 110 115
 atc tct aac ggc agt gtt ctc agt gga cct gcg gct gaa aat gca ttt 499
 Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala Ala Glu Asn Ala Phe
 120 125 130
 gca gac gcc cag caa tca ctg ctg gac cgc atg gaa gcc tat ttc ggc 547
 Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met Glu Ala Tyr Phe Gly
 135 140 145
 aac acc att cag ttc att cac tca gaa gca ccg ctc ctg atc gat ggc 595
 Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro Leu Leu Ile Asp Gly
 150 155 160 165

ctc ggc att ccc gat acc gga aat gcc att gaa ggc cgc aaa gtt ctc Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu Gly Arg Lys Val Leu 170 175 180	643
att gcc tca cca ggg gat aac cac cgc agc agg ctc aaa gaa ctc cgc Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg Leu Lys Glu Leu Arg 185 190 195	691
agc ttc atc cgc gaa tac gat cca gta ctc atc ggt gtc gat ggg gca Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile Gly Val Asp Gly Ala 200 205 210	739
gca gac acc ttg gtg gaa ttg ggg tac aag ccc gcg ctg atc gtc ggc Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro Ala Leu Ile Val Gly 215 220 225	787
aat ccc act ggt atc ggc gca gat gcg ctg cgc agt ggc gcc aac gta Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg Ser Gly Ala Asn Val 230 235 240 245	835
att ttg cca gct gat cca gac ggc cac gct gtt ggt ctg gag cgc atc Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val Gly Leu Glu Arg Ile 250 255 260	883
cag gat ctt ggc atc ggt gcg atg acc ttc cca tcc tca gta aat tcc Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro Ser Ser Val Asn Ser 265 270 275	931
tcc acg gat ctg gcg ctc ctg ctt gcg gat ttc cac aac ccg cag atg Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe His Asn Pro Gln Met 280 285 290	979
atc gtc aac gtc ggc ggt cct gtc acc ctt gat ggt gtt ttt gaa aac Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp Gly Val Phe Glu Asn 295 300 305	1027
cga gaa gat tcc gat ccc gcg gcg ctt ttg acg cgc gcc aag cta ggc Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr Arg Ala Lys Leu Gly 310 315 320 325	1075
acc aag ctt gtc gac gga tcc gtc atc gca agt ctt tac aca gtg cgc Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser Leu Tyr Thr Val Arg 330 335 340	1123
agc tcc agc aac ctt gga tgg atg tgg gca ctg tta gcc att ttg gtg Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu Leu Ala Ile Leu Val 345 350 355	1171
gtt ctt gca gtc gtg att gtt atc gct ggc acc gca gga tca ggc tct Val Leu Ala Val Val Ile Val Ile Ala Gly Thr Ala Gly Ser Gly Ser 360 365 370	1219
ttt acc gac aac ctc att gac acc tgg aac agc ttc gcg ctg aca gtg Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser Phe Ala Leu Thr Val 375 380 385	1267
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<210> 688
 <211> 394
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 688
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 Thr Arg Ile Cys Thr Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu
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 Gly Asp Leu Ala Ile Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala
 35 40 45
 Gln Arg Leu Leu Ala Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg
 50 55 60
 Phe Thr Thr Gly Ser Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp
 65 70 75 80
 Gly Gly Ile Gln Leu Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly
 85 90 95
 Thr Lys Asp Gly Lys Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe
 100 105 110
 Tyr Gly Glu Arg Leu Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala
 115 120 125
 Ala Glu Asn Ala Phe Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met
 130 135 140
 Glu Ala Tyr Phe Gly Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro
 145 150 155 160
 Leu Leu Ile Asp Gly Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu
 165 170 175
 Gly Arg Lys Val Leu Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg
 180 185 190
 Leu Lys Glu Leu Arg Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile
 195 200 205
 Gly Val Asp Gly Ala Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro
 210 215 220
 Ala Leu Ile Val Gly Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg
 225 230 235 240
 Ser Gly Ala Asn Val Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val
 245 250 255
 Gly Leu Glu Arg Ile Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro
 260 265 270
 Ser Ser Val Asn Ser Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe
 275 280 285
 His Asn Pro Gln Met Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp

290	295	300
Gly Val Phe Glu Asn Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr		
305	310	315
Arg Ala Lys Leu Gly Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser		
	325	330
Leu Tyr Thr Val Arg Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu		
	340	345
Leu Ala Ile Leu Val Val Leu Ala Val Val Ile Val Ile Ala Gly Thr		
	355	360
Ala Gly Ser Gly Ser Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser		
	370	375
Phe Ala Leu Thr Val Gln Gly Trp Phe Lys		
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<210> 689

<211> 1086

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1063)

<223> RXN01598

<400> 689

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cgcgctgaca gtgcagggtt ggttcaaata ggaaggcaac atg gct aaa cga cgt 115
                                     Met Ala Lys Arg Arg
                                     1 5

gga aga ggc gcc gca acc ttc gcc gca ctg gga ttt ggt gca gca gcc 163
Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly Phe Gly Ala Ala Ala
                        10 15 20

ggc att gcc ttt gga act tat gtg ctt gca ccc aac ctt cct gaa aac 211
Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro Asn Leu Pro Glu Asn
                        25 30 35

att gac cca aat gca cca aca tca gct gaa tta gtc gag gca gag acc 259
Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu Val Glu Ala Glu Thr
                        40 45 50

ttg gct gag gtt aat gcg gtg cag gcc gat caa gca gac agc atc att 307
Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln Ala Asp Ser Ile Ile
                        55 60 65

gac cac atc gtg gaa gac gtg gtg gct ggc aca ctg acc gat cgc ccc 355
Asp His Ile Val Glu Asp Val Val Ala Gly Thr Leu Thr Asp Arg Pro
                        70 75 80 85

gta ctg gtg atg cgc acc gct gac gct gaa gaa tca gac gtt gcc gat 403
Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu Ser Asp Val Ala Asp
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Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile Asn Ala Gly Ser Ile	
105 110 115	
aca ctt gag gag aat ttc ttc tcc caa gac ggc gcg gac cag ctg aaa	499
Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly Ala Asp Gln Leu Lys	
120 125 130	
tca atc gtg gca aat acg ttg cct gca ggc gct cag ctt tct gaa acc	547
Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala Gln Leu Ser Glu Thr	
135 140 145	
caa ctg gat cca gga act cac gct ggc gag gca ctt ggt gcc gct ttg	595
Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala Leu Gly Ala Ala Leu	
150 155 160 165	
ctg ctc aac cct gaa act ggt gaa cca cta gcc agc act gca gag cgc	643
Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala Ser Thr Ala Glu Arg	
170 175 180	
gga cta ttg ctc aac gtg ctg cgc gac aac ggt tac atc tcg tac gaa	691
Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly Tyr Ile Ser Tyr Glu	
185 190 195	
gac ggc acc att ttg cca ggc cag gtc atc gtg atg att act ggc gat	739
Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val Met Ile Thr Gly Asp	
200 205 210	
agc gac ggc tca ggt gat ggt gcc ttc gct gca gaa aca caa tcg ctg	787
Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala Glu Thr Gln Ser Leu	
215 220 225	
ttt gct cgc gca ctt gac gcc caa gga tca ggc gtg gtg gtt gca gga	835
Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly Val Val Val Ala Gly	
230 235 240 245	
cgt att cac act gct gct gat act gga gtt att gga cgg ctt cgt gcc	883
Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile Gly Arg Leu Arg Ala	
250 255 260	
aac cct gat gct gca gaa aac gtc tct aca att gat tcc gtg aat cgt	931
Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile Asp Ser Val Asn Arg	
265 270 275	
act tgg ggc aag atg gct acc gtg cta tca gtt cgt gag gaa cta gcc	979
Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val Arg Glu Glu Leu Ala	
280 285 290	
ggt agg tct gga gcg ttt ggt tcc gct gcc tcc gca gac gcg gca agt	1027
Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser Ala Asp Ala Ala Ser	
295 300 305	
ccg tct ctc gat gga act gca gca gcg cca gcg cag taggttttcc	1073
Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala Gln	
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aagcctttaaa aac	1086

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

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20 25 30

Asn Leu Pro Glu Asn Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu
35 40 45

Val Glu Ala Glu Thr Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln
50 55 60

Ala Asp Ser Ile Ile Asp His Ile Val Glu Asp Val Val Ala Gly Thr
65 70 75 80

Leu Thr Asp Arg Pro Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu
85 90 95

Ser Asp Val Ala Asp Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile
100 105 110

Asn Ala Gly Ser Ile Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly
115 120 125

Ala Asp Gln Leu Lys Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala
130 135 140

Gln Leu Ser Glu Thr Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala
145 150 155 160

Leu Gly Ala Ala Leu Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala
165 170 175

Ser Thr Ala Glu Arg Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly
180 185 190

Tyr Ile Ser Tyr Glu Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val
195 200 205

Met Ile Thr Gly Asp Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala
210 215 220

Glu Thr Gln Ser Leu Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly
225 230 235 240

Val Val Val Ala Gly Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile
245 250 255

Gly Arg Leu Arg Ala Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile
260 265 270

Asp Ser Val Asn Arg Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val
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Arg Glu Glu Leu Ala Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser
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Ala Asp Ala Ala Ser Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala
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Gln

<210> 691
 <211> 1086
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1063)
 <223> FRXA01598

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 Met Ala Lys Arg Arg
 1 5
 gga aga ggc gcc gca acc ttc gcc gca ctg gga ttt ggt gca gca gcc 163
 Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly Phe Gly Ala Ala Ala
 10 15 20
 ggc att gcc ttt gga act tat gtg ctt gca ccc aac ctt cct gaa aac 211
 Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro Asn Leu Pro Glu Asn
 25 30 35
 att gac cca aat gca cca aca tca gct gaa tta gtc gag gca gag acc 259
 Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu Val Glu Ala Glu Thr
 40 45 50
 ttg gct gag gtt aat gcg gtg cag gcc gat caa gca gac agc atc att 307
 Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln Ala Asp Ser Ile Ile
 55 60 65
 gac cac atc gtg gaa gac gtg gtg gct ggc aca ctg acc gat cgc ccc 355
 Asp His Ile Val Glu Asp Val Val Ala Gly Thr Leu Thr Asp Arg Pro
 70 75 80 85
 gta ctg gtg atg cgc acc gct gac gct gaa gaa tca gac gtt gcc gat 403
 Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu Ser Asp Val Ala Asp
 90 95 100
 gtg tca tgg ctg ttg cag caa gca gga gct att aat gct gga tcc att 451
 Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile Asn Ala Gly Ser Ile
 105 110 115
 aca ctt gag gag aat ttc ttc tcc caa gac ggc gcg gac cag ctg aaa 499
 Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly Ala Asp Gln Leu Lys
 120 125 130
 tca atc gtg gca aat acg ttg cct gca ggc gct cag ctt tct gaa acc 547
 Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala Gln Leu Ser Glu Thr
 135 140 145

caa ctg gat cca gga act cac gct ggc gag gca ctt ggt gcc gct ttg 595
 Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala Leu Gly Ala Ala Leu
 150 155 160 165

ctg ctc aac cct gaa act ggt gaa cca cta gcc agc act gca gag cgc 643
 Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala Ser Thr Ala Glu Arg
 170 175 180

gga cta ttg ctc aac gtg ctg cgc gac aac ggt tac atc tcg tac gaa 691
 Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly Tyr Ile Ser Tyr Glu
 185 190 195

gac ggc acc att ttg cca ggc cag gtc atc gtg atg att act ggc gat 739
 Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val Met Ile Thr Gly Asp
 200 205 210

agc gac ggc tca ggt gat ggt gcc ttc gct gca gaa aca caa tcg ctg 787
 Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala Glu Thr Gln Ser Leu
 215 220 225

ttt gct cgc gca ctt gac gcc caa gga tca ggc gtg gtg gtt gca gga 835
 Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly Val Val Val Ala Gly
 230 235 240 245

cgt att cac act gct gct gat act gga gtt att gga cgg ctt cgt gcc 883
 Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile Gly Arg Leu Arg Ala
 250 255 260

aac cct gat gct gca gaa aac gtc tct aca att gat tcc gtg aat cgt 931
 Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile Asp Ser Val Asn Arg
 265 270 275

act tgg ggc aag atg gct acc gtg cta tca gtt cgt gag gaa cta gcc 979
 Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val Arg Glu Glu Leu Ala
 280 285 290

ggt agg tct gga gcg ttt ggt tcc gct gcc tcc gca gac gcg gca agt 1027
 Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser Ala Asp Ala Ala Ser
 295 300 305

ccg tct ctc gat gga act gca gca gcg cca gcg cag taggttttcc 1073
 Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala Gln
 310 315 320

aagcctttaa aac 1086

<210> 692

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 692

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 20 25 30

Asn Leu Pro Glu Asn Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu
 35 40 45

Val Glu Ala Glu Thr Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln
50 55 60

Ala Asp Ser Ile Ile Asp His Ile Val Glu Asp Val Val Ala Gly Thr
65 70 75 80

Leu Thr Asp Arg Pro Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu
85 90 95

Ser Asp Val Ala Asp Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile
100 105 110

Asn Ala Gly Ser Ile Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly
115 120 125

Ala Asp Gln Leu Lys Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala
130 135 140

Gln Leu Ser Glu Thr Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala
145 150 155 160

Leu Gly Ala Ala Leu Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala
165 170 175

Ser Thr Ala Glu Arg Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly
180 185 190

Tyr Ile Ser Tyr Glu Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val
195 200 205

Met Ile Thr Gly Asp Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala
210 215 220

Glu Thr Gln Ser Leu Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly
225 230 235 240

Val Val Val Ala Gly Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile
245 250 255

Gly Arg Leu Arg Ala Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile
260 265 270

Asp Ser Val Asn Arg Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val
275 280 285

Arg Glu Glu Leu Ala Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser
290 295 300

Ala Asp Ala Ala Ser Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala
305 310 315 320

Gln

<210> 693

<211> 507

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(484)

<223> RXN01618

<400> 693

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                                         Met Ile Ile Ile Gly
                                         1 5
gca gtt ttc gcc atc ctc gca gtt cta ctg cat gtt ttc atc ttc tac 163
Ala Val Phe Ala Ile Leu Ala Val Leu Leu His Val Phe Ile Phe Tyr
                        10 15 20
atg gaa tca ttc gca tgg act agt gag aaa gca cgt gga gtt ttc ggc 211
Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala Arg Gly Val Phe Gly
                        25 30 35
acc acc gaa atc gac gcc gaa aac acc aag gag atg gcc tac aac caa 259
Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu Met Ala Tyr Asn Gln
                        40 45 50
ggc ttc tac aac ttc ttc ctg gca gtc atc gcc ggc gtg ggt gtt gcg 307
Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala Gly Val Gly Val Ala
                        55 60 65
ttc ctc ttc gct ggt tca act ggc atc ggc gca gcc ctc gca ctc gct 355
Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala Ala Leu Ala Leu Ala
                        70 75 80 85
ggc acc ggt tcc atg ctg gca gcc gct gca gtg ttg gct ttg agc tca 403
Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val Leu Ala Leu Ser Ser
                        90 95 100
ccc gac aag cgt ggt gca gcc ttc aag caa ggc acg ttc ccg ctg ctc 451
Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly Thr Phe Pro Leu Leu
                        105 110 115
gca gtg gtg ttc ctt gtg att gga ttg ctg gtt taagcagttt tttaaaggaa 504
Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
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ctt 507

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<210> 694

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 694

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      20 25 30
Arg Gly Val Phe Gly Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu
      35 40 45

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Met Ala Tyr Asn Gln Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala
 50 55 60

Gly Val Gly Val Ala Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala
 65 70 75 80

Ala Leu Ala Leu Ala Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val
 85 90 95

Leu Ala Leu Ser Ser Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly
 100 105 110

Thr Phe Pro Leu Leu Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
 115 120 125

<210> 695

<211> 507

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(484)

<223> FRXA01618

<400> 695

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 Met Ile Ile Ile Gly
 1 5

gca gtt ttc gcc atc ctc gca gtt cta ctg cat gtt ttc atc ttc tac 163
 Ala Val Phe Ala Ile Leu Ala Val Leu Leu His Val Phe Ile Phe Tyr
 10 15 20

atg gaa tca ttc gca tgg act agt gag aaa gca cgt gga gtt ttc ggc 211
 Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala Arg Gly Val Phe Gly
 25 30 35

acc acc gaa atc gac gcc gaa aac acc aag gag atg gcc tac aac caa 259
 Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu Met Ala Tyr Asn Gln
 40 45 50

ggc ttc tac aac ttc ttc ctg gca gtc atc gcc ggc gtg ggt gtt gcg 307
 Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala Gly Val Gly Val Ala
 55 60 65

ttc ctc ttc gct ggt tca act ggc atc ggc gca gcc ctc gca ctc gct 355
 Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala Ala Leu Ala Leu Ala
 70 75 80 85

ggc acc ggt tcc atg ctg gca gcc gct gca gtg ttg gct ttg agc tca 403
 Gly Thr Gly Ser Met Leu Ala Ala Ala Val Leu Ala Leu Ser Ser
 90 95 100

ccc gac aag cgt ggt gca gcc ttc aag caa ggc acg ttc ccg ctg ctc 451
 Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly Thr Phe Pro Leu Leu
 105 110 115

gca gtg gtg ttc ctt gtg att gga ttg ctg gtt taagcagttt tttaaaggaa 504
 Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
 120 125

ctt

507

<210> 696
 <211> 128
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 696
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 20 25 30
 Arg Gly Val Phe Gly Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu
 35 40 45
 Met Ala Tyr Asn Gln Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala
 50 55 60
 Gly Val Gly Val Ala Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala
 65 70 75 80
 Ala Leu Ala Leu Ala Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val
 85 90 95
 Leu Ala Leu Ser Ser Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly
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 115 120 125

<210> 697
 <211> 675
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(652)
 <223> RXN01634

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 aacggcgacc acaacggcgc ttgccctcgg tggcacgcac atg gca gtt ggt caa 115
 Met Ala Val Gly Gln
 1 5
 gaa act gat ctg ctc aac gct atg gaa aca ctc gct ggg gtt ccc tca 163
 Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu Ala Gly Val Pro Ser
 10 15 20
 gac ttg gtg gtc act gaa atc ctc ccc gat acc acc agc tat gac aat 211

Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr Thr Ser Tyr Asp Asn
 25 30 35
 ttt gaa ttc ttt gaa gtt cac aac acc ggc agt gca ccc gtg acc att 259
 Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser Ala Pro Val Thr Ile
 40 45 50
 ggg gaa ggg gag tac acc ttc gcc tat tcc ttt gac gat tcc gcc gat 307
 Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe Asp Asp Ser Ala Asp
 55 60 65
 acg tcc cgc gac aag gca ctg gat ctt ggc ggg gaa gtc acg gta gat 355
 Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly Glu Val Thr Val Asp
 70 75 80 85
 gca ggc gaa acc att gtg gtg tgg att gag tac tcc agt tca act gtt 403
 Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr Ser Ser Ser Thr Val
 90 95 100
 gat acc gct gcg ttt agt gag caa gac ttc cgt gat ttc tac ggc atg 451
 Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg Asp Phe Tyr Gly Met
 105 110 115
 gat tcc tca gcc cgc atc ttc cga gca act ggc cag gcg ggt ctc gct 499
 Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly Gln Ala Gly Leu Ala
 120 125 130
 aac ggt ggt gat cgt ggc atc cga gtt ctg tac aat ggt gaa gtt tct 547
 Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr Asn Gly Glu Val Ser
 135 140 145
 ggt tgg tcc cac tac cca tca gat agc gca gcg gtt caa aag gga att 595
 Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala Val Gln Lys Gly Ile
 150 155 160 165
 gac ttc gcg ctg cca aaa gta ggg gag cag gcc agc att gca agt gcg 643
 Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala Ser Ile Ala Ser Ala
 170 175 180
 cac caa aac tgatccaact ccaggatcaa tta 675
 His Gln Asn

<210> 698

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 698

Met Ala Val Gly Gln Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu
 1 5 10 15
 Ala Gly Val Pro Ser Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr
 20 25 30
 Thr Ser Tyr Asp Asn Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser
 35 40 45
 Ala Pro Val Thr Ile Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe
 50 55 60

Asp Asp Ser Ala Asp Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly
 65 70 75 80
 Glu Val Thr Val Asp Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr
 85 90 95
 Ser Ser Ser Thr Val Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg
 100 105 110
 Asp Phe Tyr Gly Met Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly
 115 120 125
 Gln Ala Gly Leu Ala Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr
 130 135 140
 Asn Gly Glu Val Ser Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala
 145 150 155 160
 Val Gln Lys Gly Ile Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala
 165 170 175
 Ser Ile Ala Ser Ala His Gln Asn
 180

<210> 699
 <211> 675
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(652)
 <223> FRXA01634

<400> 699
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 aacggcgacc acaacggcgc ttgccctcgg tggcacgcac atg gca gtt ggt caa 115
 Met Ala Val Gly Gln
 1 5
 gaa act gat ctg ctc aac gct atg gaa aca ctc gct ggg gtt ccc tca 163
 Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu Ala Gly Val Pro Ser
 10 15 20
 gac ttg gtg gtc act gaa atc ctc ccc gat acc acc agc tat gac aat 211
 Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr Thr Ser Tyr Asp Asn
 25 30 35
 ttt gaa ttc ttt gaa gtt cac aac acc ggc agt gca ccc gtg acc att 259
 Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser Ala Pro Val Thr Ile
 40 45 50
 ggg gaa ggg gag tac acc ttc gcc tat tcc ttt gac gat tcc gcc gat 307
 Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe Asp Asp Ser Ala Asp
 55 60 65
 acg tcc cgc gac aag gca ctg gat ctt ggc ggg gaa gtc acg gta gat 355
 Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly Glu Val Thr Val Asp

70	75	80	85	
gca ggc gaa acc att gtg gtg tgg att gag tac tcc agt tca act gtt				403
Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr Ser Ser Ser Thr Val				
	90	95	100	
gat acc gct gcg ttt agt gag caa gac ttc cgt gat ttc tac ggc atg				451
Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg Asp Phe Tyr Gly Met				
	105	110	115	
gat tcc tca gcc cgc atc ttc cga gca act ggc cag gcg ggt ctc gct				499
Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly Gln Ala Gly Leu Ala				
	120	125	130	
aac ggt ggt gat cgt ggc atc cga gtt ctg tac aat ggt gaa gtt tct				547
Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr Asn Gly Glu Val Ser				
	135	140	145	
ggt tgg tcc cac tac cca tca gat agc gca gcg gtt caa aag gga att				595
Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala Val Gln Lys Gly Ile				
	150	155	160	165
gac ttc gcg ctg cca aaa gta ggg gag cag gcc agc att gca agt gcg				643
Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala Ser Ile Ala Ser Ala				
	170	175	180	
cac caa aac tgatccaact ccaggatcaa tta				675
His Gln Asn				

<210> 700

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

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Ala	Gly	Val	Pro	Ser	Asp	Leu	Val	Val	Thr	Glu	Ile	Leu	Pro	Asp	Thr
		20					25						30		

Thr	Ser	Tyr	Asp	Asn	Phe	Glu	Phe	Phe	Glu	Val	His	Asn	Thr	Gly	Ser
		35					40					45			

Ala	Pro	Val	Thr	Ile	Gly	Glu	Gly	Glu	Tyr	Thr	Phe	Ala	Tyr	Ser	Phe
	50					55					60				

Asp	Asp	Ser	Ala	Asp	Thr	Ser	Arg	Asp	Lys	Ala	Leu	Asp	Leu	Gly	Gly
65					70					75				80	

Glu	Val	Thr	Val	Asp	Ala	Gly	Glu	Thr	Ile	Val	Val	Trp	Ile	Glu	Tyr
				85					90					95	

Ser	Ser	Ser	Thr	Val	Asp	Thr	Ala	Ala	Phe	Ser	Glu	Gln	Asp	Phe	Arg
			100					105					110		

Asp	Phe	Tyr	Gly	Met	Asp	Ser	Ser	Ala	Arg	Ile	Phe	Arg	Ala	Thr	Gly
		115					120					125			

Gln Ala Gly Leu Ala Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr
 130 135 140

Asn Gly Glu Val Ser Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala
 145 150 155 160

Val Gln Lys Gly Ile Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala
 165 170 175

Ser Ile Ala Ser Ala His Gln Asn
 180

<210> 701

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> RXN01635

<400> 701

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aaaactgatc caactccagg atcaattact tctgatcaag ttg att cct ggc gga 115
 Leu Ile Pro Gly Gly
 1 5

ttg gac act cca gaa gag cct gaa gcc cct gaa gac tct ctt ttt gaa 163
 Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu Asp Ser Leu Phe Glu
 10 15 20

ggg cgc act ccc cct agg gat gca agc acc cgc ttg atc ctc act gaa 211
 Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg Leu Ile Leu Thr Glu
 25 30 35

cta atg gtc aac tcc acc aac atg ggc agt tct gat ggt ttt gag tat 259
 Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser Asp Gly Phe Glu Tyr
 40 45 50

gtg gaa atc acc aac act act gcc gaa ccc atc gat ttt tcc gat tac 307
 Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile Asp Phe Ser Asp Tyr
 55 60 65

acc ttg aac tac ctg tac ccg cag gat gag ttc acc aac acc aac gaa 355
 Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe Thr Asn Thr Asn Glu
 70 75 80 85

gcc gtc tgg gct gcg gaa cct ggt gat gtc att att cag cct gga aaa 403
 Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile Ile Gln Pro Gly Lys
 90 95 100

tct ctc gtg ttt tgg atc aaa aat ggc ccc aat gat gag gca acc gca 451
 Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn Asp Glu Ala Thr Ala
 105 110 115

gca gat ttc aat gca gaa tat ggc acc aac ctg gag gct gga aaa gac 499
 Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu Glu Ala Gly Lys Asp
 120 125 130

ctt gtt gaa atc tcc tca ggt ggg atg gcc aat ggt act gcc aga gga 547
 Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn Gly Thr Ala Arg Gly
 135 140 145

 atg cag att cag acc aac act ggc cac ata gtc aac cgt ggt ttc tac 595
 Met Gln Ile Gln Thr Asn Thr Gly His Ile Val Asn Arg Gly Phe Tyr
 150 155 160 165

 aac atg gct ggc gct tct gat gtg aaa gcc aac gag ggt ctt cat ttc 643
 Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn Glu Gly Leu His Phe
 170 175 180

 gca gtg gat gag tct gat ctt ctg aag caa acg ctt gtc ggc agc ggt 691
 Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr Leu Val Gly Ser Gly
 185 190 195

 gcg cca acc ccg ggc act gtg tac act tcg cag att cct aat cca ctg 739
 Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln Ile Pro Asn Pro Leu
 200 205 210

 tct gcc gtt atc gct gat tct tct gta cca ctc atc aca gat aat acc 787
 Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu Ile Thr Asp Asn Thr
 215 220 225

 gca acc agt atc aac cct gcg gag ccg ttt acc ttc gcc ttc aaa tat 835
 Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr Phe Ala Phe Lys Tyr
 230 235 240 245

 cac cga tgatgtccag gtgcgcacgg caa 864
 His Arg

<210> 702
 <211> 247
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 702
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 20 25 30

 Leu Ile Leu Thr Glu Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser
 35 40 45

 Asp Gly Phe Glu Tyr Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile
 50 55 60

 Asp Phe Ser Asp Tyr Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe
 65 70 75 80

 Thr Asn Thr Asn Glu Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile
 85 90 95

 Ile Gln Pro Gly Lys Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn
 100 105 110

Asp Glu Ala Thr Ala Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu
 115 120 125
 Glu Ala Gly Lys Asp Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn
 130 135 140
 Gly Thr Ala Arg Gly Met Gln Ile Gln Thr Asn Thr Gly His Ile Val
 145 150 155 160
 Asn Arg Gly Phe Tyr Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn
 165 170 175
 Glu Gly Leu His Phe Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr
 180 185 190
 Leu Val Gly Ser Gly Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln
 195 200 205
 Ile Pro Asn Pro Leu Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu
 210 215 220
 Ile Thr Asp Asn Thr Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr
 225 230 235 240
 Phe Ala Phe Lys Tyr His Arg
 245

<210> 703

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> FRXA01635

<400> 703

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 aaaactgatc caactccagg atcaattact tctgatcaag ttg att cct ggc gga 115
 Leu Ile Pro Gly Gly
 1 5

 ttg gac act cca gaa gag cct gaa gcc cct gaa gac tct ctt ttt gaa 163
 Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu Asp Ser Leu Phe Glu
 10 15 20

 ggg cgc act ccc cct agg gat gca agc acc cgc ttg atc ctc act gaa 211
 Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg Leu Ile Leu Thr Glu
 25 30 35

 cta atg gtc aac tcc acc aac atg ggc agt tct gat ggt ttt gag tat 259
 Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser Asp Gly Phe Glu Tyr
 40 45 50

 gtg gaa atc acc aac act act gcc gaa ccc atc gat ttt tcc gat tac 307
 Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile Asp Phe Ser Asp Tyr
 55 60 65

acc ttg aac tac ctg tac ccg cag gat gag ttc acc aac acc aac gaa 355
 Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe Thr Asn Thr Asn Glu
 70 75 80 85

 gcc gtc tgg gct gcg gaa cct ggt gat gtc att att cag cct gga aaa 403
 Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile Ile Gln Pro Gly Lys
 90 95 100

 tct ctc gtg ttt tgg atc aaa aat ggc ccc aat gat gag gca acc gca 451
 Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn Asp Glu Ala Thr Ala
 105 110 115

 gca gat ttc aat gca gaa tat ggc acc aac ctg gag gct gga aaa gac 499
 Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu Glu Ala Gly Lys Asp
 120 125 130

 ctt gtt gaa atc tcc tca ggt ggg atg gcc aat ggt act gcc aga gga 547
 Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn Gly Thr Ala Arg Gly
 135 140 145

 atg cag att cag acc aac act ggc cac ata gtc aac cgt ggt ttc tac 595
 Met Gln Ile Gln Thr Asn Thr Gly His Ile Val Asn Arg Gly Phe Tyr
 150 155 160 165

 aac atg gct ggc gct tct gat gtg aaa gcc aac gag ggt ctt cat ttc 643
 Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn Glu Gly Leu His Phe
 170 175 180

 gca gtg gat gag tct gat ctt ctg aag caa acg ctt gtc ggc agc ggt 691
 Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr Leu Val Gly Ser Gly
 185 190 195

 gcg cca acc ccg ggc act gtg tac act tcg cag att cct aat cca ctg 739
 Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln Ile Pro Asn Pro Leu
 200 205 210

 tct gcc gtt atc gct gat tct tct gta cca ctc atc aca gat aat acc 787
 Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu Ile Thr Asp Asn Thr
 215 220 225

 gca acc agt atc aac cct gcg gag ccg ttt acc ttc gcc ttc aaa tat 835
 Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr Phe Ala Phe Lys Tyr
 230 235 240 245

 cac cga tgatgtccag gtgcgcacgg caa 864
 His Arg

<210> 704

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 704

Leu Ile Pro Gly Gly Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu
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Asp Ser Leu Phe Glu Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg
 20 25 30

Leu Ile Leu Thr Glu Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser
 35 40 45
 Asp Gly Phe Glu Tyr Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile
 50 55 60
 Asp Phe Ser Asp Tyr Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe
 65 70 75 80
 Thr Asn Thr Asn Glu Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile
 85 90 95
 Ile Gln Pro Gly Lys Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn
 100 105 110
 Asp Glu Ala Thr Ala Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu
 115 120 125
 Glu Ala Gly Lys Asp Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn
 130 135 140
 Gly Thr Ala Arg Gly Met Gln Ile Gln Thr Asn Thr Gly His Ile Val
 145 150 155 160
 Asn Arg Gly Phe Tyr Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn
 165 170 175
 Glu Gly Leu His Phe Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr
 180 185 190
 Leu Val Gly Ser Gly Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln
 195 200 205
 Ile Pro Asn Pro Leu Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu
 210 215 220
 Ile Thr Asp Asn Thr Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr
 225 230 235 240
 Phe Ala Phe Lys Tyr His Arg
 245

<210> 705
 <211> 1293
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1270)
 <223> RXN01647

<400> 705
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 gcataaattt ctggtgcggc gcatcgaaca tgggttggtg atg ggc gat gtg cgc 115
 Met Gly Asp Val Arg
 1 5
 atg att cat gat cca ctt ggt agg cgc cgg cgg gcg ttg gtg ttt ggg 163

Met	Ile	His	Asp	Pro	Leu	Gly	Arg	Arg	Arg	Arg	Ala	Leu	Val	Phe	Gly			
				10					15					20				
gtg	gtg	gcg	tgc	gtg	atg	ttg	gcg	gtg	gga	tca	ttg	gcg	ttg	gct	att		211	
Val	Val	Ala	Cys	Val	Met	Leu	Ala	Val	Gly	Ser	Leu	Ala	Leu	Ala	Ile			
			25					30					35					
ttt	cga	ccc	gcg	aag	gat	ccg	gcc	gat	gcg	ccg	ttg	atc	cgc	tct	gaa		259	
Phe	Arg	Pro	Ala	Lys	Asp	Pro	Ala	Asp	Ala	Pro	Leu	Ile	Arg	Ser	Glu			
		40					45					50						
tcc	ggc	gcg	ctc	ttt	gtg	cag	ctg	gat	ggg	tgc	gtg	cat	ccg	gtg	gct		307	
Ser	Gly	Ala	Leu	Phe	Val	Gln	Leu	Asp	Gly	Ser	Val	His	Pro	Val	Ala			
	55					60					65							
aat	gtg	gcc	tgc	gct	cgg	ttg	att	gtg	ggg	gag	ccg	gtg	gat	ccg	gtg		355	
Asn	Val	Ala	Ser	Ala	Arg	Leu	Ile	Val	Gly	Glu	Pro	Val	Asp	Pro	Val			
70					75				80						85			
aac	gcc	agc	gat	gcg	atc	atc	gcg	ggc	atg	ccg	cgc	gga	gtg	ccg	gtg		403	
Asn	Ala	Ser	Asp	Ala	Ile	Ile	Ala	Gly	Met	Pro	Arg	Gly	Val	Pro	Val			
				90				95					100					
ggg	gtt	cct	gat	gcg	ccg	ggg	ctt	ttc	agc	agc	acc	gaa	gaa	ccc	gag		451	
Gly	Val	Pro	Asp	Ala	Pro	Gly	Leu	Phe	Ser	Ser	Thr	Glu	Glu	Pro	Glu			
			105				110						115					
caa	gat	tgg	ttt	gtg	tgc	cag	gat	gtc	ggc	act	ggg	gat	cta	cac	att		499	
Gln	Asp	Trp	Phe	Val	Cys	Gln	Asp	Val	Gly	Thr	Gly	Asp	Leu	His	Ile			
		120					125					130						
acg	gtt	cct	agg	ggc	gga	cta	ggg	ccc	acc	ctg	att	gcg	gaa	gga	aat		547	
Thr	Val	Pro	Arg	Gly	Gly	Leu	Gly	Pro	Thr	Leu	Ile	Ala	Glu	Gly	Asn			
	135					140					145							
ggg	tgg	ctg	ggg	gcg	tgc	aaa	agc	gaa	acc	ggc	gag	gtc	acc	tgg	aac		595	
Gly	Trp	Leu	Gly	Ala	Ser	Lys	Ser	Glu	Thr	Gly	Glu	Val	Thr	Trp	Asn			
150					155					160					165			
ctg	att	acc	gcg	gac	ggg	cgc	cgc	gaa	ctg	ccg	gcg	tgg	ggc	agc	gaa		643	
Leu	Ile	Thr	Ala	Asp	Gly	Arg	Arg	Glu	Leu	Pro	Ala	Trp	Gly	Ser	Glu			
				170				175						180				
cat	ggg	cgc	att	atg	cgc	cgc	cac	ctg	ggg	att	tcc	gag	gac	acc	ccg		691	
His	Gly	Arg	Ile	Met	Arg	Arg	His	Leu	Gly	Ile	Ser	Glu	Asp	Thr	Pro			
			185					190					195					
cgc	gta	tac	ctg	acc	act	gag	ctg	ctc	aac	gcg	atc	ccc	gag	cac	gac		739	
Arg	Val	Tyr	Leu	Thr	Thr	Glu	Leu	Leu	Asn	Ala	Ile	Pro	Glu	His	Asp			
		200					205					210						
gcg	gtc	cgc	ttc	cca	gcc	ccg	ctg	ccc	gag	ctt	gtc	gac	gcc	tcc	acc		787	
Ala	Val	Arg	Phe	Pro	Ala	Pro	Leu	Pro	Glu	Leu	Val	Asp	Ala	Ser	Thr			
	215					220					225							
cgc	aac	tgg	tta	cgg	ctc	gac	ggg	gcg	ctc	gcc	gaa	atc	acg	ccg	cta		835	
Arg	Asn	Trp	Leu	Arg	Leu	Asp	Gly	Ala	Leu	Ala	Glu	Ile	Thr	Pro	Leu			
230					235					240					245			
cag	cgc	ggg	ttg	ctt	atc	gac	gcc	ggt	tcc	ggt	gtt	ttc	ccc	gac	ccc		883	
Gln	Arg	Gly	Leu	Leu	Ile	Asp	Ala	Gly	Ser	Gly	Val	Phe	Pro	Asp	Pro			

250	255	260	
acc gcg ctt ctt ggt gtg cat gaa gaa	aca gcc aac acc ttg acg ctg	931	
Thr Ala Leu Leu Gly Val His Glu Glu	Thr Ala Asn Thr Leu Thr Leu		
265	270 275		
ccc gag caa aca gtt tct tgg caa gat	ctg gac ggt ggt ttt gcc tgc	979	
Pro Glu Gln Thr Val Ser Trp Gln Asp	Leu Asp Gly Gly Phe Ala Cys		
280	285 290		
gcg gat ggt gaa ggc cag atc ggt ttc	ctg gaa act ctg gaa tcg ggg	1027	
Ala Asp Gly Glu Gly Gln Ile Gly Phe	Leu Glu Thr Leu Glu Ser Gly		
295	300 305		
gtg gcg cta tct ggt gat tcc agg gcg	aaa agt ttc agc aca aac gct	1075	
Val Ala Leu Ser Gly Asp Ser Arg Ala	Lys Ser Phe Ser Thr Asn Ala		
310	315 320 325		
ggg gca gtg ggc gtg gac agt ggc ttt	ggc tac tat gtg gtc tct	1123	
Gly Gly Ala Val Gly Val Asp Ser Gly	Phe Gly Tyr Tyr Val Val Ser		
330	335 340		
gat ttt ggg ctg atg cac cct gtt tct	act ggt gaa tcg atg gtt gcc	1171	
Asp Phe Gly Leu Met His Pro Val Ser	Thr Gly Glu Ser Met Val Ala		
345	350 355		
cta gga atc act gac gtg cag gtc gtg	ccg tgg agc gtg ctg cga ttg	1219	
Leu Gly Ile Thr Asp Val Gln Val Val	Pro Trp Ser Val Leu Arg Leu		
360	365 370		
ttg ccg cag gga agt gaa tta gca aaa	gag aca gcg ctg gcg ccc acc	1267	
Leu Pro Gln Gly Ser Glu Leu Ala Lys	Glu Thr Ala Leu Ala Pro Thr		
375	380 385		
tat taaggagtat ggtggcctta cat		1293	
Tyr			
390			

<210> 706
 <211> 390
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 706
 Met Gly Asp Val Arg Met Ile His Asp Pro Leu Gly Arg Arg Arg Arg
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 20 25 30
 Leu Ala Leu Ala Ile Phe Arg Pro Ala Lys Asp Pro Ala Asp Ala Pro
 35 40 45
 Leu Ile Arg Ser Glu Ser Gly Ala Leu Phe Val Gln Leu Asp Gly Ser
 50 55 60
 Val His Pro Val Ala Asn Val Ala Ser Ala Arg Leu Ile Val Gly Glu
 65 70 75 80
 Pro Val Asp Pro Val Asn Ala Ser Asp Ala Ile Ile Ala Gly Met Pro

85	90	95
Arg Gly Val Pro Val Gly Val Pro	Asp Ala Pro Gly Leu Phe Ser Ser	
100	105	110
Thr Glu Glu Pro Glu Gln Asp Trp	Phe Val Cys Gln Asp Val Gly Thr	
115	120	125
Gly Asp Leu His Ile Thr Val Pro	Arg Gly Gly Leu Gly Pro Thr Leu	
130	135	140
Ile Ala Glu Gly Asn Gly Trp Leu	Gly Ala Ser Lys Ser Glu Thr Gly	
145	150	155
Glu Val Thr Trp Asn Leu Ile Thr	Ala Asp Gly Arg Arg Glu Leu Pro	
165	170	175
Ala Trp Gly Ser Glu His Gly Arg	Ile Met Arg Arg His Leu Gly Ile	
180	185	190
Ser Glu Asp Thr Pro Arg Val Tyr	Leu Thr Thr Glu Leu Leu Asn Ala	
195	200	205
Ile Pro Glu His Asp Ala Val Arg	Phe Pro Ala Pro Leu Pro Glu Leu	
210	215	220
Val Asp Ala Ser Thr Arg Asn Trp	Leu Arg Leu Asp Gly Ala Leu Ala	
225	230	235
Glu Ile Thr Pro Leu Gln Arg Gly	Leu Leu Ile Asp Ala Gly Ser Gly	
245	250	255
Val Phe Pro Asp Pro Thr Ala Leu	Leu Gly Val His Glu Glu Thr Ala	
260	265	270
Asn Thr Leu Thr Leu Pro Glu Gln	Thr Val Ser Trp Gln Asp Leu Asp	
275	280	285
Gly Gly Phe Ala Cys Ala Asp Gly	Glu Gly Gln Ile Gly Phe Leu Glu	
290	295	300
Thr Leu Glu Ser Gly Val Ala Leu	Ser Gly Asp Ser Arg Ala Lys Ser	
305	310	315
Phe Ser Thr Asn Ala Gly Gly Ala	Val Gly Val Asp Ser Gly Phe Gly	
325	330	335
Tyr Tyr Val Val Ser Asp Phe Gly	Leu Met His Pro Val Ser Thr Gly	
340	345	350
Glu Ser Met Val Ala Leu Gly Ile	Thr Asp Val Gln Val Val Pro Trp	
355	360	365
Ser Val Leu Arg Leu Leu Pro Gln	Gly Ser Glu Leu Ala Lys Glu Thr	
370	375	380
Ala Leu Ala Pro Thr Tyr		
385	390	

<210> 707

<211> 911
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(888)
 <223> FRXA01647

<400> 707
 atg ccg cgc gga gtg ccg gtg ggg gtt cct gat gcg ccg ggg ctt ttc 48
 Met Pro Arg Gly Val Pro Val Gly Val Pro Asp Ala Pro Gly Leu Phe
 1 5 10 15
 agc agc acc gaa gaa ccc gag caa gat tgg ttt gtg tgc cag gat gtc 96
 Ser Ser Thr Glu Glu Pro Glu Gln Asp Trp Phe Val Cys Gln Asp Val
 20 25 30
 ggc act ggg gat cta cac att acg gtt cct agg ggc gga cta ggg ccc 144
 Gly Thr Gly Asp Leu His Ile Thr Val Pro Arg Gly Gly Leu Gly Pro
 35 40 45
 acc ctg att gcg gaa gga aat ggg tgg ctg ggg gcg tcg aaa agc gaa 192
 Thr Leu Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu
 50 55 60
 acc ggc gag gtc acc tgg aac ctg att acc gcg gac ggg cgc cgc gaa 240
 Thr Gly Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu
 65 70 75 80
 ctg ccg gcg tgg ggc agc gaa cat ggg cgc att atg cgc cgc cac ctg 288
 Leu Pro Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu
 85 90 95
 ggg att tcc gag gac acc ccg cgc gta tac ctg acc act gag ctg ctc 336
 Gly Ile Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu
 100 105 110
 aac gcg atc ccc gag cac gac gcg gtc cgc ttc cca gcc ccg ctg ccc 384
 Asn Ala Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro
 115 120 125
 gag ctt gtc gac gcc tcc acc cgc aac tgg tta cgg ctc gac ggg gcg 432
 Glu Leu Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala
 130 135 140
 ctc gcc gaa atc acg ccg cta cag cgc ggg ttg ctt atc gac gcc ggt 480
 Leu Ala Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly
 145 150 155 160
 tcc ggt gtt ttc ccc gac ccc acc gcg ctt ctt ggt gtg cat gaa gaa 528
 Ser Gly Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu
 165 170 175
 aca gcc aac acc ttg acg ctg ccc gag caa aca gtt tct tgg caa gat 576
 Thr Ala Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp
 180 185 190
 ctg gac ggt ggt ttt gcc tgc gcg gat ggt gaa ggc cag atc ggt ttc 624
 Leu Asp Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe
 195 200 205

ctg gaa act ctg gaa tcg ggg gtg gcg cta tct ggt gat tcc agg gcg 672
 Leu Glu Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala
 210 215 220

aaa agt ttc agc aca aac gct ggt ggg gca gtg ggc gtg gac agt ggc 720
 Lys Ser Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly
 225 230 235 240

ttt ggc tac tat gtg gtc tct gat ttt ggg ctg atg cac cct gtt tct 768
 Phe Gly Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser
 245 250 255

act ggt gaa tcg atg gtt gcc cta gga atc act gac gtg cag gtc gtg 816
 Thr Gly Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val
 260 265 270

ccg tgg agc gtg ctg cga ttg ttg ccg cag gga agt gaa tta gca aaa 864
 Pro Trp Ser Val Leu Arg Leu Leu Pro Gln Gly Ser Glu Leu Ala Lys
 275 280 285

gag aca gcg ctc gcg ccc acc tat taaggagtat ggtggcctta cat 911
 Glu Thr Ala Leu Ala Pro Thr Tyr
 290 295

<210> 708

<211> 296

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

Met Pro Arg Gly Val Pro Val Gly Val Pro Asp Ala Pro Gly Leu Phe
 1 5 10 15

Ser Ser Thr Glu Glu Pro Glu Gln Asp Trp Phe Val Cys Gln Asp Val
 20 25 30

Gly Thr Gly Asp Leu His Ile Thr Val Pro Arg Gly Gly Leu Gly Pro
 35 40 45

Thr Leu Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu
 50 55 60

Thr Gly Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu
 65 70 75 80

Leu Pro Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu
 85 90 95

Gly Ile Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu
 100 105 110

Asn Ala Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro
 115 120 125

Glu Leu Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala
 130 135 140

Leu Ala Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly
 145 150 155 160

Ser Gly Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu
 165 170 175

Thr Ala Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp
 180 185 190

Leu Asp Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe
 195 200 205

Leu Glu Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala
 210 215 220

Lys Ser Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly
 225 230 235 240

Phe Gly Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser
 245 250 255

Thr Gly Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val
 260 265 270

Pro Trp Ser Val Leu Arg Leu Leu Pro Gln Gly Ser Glu Leu Ala Lys
 275 280 285

Glu Thr Ala Leu Ala Pro Thr Tyr
 290 295

<210> 709
 <211> 1856
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1833)
 <223> RXN01658

<400> 709
 gat cca cag atc ctg tca cca acc ttc acc cag caa cag cag ctg cga 48
 Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
 1 5 10 15

aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta 96
 Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
 20 25 30

gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca 144
 Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
 35 40 45

aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt 192
 Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
 50 55 60

tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat 240
 Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65 70 75 80

gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac 288

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr	85	90	95	
acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat				336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp	100	105	110	
gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga				384
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly	115	120	125	
cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt				432
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly	130	135	140	
gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac				480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr	145	150	155	160
acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt				528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg	165	170	175	
gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat				576
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp	180	185	190	
cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc				624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser	195	200	205	
cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac				672
Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr	210	215	220	
cca act gtg att gat ggt cgc atc aag tgg atc gtc gat ggc tac acc				720
Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr	225	230	235	240
acc ttg gat agt ctt ccg tac tcc acg cgc acc tca ctg acg gaa gcg				768
Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala	245	250	255	
act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca				816
Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr	260	265	270	
gat agg gtc ggt tac atc cgc aac tcc gtg aag gct gtt gtt gat gcg				864
Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala	275	280	285	
tac gac gga act gtt gaa ctc tac gaa ttc gac acc gaa gat cct gtt				912
Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val	290	295	300	
ctg aag gca tgg cgt ggc gtg ttc cca gac acc gtg aag gac ggg tcg				960
Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser	305	310	315	320
gag att tcc gat gag ctt cgc gca cac ctg cgt tac cca gaa gat ttg				1008
Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu				

325	330	335	
ttc aag gtc cag cgt gac atg ctg gcc aag tac aac gtt gat gat tct Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser 340 345 350			1056
gga aca ttc ttc acc aac gat gcg ttc tgg tct gtc cca ggt gac cca Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro 355 360 365			1104
act gca gcg gag ggc cgc cag gaa ctt aag cag cct cct tac tac gtg Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val 370 375 380			1152
gtg gca gca gac cca gag acc ggt gag tcc agc ttc cag ctg atc acc Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr 385 390 395 400			1200
ccg ttc cgt gga ctt cag cgc gag tac ctc tct gca cac atg tct gcg Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala 405 410 415			1248
tcg tct gat cca gtt acc tac ggt gaa atc act gtt cgt gtg ctg cct Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro 420 425 430			1296
acc gat tct gtg acc cag ggt cca aag cag gcc cag gat gcg atg atg Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met 435 440 445			1344
tca tct gac cag gtt gct cag gac caa aca ctg tgg cgt gga tcg aac Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn 450 455 460			1392
gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu 465 470 475 480			1440
atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca tcg Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser 485 490 495			1488
gcc ttc ccg aag ctt ctg cgc gtg ctg gtc ttc tac aag ggt cag gtt Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val 500 505 510			1536
ggt tac gca cca acg atc gct gaa gcc cta tcg cag gtc ggc att gat Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp 515 520 525			1584
ccg aag gaa gcg cag gac atc gaa gag gta gat ggc acc gct acg acg Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr 530 535 540			1632
cca tcg act gat gag act gac act gac act gat cag cct gca acc gaa Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu 545 550 555 560			1680
acc cca act gca cca gtg agt gag gcg gaa gga atc gcg gcc atc aac Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn 565 570 575			1728

gat gcg ttg agc aac ctt gaa gct gct cgc gat agc tct ttc gaa gag 1776
Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
580 585 590

tat ggt cgt gca ctc gat gcg ctt gat cgt gcc gtc gat agc tac cag 1824
Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
595 600 605

tcc gca cag tagcgtttga gtaaacagcc cga 1856
Ser Ala Gln
610

<210> 710

<211> 611

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
1 5 10 15

Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
20 25 30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
35 40 45

Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
50 55 60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
65 70 75 80

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
85 90 95

Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
100 105 110

Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
115 120 125

Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
130 135 140

Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145 150 155 160

Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
165 170 175

Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
180 185 190

Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
195 200 205

Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
210 215 220

Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
 225 230 235 240
 Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
 245 250 255
 Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
 260 265 270
 Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
 275 280 285
 Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
 290 295 300
 Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
 305 310 315 320
 Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
 325 330 335
 Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
 340 345 350
 Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
 355 360 365
 Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
 370 375 380
 Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
 385 390 395 400
 Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
 405 410 415
 Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
 420 425 430
 Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
 435 440 445
 Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
 450 455 460
 Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
 465 470 475 480
 Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
 485 490 495
 Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
 500 505 510
 Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
 515 520 525
 Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
 530 535 540

Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
 545 550 555 560

Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
 565 570 575

Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
 580 585 590

Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
 595 600 605

Ser Ala Gln
 610

<210> 711
 <211> 1485
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1485)
 <223> FRXA01658

<400> 711
 gat cca cag atc ctg tca cca acc ttc acc cag caa cag cag ctg cga 48
 Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
 1 5 10 15

aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta 96
 Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
 20 25 30

gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca 144
 Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
 35 40 45

aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt 192
 Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
 50 55 60

tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat 240
 Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65 70 75 80

gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac 288
 Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
 85 90 95

acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat 336
 Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
 100 105 110

gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga 384
 Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
 115 120 125

cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt 432
 Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly

130	135	140	
gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr 145 150 155 160			480
acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg 165 170 175			528
gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp 180 185 190			576
cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser 195 200 205			624
cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr 210 215 220			672
cca act gtg att gat ggt cgc atc aag tgg atc gtc gat ggc tac acc Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr 225 230 235 240			720
acc ttg gat agt ctt ccg tac tcc acg cgc acc tca ctg acg gaa gcg Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala 245 250 255			768
act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr 260 265 270			816
gat agg gtc ggt tac atc cgc aac tcc gtg aag gct gtt gtt gat gcg Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala 275 280 285			864
tac gac gga act gtt gaa ctc tac gaa ttc gac acc gaa gat cct gtt Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val 290 295 300			912
ctg aag gca tgg cgt ggc gtg ttc cca gac acc gtg aag gac ggg tcg Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser 305 310 315 320			960
gag att tcc gat gag ctt cgc gca cac ctg cgt tac cca gaa gat ttg Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu 325 330 335			1008
ttc aag gtc cag cgt gac atg ctg gcc aag tac aac gtt gat gat tct Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser 340 345 350			1056
gga aca ttc ttc acc aac gat gcg ttc tgg tct gtc cca ggt gac cca Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro 355 360 365			1104
act gca gcg gag ggc cgc cag gaa ctt aag cag cct cct tac tac gtg Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val 370 375 380			1152

gtg gca gca gac cca gag acc ggt gag tcc agc ttc cag ctg atc acc 1200
 Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
 385 390 395 400

ccg ttc cgt gga ctt cag cgc gag tac ctc tct gca cac atg tct gcg 1248
 Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
 405 410 415

tcg tct gat cca gtt acc tac ggt gaa atc act gtt cgt gtg ctg cct 1296
 Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
 420 425 430

acc gat tct gtg acc cag ggt cca aag cag gcc cag gat gcg atg atg 1344
 Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
 435 440 445

tca tct gac cag gtt gct cag gac caa aca ctg tgg cgt gga tcg aac 1392
 Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
 450 455 460

gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag 1440
 Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
 465 470 475 480

atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca 1485
 Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala
 485 490 495

<210> 712

<211> 495

<212> PRT

<213> Corynebacterium glutamicum

<400> 712

Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
 1 5 10 15

Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
 20 25 30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
 35 40 45

Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
 50 55 60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65 70 75 80

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
 85 90 95

Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
 100 105 110

Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
 115 120 125

Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly

130	135	140
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr		
145	150	155 160
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg		
	165	170 175
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp		
	180	185 190
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser		
	195	200 205
Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr		
	210	215 220
Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr		
	225	230 235 240
Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala		
	245	250 255
Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr		
	260	265 270
Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala		
	275	280 285
Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val		
	290	295 300
Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser		
	305	310 315 320
Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu		
	325	330 335
Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser		
	340	345 350
Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro		
	355	360 365
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val		
	370	375 380
Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr		
	385	390 395 400
Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala		
	405	410 415
Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro		
	420	425 430
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met		
	435	440 445
Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn		
	450	455 460

Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465 470 475 480

Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala
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<210> 713

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXN01659

<400> 713

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                               Val Ala Gly Val Ala
                               1 5
cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca 163
Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro
                               10 15 20
gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa 211
Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu
                               25 30 35
acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg 259
Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro
                               40 45 50
ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg 307
Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr
                               55 60 65
cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag 355
Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys
                               70 75 80 85
ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa 403
Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu
                               90 95 100
gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg 451
Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met
                               105 110 115
ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca 499
Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser
                               120 125 130
ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt 547
Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg
                               135 140 145

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ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag 595
 Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln
 150 155 160 165

tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag 643
 Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys
 170 175 180

tgg tagaaaactg gtgttttttcg gcc 669
 Trp

<210> 714

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 714

Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly
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Leu Asp Ser Met Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp
 20 25 30

Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu
 35 40 45

Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu
 50 55 60

Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu
 65 70 75 80

Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro
 85 90 95

Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu
 100 105 110

Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val
 115 120 125

Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu
 130 135 140

Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg
 145 150 155 160

Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp
 165 170 175

Glu Pro Pro Lys Lys Trp
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<210> 715

<211> 509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(486)

<223> FRXA01659

<400> 715

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Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala
 1          5          10          15

gaa acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg 96
Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg
          20          25          30

ccg ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc 144
Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser
          35          40          45

acg cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg 192
Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu
          50          55          60

aag ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa 240
Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu
          65          70          75          80

gaa gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag 288
Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln
          85          90          95

atg ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg 336
Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg
          100          105          110

tca ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag 384
Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu
          115          120          125

cgt ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt 432
Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly
          130          135          140

cag tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa 480
Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys
          145          150          155          160

aag tgg tagaaaactg gtgttttttcg gcc 509
Lys Trp

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<210> 716

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

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Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala
 1          5          10          15

Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg

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Pro	Leu	Ala	Leu	Leu	Thr	Asp	Ala	Ser	Phe	Thr	Leu	Pro	Pro	Arg	Ser				
		35						40					45						
Thr	Arg	Ala	Gln	Thr	Leu	Asp	Leu	Lys	His	Leu	Glu	Pro	Ser	Arg	Leu				
	50					55					60								
Lys	Pro	Glu	Gln	Pro	Glu	Lys	Pro	Ala	Phe	Thr	Pro	Asn	Ala	Ser	Glu				
	65				70					75					80				
Glu	Asp	Leu	Ser	Gln	Pro	Leu	Val	Ile	Arg	Pro	Glu	Glu	Pro	Leu	Gln				
				85					90					95					
Met	Pro	Val	Arg	Gly	Val	Gln	Glu	Ser	Arg	Gly	Val	Val	Glu	Pro	Arg				
		100						105					110						
Ser	Leu	Gly	Ala	Asp	Asp	Val	Glu	Ser	Ile	Ala	Glu	Gly	Asp	Pro	Glu				
		115					120					125							
Arg	Pro	Ser	Asp	Leu	Tyr	Gly	Thr	Arg	Val	Leu	Arg	Asp	Leu	Asn	Gly				
	130					135					140								
Gln	Ser	Ser	Ile	Phe	Gln	Asp	Ser	Thr	Asp	Ala	Asp	Glu	Pro	Pro	Lys				
	145				150					155					160				
Lys	Trp																		

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(958)
 <223> RXN01663

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 cgtggcttga gtacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc 115
 Met Glu Ile Ser Val
 1 5
 ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc 163
 Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
 10 15 20
 gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc 211
 Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
 25 30 35
 tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag 259
 Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
 40 45 50
 ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag 307
 Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu

55	60	65	
ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag			355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu			
70	75	80	85
ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat			403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp			
	90	95	100
gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac			451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr			
	105	110	115
ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg			499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala			
	120	125	130
gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt			547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe			
	135	140	145
ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg			595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala			
	150	155	160
gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat			643
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp			
	170	175	180
gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg			691
Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val			
	185	190	195
gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg			739
Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala			
	200	205	210
ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc			787
Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val			
	215	220	225
att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa			835
Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu			
	230	235	240
tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc			883
Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu			
	250	255	260
agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg			931
Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr			
	265	270	275
tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa			978
Ser Val Trp Ile Pro Cys Gln Lys Leu			
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tct			981

<210> 718
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 718

Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
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Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
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Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
35 40 45
Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
50 55 60
Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
65 70 75 80
Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
85 90 95
Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
100 105 110
Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
115 120 125
Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
130 135 140
Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu
145 150 155 160
Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp
165 170 175
Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala
180 185 190
Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His
195 200 205
Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
210 215 220
Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
225 230 235 240
Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
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Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
260 265 270
Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu
275 280 285

<400> 721																
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gggtcacgac	caccatcacc	ccaccggatt	caaaggattt	ttg	tac	gag	att	ttc								115
					Leu	Tyr	Glu	Ile	Phe							
					1				5							
ggt	cca	cac	tcc	cat	gac	acc	gcc	gac	tcg	att	gat	gat	gct	atg	gag	163
Val	Pro	His	Ser	His	Asp	Thr	Ala	Asp	Ser	Ile	Asp	Asp	Ala	Met	Glu	
				10					15					20		
gcg	aac	tca	gag	ggt	att	cga	gcg	ctg	aag	ttt	agc	ctt	gta	ttg	atg	211
Ala	Asn	Ser	Glu	Gly	Ile	Arg	Ala	Leu	Lys	Phe	Ser	Leu	Val	Leu	Met	
				25					30					35		
ctg	ctc	acg	acg	ggt	ttg	cag	gct	atc	att	gtg	tct	ttt	tct	gga	tct	259
Leu	Leu	Thr	Thr	Val	Leu	Gln	Ala	Ile	Ile	Val	Ser	Phe	Ser	Gly	Ser	
				40					45					50		
ggt	gca	ctg	ttg	gcg	gat	acg	ggt	cac	aac	ctt	tcc	gac	gca	ttg	act	307
Val	Ala	Leu	Leu	Ala	Asp	Thr	Val	His	Asn	Leu	Ser	Asp	Ala	Leu	Thr	

55	60	65	
gcg att cct ctt tgg att gct ttc ata ctt tcc cgg cgc gca gcg act			355
Ala Ile Pro Leu Trp Ile Ala Phe Ile Leu Ser Arg Arg Ala Ala Thr			
70	75	80	85
caa aaa tat acg tat gga ttc aat cgt gca gag gat tta gcg ggg ttg			403
Gln Lys Tyr Thr Tyr Gly Phe Asn Arg Ala Glu Asp Leu Ala Gly Leu			
	90	95	100
ttt att gtc gcg atg att gct ctt tcg gcg att gtt gct gca tgg cag			451
Phe Ile Val Ala Met Ile Ala Leu Ser Ala Ile Val Ala Ala Trp Gln			
	105	110	115
gcg atc gac cgg atg att aat cct cgc ccg atg gag aat att gaa tgg			499
Ala Ile Asp Arg Met Ile Asn Pro Arg Pro Met Glu Asn Ile Glu Trp			
	120	125	130
gtg att gcg gca ggt gtt att ggt ttc tta gga aat gag gct gtg gca			547
Val Ile Ala Ala Gly Val Ile Gly Phe Leu Gly Asn Glu Ala Val Ala			
	135	140	145
atg tat cgc att cgg gtt ggt aag agg att ggc tcg gct gct ttg gtt			595
Met Tyr Arg Ile Arg Val Gly Lys Arg Ile Gly Ser Ala Ala Leu Val			
	150	155	160
gca gat ggc gtt cat gct cgc acg gat ggt ttt act tca ctt gca gtt			643
Ala Asp Gly Val His Ala Arg Thr Asp Gly Phe Thr Ser Leu Ala Val			
	170	175	180
gtc gca ggt ggt gtt gga gtt ttt ctg gga ttc ccc ctg gct gac cca			691
Val Ala Gly Gly Val Gly Val Phe Leu Gly Phe Pro Leu Ala Asp Pro			
	185	190	195
att atc gga ttg atc att tct gcg atg att gcc acc ctt ctt gtt ggt			739
Ile Ile Gly Leu Ile Ile Ser Ala Met Ile Ala Thr Leu Leu Val Gly			
	200	205	210
acg atc cgt tcg gtt ggc aga cgc ctc atg gat gga att gag ccg gag			787
Thr Ile Arg Ser Val Gly Arg Arg Leu Met Asp Gly Ile Glu Pro Glu			
	215	220	225
ttg gta gag aag gct acg cac gcg atc tgg cat gtg aag gaa att gag			835
Leu Val Glu Lys Ala Thr His Ala Ile Trp His Val Lys Glu Ile Glu			
	230	235	240
tcg att gat cga ctg agg ttg agg tgg gtt gga cac cgt ctt cac ggc			883
Ser Ile Asp Arg Leu Arg Leu Arg Trp Val Gly His Arg Leu His Gly			
	250	255	260
gat gcc acg gtc agc act tct aca tca tcg cta tcg gaa gcc acc gca			931
Asp Ala Thr Val Ser Thr Ser Thr Ser Leu Ser Glu Ala Thr Ala			
	265	270	275
atc gcc ctt gag gct gag ctt tcc gtc aaa caa cat ctt ccc aat gtg			979
Ile Ala Leu Glu Ala Glu Leu Ser Val Lys Gln His Leu Pro Asn Val			
	280	285	290
gat gaa atg act gtg acc atc acc cct tcc aaa cct tgaggtcccgt			1025
Asp Glu Met Thr Val Thr Ile Thr Pro Ser Lys Pro			
	295	300	305

gatacaattg ttg

1038

<210> 722

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

Leu Tyr Glu Ile Phe Val Pro His Ser His Asp Thr Ala Asp Ser Ile
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Asp Asp Ala Met Glu Ala Asn Ser Glu Gly Ile Arg Ala Leu Lys Phe
 20 25 30

Ser Leu Val Leu Met Leu Leu Thr Thr Val Leu Gln Ala Ile Ile Val
 35 40 45

Ser Phe Ser Gly Ser Val Ala Leu Leu Ala Asp Thr Val His Asn Leu
 50 55 60

Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe Ile Leu Ser
 65 70 75 80

Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn Arg Ala Glu
 85 90 95

Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu Ser Ala Ile
 100 105 110

Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro Arg Pro Met
 115 120 125

Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly Phe Leu Gly
 130 135 140

Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys Arg Ile Gly
 145 150 155 160

Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr Asp Gly Phe
 165 170 175

Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe Leu Gly Phe
 180 185 190

Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala Met Ile Ala
 195 200 205

Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg Leu Met Asp
 210 215 220

Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala Ile Trp His
 225 230 235 240

Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg Trp Val Gly
 245 250 255

His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr Ser Ser Leu
 260 265 270

Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser Val Lys Gln
 275 280 285

His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr Pro Ser Lys
 290 295 300

Pro
 305

<210> 723

<211> 755

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(732)

<223> FRXA01669

<400> 723

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His Asn Leu Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe	
1 5 10 15	
ata ctt tcc cgg cgc gca gcg act caa aaa tat acg tat gga ttc aat	96
Ile Leu Ser Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn	
20 25 30	
cgt gca gag gat tta gcg ggg ttg ttt att gtc gcg atg att gct ctt	144
Arg Ala Glu Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu	
35 40 45	
tcg gcg att gtt gct gca tgg cag gcg atc gac cgg atg att aat cct	192
Ser Ala Ile Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro	
50 55 60	
cgc ccg atg gag aat att gaa tgg gtg att gcg gca ggt gtt att ggt	240
Arg Pro Met Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly	
65 70 75 80	
ttc tta gga aat gag gct gtg gca atg tat cgc att cgg gtt ggt aag	288
Phe Leu Gly Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys	
85 90 95	
agg att ggc tcg gct gct ttg gtt gca gat ggc gtt cat gct cgc acg	336
Arg Ile Gly Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr	
100 105 110	
gat ggt ttt act tca ctt gca gtt gtc gca ggt ggt gtt gga gtt ttt	384
Asp Gly Phe Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe	
115 120 125	
ctg gga ttc ccc ctg gct gac cca att atc gga ttg atc att tct gcg	432
Leu Gly Phe Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala	
130 135 140	
atg att gcc acc ctt ctt gtt ggt acg atc cgt tcg gtt ggc aga cgc	480
Met Ile Ala Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg	
145 150 155 160	

ctc atg gat gga att gag ccg gag ttg gta gag aag gct acg cac gcg 528
Leu Met Asp Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala
165 170 175

atc tgg cat gtg aag gaa att gag tcg att gat cga ctg agg ttg agg 576
Ile Trp His Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg
180 185 190

tgg gtt gga cac cgt ctt cac ggc gat gcc acg gtc agc act tct aca 624
Trp Val Gly His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr
195 200 205

tca tcg cta tcg gaa gcc acc gca atc gcc ctt gag gct gag ctt tcc 672
Ser Ser Leu Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser
210 215 220

gtc aaa caa cat ctt ccc aat gtg gat gaa atg act gtg acc atc acc 720
Val Lys Gln His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr
225 230 235 240

cct tcc aaa cct tgagtcccgt gatacaattg ttg 755
Pro Ser Lys Pro

<210> 724
<211> 244
<212> PRT
<213> Corynebacterium glutamicum

<400> 724
His Asn Leu Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe
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Ile Leu Ser Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn
20 25 30

Arg Ala Glu Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu
35 40 45

Ser Ala Ile Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro
50 55 60

Arg Pro Met Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly
65 70 75 80

Phe Leu Gly Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys
85 90 95

Arg Ile Gly Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr
100 105 110

Asp Gly Phe Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe
115 120 125

Leu Gly Phe Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala
130 135 140

Met Ile Ala Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg
145 150 155 160

Phe Gly Gly Leu Gln Ile Gln Leu Gln Glu Glu Val Asp
 105 110

aacacaaacc cct

465

<210> 726

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

Met Ala Ser Arg Glu Val Ser Ile Thr Arg Ile Ser Pro Leu Ala Thr
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Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly Leu Val Ala Trp Ile
 20 25 30

Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn Val Ala Gly Val Trp
 35 40 45

Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly Ala Glu Gln Thr Ile
 50 55 60

Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu Leu Gly Ala Ile Gly
 65 70 75 80

Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys Ala Ile Ile Tyr Asn
 85 90 95

Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile Gln Leu Gln Glu Glu
 100 105 110

Val Asp

<210> 727

<211> 332

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(309)

<223> FRXA01672

<400> 727

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ctc gtg gcg tgg atc atc tgc gta acc gtc ctc tat ttc gga ctt aac 96
 Leu Val Ala Trp Ile Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn
 20 25 30

gtg gct ggc gtc tgg cag aac ttc aac gat gtc atc ggc ggt gtt ggt 144
 Val Ala Gly Val Trp Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly
 35 40 45

gca gaa caa acc atc acc ttc ggg ctc gtc ctg agc att tcc gca ctt 192

Ala Glu Gln Thr Ile Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu
 50 55 60

ctg gga gct atc gga gcg att acc gtc gct gtg ctt gca cca ttg tgt 240
 Leu Gly Ala Ile Gly Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys
 65 70 75 80

gca atc atc tac aac tcg att gtt gac ctc ttc ggt gga ctg cag att 288
 Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile
 85 90 95

caa ctg caa gaa gaa gta gac taacctctga aacacaaacc cct 332
 Gln Leu Gln Glu Glu Val Asp
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<210> 728
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Val Ala Gly Val Trp Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly
 35 40 45

Ala Glu Gln Thr Ile Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu
 50 55 60

Leu Gly Ala Ile Gly Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys
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Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile
 85 90 95

Gln Leu Gln Glu Glu Val Asp
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 <223> RXN01694

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ttcgaaaagc catgtccacc acgtgttcta tcctggcggc atg caa aaa atc acc 115
 Met Gln Lys Ile Thr
 1 5

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Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu Ala Ala Glu Phe Tyr	
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gtc aat gcg ttt tct gag ttt ccg ggt ggc gca gaa gta ctc acc aca	211
Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala Glu Val Leu Thr Thr	
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gtt aag tat ccc gaa gct ggc ttg ctg gac ttc cag gag cct ttc gca	259
Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe Gln Glu Pro Phe Ala	
40 45 50	
gga aaa acc ttg acg gtg gaa ctc gct atc tca ggc ttt aag atc atc	307
Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser Gly Phe Lys Ile Ile	
55 60 65	
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Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn Pro Ser Ile Ser Phe	
70 75 80 85	
atg gtg aat ttt gat gcg gtg cgt gat gaa aat gcc aaa gag cac ctt	403
Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn Ala Lys Glu His Leu	
90 95 100	
gat gcg gtg tgg gaa aaa ctc cat gaa ggc ggc agc aca ctg atg cca	451
Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly Ser Thr Leu Met Pro	
105 110 115	
gtc gat act tac cca ttt tcg gaa tac tac ggg tgg gta caa gac aaa	499
Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly Trp Val Gln Asp Lys	
120 125 130	
tat ggt gtg agc tgg caa ttg atg ctc agc cgc cca gaa gaa aag cca	547
Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg Pro Glu Glu Lys Pro	
135 140 145	
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Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly Gly Ala Ala Gln Asn	
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Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu Val Phe Pro Asn Ser	
170 175 180	
caa ctt ggt gat cgt gca cct tat gga cag caa aca ggt cct gcc act	691
Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln Thr Gly Pro Ala Thr	
185 190 195	
cct gag gcc ctc atg ttt tcc cag ttc caa ctc gac ggt cag tgg att	739
Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu Asp Gly Gln Trp Ile	
200 205 210	
ttc gcg atg gat tcc gga gtt gag caa gat ttc acc ttc agt gag ggt	787
Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe Thr Phe Ser Glu Gly	
215 220 225	
gtc tca ttg atg tat gaa gct cat ggt caa gaa gaa ctc gat gcc atc	835
Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu Glu Leu Asp Ala Ile	
230 235 240 245	
tgg aat gca ctc tcg gca gtt cca gaa gct gag gct tgt ggt tgg ttg	883

Thr Gly Pro Ala Thr Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu
195 200 205

Asp Gly Gln Trp Ile Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe
 210 215 220

Thr Phe Ser Glu Gly Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu
 225 230 235 240

Glu Leu Asp Ala Ile Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu
 245 250 255

Ala Cys Gly Trp Leu Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val
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Pro Asp Asn Met Glu Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys
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Leu Leu Ala Met Lys Lys Ile Asn Ile Ala Glu Phe
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 Met Gln Lys Ile Thr
 1 5

cca aac atc tgg tgc caa ggc acc gca gac gaa gca gcc gaa ttc tac 163
 Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu Ala Ala Glu Phe Tyr
 10 15 20

gtc aat gcg ttt tct gag ttt ccg ggt ggc gca gaa gta ctc acc aca 211
 Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala Glu Val Leu Thr Thr
 25 30 35

gtt aag tat ccc gaa gct ggc ttg ctg gac ttc cag gag cct ttc gca 259
 Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe Gln Glu Pro Phe Ala
 40 45 50

gga aaa acc ttg acg gtg gaa ctc gct atc tca ggc ttt aag atc atc 307
 Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser Gly Phe Lys Ile Ile
 55 60 65

ttg atc aat gct ggt gaa gag ttc act ccc aac cca tcg atc agc ttc 355
 Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn Pro Ser Ile Ser Phe
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atg gtg aat ttt gat gcg gtg cgt gat gaa aat gcc aaa gag cac ctt 403
 Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn Ala Lys Glu His Leu
 90 95 100

gat gcg gtg tgg gaa aaa ctc cat gaa ggc ggc agc aca ctg atg cca 451

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Val	Asp	Thr	Tyr	Pro	Phe	Ser	Glu	Tyr	Tyr	Gly	Trp	Val	Gln	Asp	Lys		
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Tyr	Gly	Val	Ser	Trp	Gln	Leu	Met	Leu	Ser	Arg	Pro	Glu	Glu	Lys	Pro		
		135				140					145						
ggg	ccc	gca	gta	atc	cca	acg	ctc	tta	ttt	ggg	ggg	gca	gct	caa	aat	595	
Gly	Pro	Ala	Val	Ile	Pro	Thr	Leu	Leu	Phe	Gly	Gly	Ala	Ala	Gln	Asn		
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Gln	Ala	Gly	Pro	Ala	Gln	Glu	Asn	Tyr	Val	Glu	Val	Phe	Pro	Asn	Ser		
			170						175					180			
caa	ctt	ggg	gat	cgt	gca	cct	tat	gga	cag	caa	aca	ggg	cct	gcc	act	691	
Gln	Leu	Gly	Asp	Arg	Ala	Pro	Tyr	Gly	Gln	Gln	Thr	Gly	Pro	Ala	Thr		
			185					190					195				
cct	gag	gcc	ctc	atg	ttt	tcc	cag	ttc	caa	ctc	gac	ggg	cag	tgg	att	739	
Pro	Glu	Ala	Leu	Met	Phe	Ser	Gln	Phe	Gln	Leu	Asp	Gly	Gln	Trp	Ile		
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Phe	Ala	Met	Asp	Ser	Gly	Val	Glu	Gln	Asp	Phe	Thr	Phe	Ser	Glu	Gly		
		215				220					225						
gtc	tca	ttg	atg	tat	gaa	gct	cat	ggg	caa	gaa	gaa	ctc	gat	gcc	atc	835	
Val	Ser	Leu	Met	Tyr	Glu	Ala	His	Gly	Gln	Glu	Glu	Leu	Asp	Ala	Ile		
230					235					240					245		
tgg	aat	gca	ctc	tcg	gca	gtt	cca	gaa	gct	gag	gct	tgt	ggg	tgg	ttg	883	
Trp	Asn	Ala	Leu	Ser	Ala	Val	Pro	Glu	Ala	Glu	Ala	Cys	Gly	Trp	Leu		
			250						255					260			
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Lys	Asp	Lys	Phe	Gly	Val	Ser	Trp	Gln	Ile	Val	Pro	Asp	Asn	Met	Glu		
			265					270					275				
gag	ctc	atg	gct	aaa	ccc	ggc	gcg	tat	gaa	aag	ctt	ctt	gcg	atg	aag	979	
Glu	Leu	Met	Ala	Lys	Pro	Gly	Ala	Tyr	Glu	Lys	Leu	Leu	Ala	Met	Lys		
		280					285					290					
aag	atc	aat	atc	gcg	gag	ttc	tagcagttct	aagcgctcca	cgc							1023	
Lys	Ile	Asn	Ile	Ala	Glu	Phe											
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35 40 45
Gln Glu Pro Phe Ala Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser
50 55 60
Gly Phe Lys Ile Ile Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn
65 70 75 80
Pro Ser Ile Ser Phe Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn
85 90 95
Ala Lys Glu His Leu Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly
100 105 110
Ser Thr Leu Met Pro Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly
115 120 125
Trp Val Gln Asp Lys Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg
130 135 140
Pro Glu Glu Lys Pro Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly
145 150 155 160
Gly Ala Ala Gln Asn Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu
165 170 175
Val Phe Pro Asn Ser Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln
180 185 190
Thr Gly Pro Ala Thr Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu
195 200 205
Asp Gly Gln Trp Ile Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe
210 215 220
Thr Phe Ser Glu Gly Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu
225 230 235 240
Glu Leu Asp Ala Ile Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu
245 250 255
Ala Cys Gly Trp Leu Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val
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Pro Asp Asn Met Glu Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys
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Leu Leu Ala Met Lys Lys Ile Asn Ile Ala Glu Phe
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1279)

<223> RXN01696

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                                   Leu Ser Thr Pro Ile
                                   1 5

ggc ctt ggc ctt cct ccg acc cca cct cca gtg ttg gcg cca cgt cgt 163
Gly Leu Gly Leu Pro Pro Thr Pro Pro Pro Val Leu Ala Pro Arg Arg
                                   10 15 20

aaa aca cgc caa ctc atg gtc ggc aaa gtg ggc gtt ggt tcg gat cac 211
Lys Thr Arg Gln Leu Met Val Gly Lys Val Gly Val Gly Ser Asp His
                                   25 30 35

ccg att tcc gtc cag tcg atg acc acc acc aaa acc cac gac atc aac 259
Pro Ile Ser Val Gln Ser Met Thr Thr Thr Lys Thr His Asp Ile Asn
                                   40 45 50

ggc acc ctg caa cag atc gca cag ttg aca gcc acc ggt tgt gac atc 307
Gly Thr Leu Gln Gln Ile Ala Gln Leu Thr Ala Thr Gly Cys Asp Ile
                                   55 60 65

gtc cgc gtt gcc tgc cca aag act gtt gat gcg gaa gca ctg ccg atc 355
Val Arg Val Ala Cys Pro Lys Thr Val Asp Ala Glu Ala Leu Pro Ile
                                   70 75 80 85

atc gca aag aag tct ccg atc cca gtg atc gca gat atc cac ttc cag 403
Ile Ala Lys Lys Ser Pro Ile Pro Val Ile Ala Asp Ile His Phe Gln
                                   90 95 100

ccc aag tac atc ttc gcg gca atc gat gca ggt tgc gcc gcc gtt cgt 451
Pro Lys Tyr Ile Phe Ala Ala Ile Asp Ala Gly Cys Ala Ala Val Arg
                                   105 110 115

gtg aac cca ggc aac atc aag gaa ttc gat ggt gcg gtt aaa gaa gta 499
Val Asn Pro Gly Asn Ile Lys Glu Phe Asp Gly Arg Val Lys Glu Val
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gca aaa gct gca ggc gat gcc gga att cca att cgt att ggt gtc aac 547
Ala Lys Ala Ala Gly Asp Ala Gly Ile Pro Ile Arg Ile Gly Val Asn
                                   135 140 145

ggc gga tcc ctg gat aag cgc atc ctg gac aaa tac cac ggc aaa gcc 595
Gly Gly Ser Leu Asp Lys Arg Ile Leu Asp Lys Tyr His Gly Lys Ala
                                   150 155 160 165

acc cca gaa gct ctc gtg gaa tcc gca atg tgg gaa gcc ggc ctg ttt 643
Thr Pro Glu Ala Leu Val Glu Ser Ala Met Trp Glu Ala Gly Leu Phe
                                   170 175 180

gaa gag cac ggc ttc ggc gac atc gca atc tct gtg aag cac tcc gac 691
Glu Glu His Gly Phe Gly Asp Ile Ala Ile Ser Val Lys His Ser Asp
                                   185 190 195

cca gta ctc atg gtg gag gcc tac cgc cag ctc gct gaa caa agc gac 739
Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu Gln Ser Asp

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aca atc aag tct tcc gta gca ttc ggc gct ctg ctg tcc cag ggc atc Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser Gln Gly Ile 230 235 240 245			835
ggc gac act atc cgt gtg tct ctt tct gct gac cca gtg gaa gaa atc Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val Glu Glu Ile 250 255 260			883
aag gtt ggc gac cag att ctg cag tcc ctc aac ctg cgc cca cgc aag Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg Pro Arg Lys 265 270 275			931
ctg gaa atc gtg tcc tgc cca tca tgt ggc cgc gca cag gtc gat gtg Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln Val Asp Val 280 285 290			979
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cca ctg cgc gtc gct gtc atg ggt tgc gtt gtt aac ggc cca ggt gag Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly Pro Gly Glu 310 315 320 325			1075
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<212> PRT

<213> Corynebacterium glutamicum

<400> 734

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Leu Ala Pro Arg Arg Lys Thr Arg Gln Leu Met Val Gly Lys Val Gly

20										25					30				
Val	Gly	Ser	Asp	His	Pro	Ile	Ser	Val	Gln	Ser	Met	Thr	Thr	Thr	Lys				
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Thr	His	Asp	Ile	Asn	Gly	Thr	Leu	Gln	Gln	Ile	Ala	Gln	Leu	Thr	Ala				
50					55					60									
Thr	Gly	Cys	Asp	Ile	Val	Arg	Val	Ala	Cys	Pro	Lys	Thr	Val	Asp	Ala				
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Glu	Ala	Leu	Pro	Ile	Ile	Ala	Lys	Lys	Ser	Pro	Ile	Pro	Val	Ile	Ala				
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Asp	Ile	His	Phe	Gln	Pro	Lys	Tyr	Ile	Phe	Ala	Ala	Ile	Asp	Ala	Gly				
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Cys	Ala	Ala	Val	Arg	Val	Asn	Pro	Gly	Asn	Ile	Lys	Glu	Phe	Asp	Gly				
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Arg	Val	Lys	Glu	Val	Ala	Lys	Ala	Ala	Gly	Asp	Ala	Gly	Ile	Pro	Ile				
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Glu	Ala	Gly	Leu	Phe	Glu	Glu	His	Gly	Phe	Gly	Asp	Ile	Ala	Ile	Ser				
180					185					190									
Val	Lys	His	Ser	Asp	Pro	Val	Leu	Met	Val	Glu	Ala	Tyr	Arg	Gln	Leu				
195					200					205									
Ala	Glu	Gln	Ser	Asp	Tyr	Pro	Leu	His	Leu	Gly	Val	Thr	Glu	Ala	Gly				
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Pro	Lys	Phe	Met	Gly	Thr	Ile	Lys	Ser	Ser	Val	Ala	Phe	Gly	Ala	Leu				
225					230					235					240				
Leu	Ser	Gln	Gly	Ile	Gly	Asp	Thr	Ile	Arg	Val	Ser	Leu	Ser	Ala	Asp				
245					250					255									
Pro	Val	Glu	Glu	Ile	Lys	Val	Gly	Asp	Gln	Ile	Leu	Gln	Ser	Leu	Asn				
260					265					270									
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275					280					285									
Ala	Gln	Val	Asp	Val	Tyr	Ser	Leu	Ala	Glu	Glu	Val	Thr	Glu	Ala	Leu				
290					295					300									
Asp	Gly	Met	Glu	Val	Pro	Leu	Arg	Val	Ala	Val	Met	Gly	Cys	Val	Val				
305					310					315					320				
Asn	Gly	Pro	Gly	Glu	Ala	Arg	Asp	Ala	Asp	Leu	Gly	Val	Ala	Ser	Gly				
325					330					335									
Asn	Gly	Lys	Gly	Gln	Ile	Phe	Val	Lys	Gly	Glu	Val	Ile	Lys	Thr	Val				
340					345					350									

Pro Glu Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile
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Ala Glu Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly
 370 375 380

Met Lys Ala Glu Val Lys Val Thr Lys
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<211> 620

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(597)

<223> FRXA01696

<400> 735

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caa agc gac tac cca ctg cac ctc ggt gtt act gaa gct ggt ccc aag 96
 Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys
 20 25 30

ttc atg gga aca atc aag tct tcc gta gca ttc ggc gct ctg ctg tcc 144
 Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser
 35 40 45

cag ggc atc ggc gac act atc cgt gtg tct ctt tct gct gac cca gtg 192
 Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
 50 55 60

gaa gaa atc aag gtt ggc gac cag att ctg cag tcc ctc aac ctg cgc 240
 Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg
 65 70 75 80

cca cgc aag ctg gaa atc gtg tcc tgc cca tca tgt ggc cgc gca cag 288
 Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln
 85 90 95

gtc gat gtg tac tca ctt gct gaa gaa gtc acc gaa gca ctc gac ggc 336
 Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly
 100 105 110

atg gaa gtt cca ctg cgc gtc gct gtc atg ggt tgc gtt gtt aac ggc 384
 Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly
 115 120 125

cca ggt gag gct cgc gac gct gac ctc ggt gtt gca tcc ggt aac ggc 432
 Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly
 130 135 140

aag ggc cag atc ttt gtc aag ggc gaa gtc atc aag act gtc cca gaa 480
 Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu
 145 150 155 160

tcc cag atc gtg gaa acc ctc atc gaa gaa gca atg cgt atc gca gag 528
Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu
165 170 175

gaa atg gac cca gaa gtc ctc gct gca gca agt gct tcc ggt atg aag 576
Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys
180 185 190

gct gaa gtg aag gta acc aag taagttttgg ttaattaagg cac 620
Ala Glu Val Lys Val Thr Lys
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<210> 736

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 736

His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu
1 5 10 15

Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys
20 25 30

Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser
35 40 45

Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
50 55 60

Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg
65 70 75 80

Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln
85 90 95

Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly
100 105 110

Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly
115 120 125

Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly
130 135 140

Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu
145 150 155 160

Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu
165 170 175

Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys
180 185 190

Ala Glu Val Lys Val Thr Lys
195

<210> 737

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXN01697

<400> 737

tagatcaact aagtatgaac gcgaatccga ctttggctgt actgcaagaa tcgaccagag 60

```

cccgattaaa aaatgcccc gcgcaacgaa actagtaatc atg ttt caa gga cta 115
                                   Met Phe Gln Gly Leu
                                   1 5

```

```

aaa gaa ctc acc gca gca aaa ggc cgc acg ctg ctg atc acc gtc acc 163
Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu Leu Ile Thr Val Thr
      10 15 20

```

```

gtc ggg ctg atc gcc gtg ctg gtt act ttc ctc tct gcc ctc acc gcc 211
Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu Ser Ala Leu Thr Ala
      25 30 35

```

```

ggg ctt ggc cac caa tca gta tcc gca ctg aaa tac cta gcg ggt gat 259
Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys Tyr Leu Ala Gly Asp
      40 45 50

```

```

aat gaa ctt atc ctc gcc gat tcc gga tcc acc acg ctt tcc gcg tcc 307
Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr Thr Leu Ser Ala Ser
      55 60 65

```

```

acg ctt tct gat caa gca gtt gcc caa ctc gaa gac gaa ggc gca cag 355
Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu Asp Glu Gly Ala Gln
      70 75 80 85

```

```

atg ctg tgg cag gtc cgc gac cga gta gca gac acc ccc acc atg ctc 403
Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp Thr Pro Thr Met Leu
      90 95 100

```

```

ctc aac tcc cct gac ctt gcg cct ggt gaa gta tcc ctt cct gcc gaa 451
Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val Ser Leu Pro Ala Glu
      105 110 115

```

```

ctc gct gat tcg gaa ctc gct act gcg cat gat gta gtg gat tct tcc 499
Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp Val Val Asp Ser Ser
      120 125 130

```

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aac gat ctg tac ctc gat cac ctg ccc gtg gta ttg atg aac acc tcc 547
Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val Leu Met Asn Thr Ser
      135 140 145

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```

gat tta gcc tca ctc gcg caa gtc cga ggc gtg aca gga cca gca ggc 595
Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val Thr Gly Pro Ala Gly
      150 155 160 165

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gca ttc gcc tct gac gtt gcg ctc ccc tcc gac acc gtt gcg ctc tct 643
Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp Thr Val Ala Leu Ser
      170 175 180

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gga tcc gaa cgg tgg aac gca tcc gcc tcc tac cag ggc gaa cag atg 691

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Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr Gln Gly Glu Gln Met
 185 190 195
 tca ctc aac ctc atg atc gtc atg ctg tat gtt atc tcc gca ctc gtg 739
 Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val Ile Ser Ala Leu Val
 200 205 210
 ctc ggc gca ttc ttc acc gtc tgg acc atc caa cgc ctc cgc ggc atc 787
 Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln Arg Leu Arg Gly Ile
 215 220 225
 gcc atc tct agt gct ttg gga gca gcc cgc cga gta ctt atc gcc gac 835
 Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg Val Leu Ile Ala Asp
 230 235 240 245
 gct ctc ggc caa gcc atc atc gtc tta gga atc ggc atc acc gca ggc 883
 Ala Leu Gly Gln Ala Ile Ile Val Leu Gly Ile Gly Ile Thr Ala Gly
 250 255 260
 aca ttg atc aca gtc atc tcc gca ttc ggc atg gga gac gca atg ccc 931
 Thr Leu Ile Thr Val Ile Ser Ala Phe Gly Met Gly Asp Ala Met Pro
 265 270 275
 gtg gtc atc tcc tcc tcc acc acg ctc ttc ccc gca ctt atc ctc gcc 979
 Val Val Ile Ser Ser Ser Thr Thr Leu Phe Pro Ala Leu Ile Leu Ala
 280 285 290
 gca gca gga ctc atc ggt gcc gcc att tca ctc ggc ccc atc ctt cgc 1027
 Ala Ala Gly Leu Ile Gly Ala Ala Ile Ser Leu Gly Pro Ile Leu Arg
 295 300 305
 gtc gaa cca cgc tcc gca ctc atg aac gca taagaaaagg aacctcacat 1077
 Val Glu Pro Arg Ser Ala Leu Met Asn Ala
 310 315
 gac 1080

<210> 738
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 738
 Met Phe Gln Gly Leu Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu
 1 5 10 15
 Leu Ile Thr Val Thr Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu
 20 25 30
 Ser Ala Leu Thr Ala Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys
 35 40 45
 Tyr Leu Ala Gly Asp Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr
 50 55 60
 Thr Leu Ser Ala Ser Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu
 65 70 75 80
 Asp Glu Gly Ala Gln Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp
 85 90 95

Thr Pro Thr Met Leu Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val
 100 105 110
 Ser Leu Pro Ala Glu Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp
 115 120 125
 Val Val Asp Ser Ser Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val
 130 135 140
 Leu Met Asn Thr Ser Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val
 145 150 155 160
 Thr Gly Pro Ala Gly Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp
 165 170 175
 Thr Val Ala Leu Ser Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr
 180 185 190
 Gln Gly Glu Gln Met Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val
 195 200 205
 Ile Ser Ala Leu Val Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln
 210 215 220
 Arg Leu Arg Gly Ile Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg
 225 230 235 240
 Val Leu Ile Ala Asp Ala Leu Gly Gln Ala Ile Ile Val Leu Gly Ile
 245 250 255
 Gly Ile Thr Ala Gly Thr Leu Ile Thr Val Ile Ser Ala Phe Gly Met
 260 265 270
 Gly Asp Ala Met Pro Val Val Ile Ser Ser Ser Thr Thr Leu Phe Pro
 275 280 285
 Ala Leu Ile Leu Ala Ala Ala Gly Leu Ile Gly Ala Ala Ile Ser Leu
 290 295 300
 Gly Pro Ile Leu Arg Val Glu Pro Arg Ser Ala Leu Met Asn Ala
 305 310 315

 <210> 739
 <211> 826
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(826)
 <223> FRXA01697

 <400> 739
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 cccgattaaa aaatgcccc gcgcaacgaa actagtaatc atg ttt caa gga cta 115
 Met Phe Gln Gly Leu
 1 5

aaa gaa ctc acc gca gca aaa ggc cgc acg ctg ctg atc acc gtc acc	163
Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu Leu Ile Thr Val Thr	
10 15 20	
gtc ggg ctg atc gcc gtg ctg gtt act ttc ctc tct gcc ctc acc gcc	211
Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu Ser Ala Leu Thr Ala	
25 30 35	
ggg ctt ggc cac caa tca gta tcc gca ctg aaa tac cta gcg ggt gat	259
Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys Tyr Leu Ala Gly Asp	
40 45 50	
aat gaa ctt atc ctc gcc gat tcc gga tcc acc acg ctt tcc gcg tcc	307
Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr Thr Leu Ser Ala Ser	
55 60 65	
acg ctt tct gat caa gca gtt gcc caa ctc gaa gac gaa ggc gca cag	355
Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu Asp Glu Gly Ala Gln	
70 75 80 85	
atg ctg tgg cag gtc cgc gac cga gta gca gac acc ccc acc atg ctc	403
Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp Thr Pro Thr Met Leu	
90 95 100	
ctc aac tcc cct gac ctt gcg cct ggt gaa gta tcc ctt cct gcc gaa	451
Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val Ser Leu Pro Ala Glu	
105 110 115	
ctc gct gat tcg gaa ctc gct act gcg cat gat gta gtg gat tct tcc	499
Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp Val Val Asp Ser Ser	
120 125 130	
aac gat ctg tac ctc gat cac ctg ccc gtg gta ttg atg aac acc tcc	547
Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val Leu Met Asn Thr Ser	
135 140 145	
gat tta gcc tca ctc gcg caa gtc cga ggc gtg aca gga cca gca ggc	595
Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val Thr Gly Pro Ala Gly	
150 155 160 165	
gca ttc gcc tct gac gtt gcg ctc ccc tcc gac acc gtt gcg ctc tct	643
Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp Thr Val Ala Leu Ser	
170 175 180	
gga tcc gaa cgg tgg aac gca tcc gcc tcc tac cag ggc gaa cag atg	691
Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr Gln Gly Glu Gln Met	
185 190 195	
tca ctc aac ctc atg atc gtc atg ctg tat gtc atc tcc gca ctc gtg	739
Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val Ile Ser Ala Leu Val	
200 205 210	
ctc ggc gca ttc ttc acc gtc tgg acc atc caa cgc ctc cgc ggc atc	787
Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln Arg Leu Arg Gly Ile	
215 220 225	
gcc atc tct agt gct ttg gga gca gcc cgc cga gta ctt	826
Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg Val Leu	
230 235 240	

<210> 740
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 740
Met Phe Gln Gly Leu Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu
1 5 10 15
Leu Ile Thr Val Thr Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu
20 25 30
Ser Ala Leu Thr Ala Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys
35 40 45
Tyr Leu Ala Gly Asp Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr
50 55 60
Thr Leu Ser Ala Ser Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu
65 70 75 80
Asp Glu Gly Ala Gln Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp
85 90 95
Thr Pro Thr Met Leu Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val
100 105 110
Ser Leu Pro Ala Glu Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp
115 120 125
Val Val Asp Ser Ser Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val
130 135 140
Leu Met Asn Thr Ser Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val
145 150 155 160
Thr Gly Pro Ala Gly Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp
165 170 175
Thr Val Ala Leu Ser Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr
180 185 190
Gln Gly Glu Gln Met Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val
195 200 205
Ile Ser Ala Leu Val Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln
210 215 220
Arg Leu Arg Gly Ile Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg
225 230 235 240
Val Leu

<210> 741
<211> 472
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(472)

<223> RXN01701

<400> 741

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gccgatcaaa ttcattgatt gttaatcgga agtttttttga acaggtaaag ctaggggacc 60
tggttcagtgc ctggttgccgg atgtattaag gagaatgccc atg ctg agc cac gaa 115
                                         Met Leu Ser His Glu
                                         1      5

gaa att gtt gcg atc gca gaa gat ttg ctg tct aaa cgc tac ggc ggt 163
Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser Lys Arg Tyr Gly Gly
          10                      15                      20

gta caa act ctt tct gac gtg gag cag ctc aac ggt tcc ggc acc tcc 211
Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn Gly Ser Gly Thr Ser
          25                      30                      35

gcg gtg ctg cgt gcc agg gtg gct aac tcc cca ttc ctc caa cag cgc 259
Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro Phe Leu Gln Gln Arg
          40                      45                      50

tcc gtg gtg ctg aag tac gtg ccc agc acc gga gac gtc ttt gat gat 307
Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly Asp Val Phe Asp Asp
          55                      60                      65

tct gcg ctg gtg cgt gaa atc gtc tcc tac cag ttc acc acc tcc ttg 355
Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln Phe Thr Thr Ser Leu
          70                      75                      80                      85

tcg gaa gat gtc cgc cca ggg cca gtc att ttg gcc tat gac att gac 403
Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu Ala Tyr Asp Ile Asp
          90                      95                      100

aag cgc atc ctg gtc att tca gat tcc ggc aac ggc gac acc ttt gcg 451
Lys Arg Ile Leu Val Ile Ser Asp Ser Gly Asn Gly Asp Thr Phe Ala
          105                      110                      115

gat ctg atc gat cag cgt ccg 472
Asp Leu Ile Asp Gln Arg Pro
          120

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<210> 742

<211> 124

<212> PRT

<213> Corynebacterium glutamicum

<400> 742

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Met Leu Ser His Glu Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser
  1              5              10              15

Lys Arg Tyr Gly Gly Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn
  20              25              30

Gly Ser Gly Thr Ser Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro
  35              40              45

Phe Leu Gln Gln Arg Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly
  50              55              60

```

Asp Val Phe Asp Asp Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln
65 70 75 80

Phe Thr Thr Ser Leu Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu
85 90 95

Ala Tyr Asp Ile Asp Lys Arg Ile Leu Val Ile Ser Asp Ser Gly Asn
100 105 110

Gly Asp Thr Phe Ala Asp Leu Ile Asp Gln Arg Pro
115 120

<210> 743

<211> 433

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(433)

<223> FRXA01701

<400> 743

gccgatcaaa ttcattgatt gttaatcgga agttttttga acaggtaaag ctaggggacc 60

tggtcagtgct ctggtggcgg atgtattaag gagaatgccc atg ctg agc cac gaa 115
Met Leu Ser His Glu
1 5

gaa att gtt gcg atc gca gaa gat ttg ctg tct aaa cgc tac ggc ggt 163
Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser Lys Arg Tyr Gly Gly
10 15 20

gta caa act ctt tct gac gtg gag cag ctc aac ggt tcc ggc acc tcc 211
Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn Gly Ser Gly Thr Ser
25 30 35

gcg gtg ctg cgt gcc agg gtg gct aac tcc cca ttc ctc caa cag cgc 259
Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro Phe Leu Gln Gln Arg
40 45 50

tcc gtg gtg ctg aag tac gtg ccc agc acc gga gac gtc ttt gat gat 307
Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly Asp Val Phe Asp Asp
55 60 65

tct gcg ctg gtg cgt gaa atc gtc tcc tac cag ttc acc acc tcc ttg 355
Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln Phe Thr Thr Ser Leu
70 75 80 85

tcg gaa gat gtc cgc cca ggg cca gtc att ttg gcc tat gac att gac 403
Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu Ala Tyr Asp Ile Asp
90 95 100

aag cgc atc ctg gtc att tca gat tcc ggc 433
Lys Arg Ile Leu Val Ile Ser Asp Ser Gly
105 110

<210> 744

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<400> 744
Met Leu Ser His Glu Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser
  1          5          10          15

Lys Arg Tyr Gly Gly Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn
          20          25          30

Gly Ser Gly Thr Ser Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro
          35          40          45

Phe Leu Gln Gln Arg Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly
  50          55          60

Asp Val Phe Asp Asp Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln
  65          70          75          80

Phe Thr Thr Ser Leu Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu
          85          90          95

Ala Tyr Asp Ile Asp Lys Arg Ile Leu Val Ile Ser Asp Ser Gly
          100          105          110

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<220>
<221> CDS
<222> (101)..(1213)
<223> RXN01703
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<400> 745
gttagacaaa tgggtaaaca gagctgacct agcggaatcc gccatcaacg aaaggcattc 60

cgcgagggtt tgggggtctgc ctcgaacaaa tcttggggttt  gtg gca tgg cca tcc 115
Val Ala Trp Pro Ser
1 5

aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg 163
Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
10 15 20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag 211
His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
25 30 35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc 259
Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
40 45 50

aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg 307
Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
55 60 65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca 355

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Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr	
70 75 80 85	
cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat	403
Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp	
90 95 100	
tcc ctt act ggt gtg ctg ccg tgg cgt tcc ggc gaa acc ttc tac aac	451
Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly Glu Thr Phe Tyr Asn	
105 110 115	
gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt	499
Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg	
120 125 130	
ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc	547
Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile	
135 140 145	
gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga	595
Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly	
150 155 160 165	
cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att	643
Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile	
170 175 180	
ggt gcg tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg	691
Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu	
185 190 195	
acc act act gtg gtg gat cac tgg tcg gat gcc gat aag gca gaa gac	739
Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Lys Ala Glu Asp	
200 205 210	
tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg	787
Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser	
215 220 225	
cgg aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac	835
Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp	
230 235 240 245	
ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat	883
Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp	
250 255 260	
gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa	931
Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys	
265 270 275	
aag att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac	979
Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn	
280 285 290	
cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca	1027
His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr	
295 300 305	
acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg	1075
Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu	

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310          315          320          325
agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg 1123
Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val
          330          335          340

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa 1171
Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu
          345          350          355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga 1213
Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
          360          365          370

tagccccgat agtgtatgtg ctg 1236

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<210> 746

<211> 371

<212> PRT

<213> Corynebacterium glutamicum

<400> 746

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Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His
  1              5              10              15

Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg
      20              25              30

Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg
      35              40              45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr
      50              55              60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val
      65              70              75              80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile
      85              90              95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly
      100             105             110

Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met
      115             120             125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile
      130             135             140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg
      145             150             155             160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys
      165             170             175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg
      180             185             190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala
      195             200             205

```

Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val
 210 215 220
 Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp
 225 230 235 240
 Trp Asp Thr Gly Asp Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val
 245 250 255
 Arg Tyr Leu Ala Asp Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr
 260 265 270
 Asn Arg Glu Thr Lys Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala
 275 280 285
 Glu Ser Val Trp Asn His Arg Leu Glu Val Asp Gly Leu Pro Val Phe
 290 295 300
 Ala Thr Asp Trp Thr Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu
 305 310 315 320
 Ser Ser Ser Ser Leu Ser Asp Leu Val Ser Val Val Arg Val Asp Glu
 325 330 335
 Arg Asp Leu Ser Val Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala
 340 345 350
 Ala Lys Val Ala Glu Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly
 355 360 365
 Arg Ser Arg
 370

<210> 747
 <211> 494
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(471)
 <223> FRXA01703

<400> 747
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 Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser Arg
 1 5 10 15
 aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac ggc 96
 Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly
 20 25 30
 gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat gtg 144
 Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val
 35 40 45
 gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa aag 192
 Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys Lys
 50 55 60

att gca gca cgc ctg gta ctg gaa tgc gcg gaa agc gta tgg aac cac 240
 Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn His
 65 70 75 80

cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca acg 288
 Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr Thr
 85 90 95

gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg agc 336
 Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu Ser
 100 105 110

gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg caa 384
 Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val Gln
 115 120 125

ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa gaa 432
 Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu Glu
 130 135 140

ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga tagccccgat 481
 Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
 145 150 155

agtgtatgtg ctg 494

<210> 748

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

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Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly
 20 25 30

Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val
 35 40 45

Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys Lys
 50 55 60

Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn His
 65 70 75 80

Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr Thr
 85 90 95

Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu Ser
 100 105 110

Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val Gln
 115 120 125

Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu Glu
 130 135 140

Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
 145 150 155

<210> 749
 <211> 555
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(532)
 <223> RXN01709

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 gaaattaggt gtcgatgcag caatacggaa ctttgccaat gtg ttt gaa caa gct 115
 Val Phe Glu Gln Ala
 1 5
 ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg 163
 Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Ala Gly
 10 15 20
 ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc 211
 Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser
 25 30 35
 ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca 259
 Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala
 40 45 50
 cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc 307
 Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr
 55 60 65
 ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa 355
 Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys
 70 75 80 85
 gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca 403
 Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala
 90 95 100
 atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451
 Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
 105 110 115
 tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499
 Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
 120 125 130
 atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
 Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
 135 140
 gat 555

<210> 750

<211> 144
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 750
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 35 40 45
 Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
 50 55 60
 Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
 65 70 75 80
 Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
 85 90 95
 Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
 100 105 110
 Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
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 Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
 130 135 140

<210> 751
 <211> 368
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (16)..(345)
 <223> FRXA01709

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 Gly Gly Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu
 15 20 25
 gga cgc att gat gca cag acc ctc agc ggg aaa gct cct act gga atc 147
 Gly Arg Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile
 30 35 40
 gcc aaa cgg gca cgt gcg aaa gga att cca gta ctg gcg gtt tgt ggg 195
 Ala Lys Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly
 45 50 55 60
 cag agc cta ttg ggt cca gca atc tca aat gag cta ttt gaa gac atc 243

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<400> 753
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gtgggatagc atcggcaacg cggttgcatg gccgttggcc atg ttg ttg atg gcg      115
               Met Leu Leu Met Ala
                   1           5

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cat cgc ttc ttc gtg ctt gcg att aac ggc gca gtc acc gac gat ttc	163
His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala Val Thr Asp Asp Phe	
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acg acg gtt tat agt gct tta cga cgt ttc gtt gaa ggt att ccg gtc	211
Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val Glu Gly Ile Pro Val	
25 30 35	
tac aac gag gtc tac cac ttc gtc gat ccg cac tac ctc tat aac ccg	259
Tyr Asn Glu Val Tyr His Phe Val Asp Pro His Tyr Leu Tyr Asn Pro	
40 45 50	
ggc gcc acc ctc cta ttg gca cca ttg gga tat atc acc cat ttc acg	307
Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr Ile Thr His Phe Thr	
55 60 65	
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Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu Leu Ala Ile Val Leu	
70 75 80 85	
gcg ttc ggg ctg ctg acc aga ctc tcc ggt tgg gcg ctg cgc agc atg	403
Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp Ala Leu Arg Ser Met	
90 95 100	
gtg tgg ccg att gcg atc gcc ttg gcg atg ctg aca gaa acc gtg caa	451
Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu Thr Glu Thr Val Gln	
105 110 115	
aac acc ctc att ttc tcc aac atc aac ggc atc ctg ctg ctc atg ttg	499
Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile Leu Leu Leu Met Leu	
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gcg att ttc ctg tgg tgc gtg gtg cac aaa aaa tcc tgg ttg ggc gga	547
Ala Ile Phe Leu Trp Cys Val Val His Lys Lys Ser Trp Leu Gly Gly	
135 140 145	
cta gtc att ggt ttg gcc att ttg atc aaa ccc atg ttc ctg cca ctt	595
Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro Met Phe Leu Pro Leu	
150 155 160 165	
ctc ttc cta cct ttg gtg aaa aag caa tgg gga tcg ctc atc ctc ggc	643
Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly	
170 175 180	
att tta acc cca gtg att ttc aat gca gtg gcc tgg ttc tta gtt ccg	691
Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro	
185 190 195	
gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctt ggt gaa act	739
Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Glu Thr	
200 205 210	
cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga	787
Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly	
215 220 225	
atg ccc acc tgg atg gaa atc acc tgg ttc ctc atc ttc ggc gca atg	835
Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met	
230 235 240 245	
gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca	883

Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
 250 255 260
 tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc 931
 Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
 265 270 275
 ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct 979
 Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
 280 285 290
 atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt 1027
 Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
 295 300 305
 gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc 1075
 Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
 310 315 320 325
 cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc 1123
 Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
 330 335 340
 gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc 1171
 Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
 345 350 355
 tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att 1219
 Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
 360 365 370
 acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt 1268
 Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
 375 380 385
 caaactcatc agc 1281

<210> 754
 <211> 386
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 754
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 Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His
 35 40 45
 Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr
 50 55 60
 Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu
 65 70 75 80
 Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp
 85 90 95

Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu
100 105 110

Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile
115 120 125

Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys
130 135 140

Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro
145 150 155 160

Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly
165 170 175

Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala
180 185 190

Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro
195 200 205

Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu
210 215 220

Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu
225 230 235 240

Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe
245 250 255

Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu
260 265 270

Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser
275 280 285

Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val
290 295 300

Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro
305 310 315 320

Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu
325 330 335

Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe
340 345 350

Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr
355 360 365

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
370 375 380

Thr Ala
385

<210> 755

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> FRXA01711

<400> 755

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gtgggatagc atcggcaacg cggttgcatg gccgttggcc atg ttg ttg atg gcg 115
Met Leu Leu Met Ala
1 5
cat cgc ttc ttc gtg ctt gcg att aac ggc gca gtc acc gac gat ttc 163
His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala Val Thr Asp Asp Phe
10 15 20
acg acg gtt tat agt gct tta cga cgt ttc gtt gaa ggt att ccg gtc 211
Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val Glu Gly Ile Pro Val
25 30 35
tac aac gag gtc tac cac ttc gtc gat ccg cac tac ctc tat aac ccg 259
Tyr Asn Glu Val Tyr His Phe Val Asp Pro His Tyr Leu Tyr Asn Pro
40 45 50
ggc gcc acc ctc cta ttg gca cca ttg gga tat atc acc cat ttc acg 307
Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr Ile Thr His Phe Thr
55 60 65
ttg gct cgg tgg atg ttc atc gcg gtg aac ctc ctt gcc att gtt tta 355
Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu Leu Ala Ile Val Leu
70 75 80 85
gcg ttc ggg ctg ctg acc aga ctc tcc ggt tgg gcg ctg cgc agc atg 403
Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp Ala Leu Arg Ser Met
90 95 100
gtg tgg ccg att gcg atc gcc ttg gcg atg ctg aca gaa acc gtg caa 451
Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu Thr Glu Thr Val Gln
105 110 115
aac acc ctc att ttc tcc aac atc aac ggc atc ctg ctg ctc atg ttg 499
Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile Leu Leu Leu Met Leu
120 125 130
gcg att ttc ctg tgg tgc gtg gtg cac aaa aaa tcc tgg ttg ggc gga 547
Ala Ile Phe Leu Trp Cys Val Val His Lys Lys Ser Trp Leu Gly Gly
135 140 145
cta gtc att ggt ttg gcc att ttg atc aaa ccc atg ttc ctg cca ctt 595
Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro Met Phe Leu Pro Leu
150 155 160 165
ctc ttc cta cct ttg gtg aaa aag caa tgg gga tgc ctc atc ctc ggc 643
Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly
170 175 180
att tta acc cca gtg att ttc aat gca gtg gcc tgg ttc tta gtt ccg 691
Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro

185	190	195	
gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctt ggt gaa act			739
Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Glu Thr			
200	205	210	
cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga			787
Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly			
215	220	225	
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Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met			
230	235	240	245
gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca			883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro			
250	255	260	
tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc			931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe			
265	270	275	
ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct			979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro			
280	285	290	
atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt			1027
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val			
295	300	305	
gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc			1075
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser			
310	315	320	325
cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc			1123
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr			
330	335	340	
gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc			1171
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile			
345	350	355	
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att			1219
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile			
360	365	370	
acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt			1268
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala			
375	380	385	
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<210> 756

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 756

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 20 25 30
 Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His
 35 40 45
 Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr
 50 55 60
 Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu
 65 70 75 80
 Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp
 85 90 95
 Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu
 100 105 110
 Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile
 115 120 125
 Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys
 130 135 140
 Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro
 145 150 155 160
 Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly
 165 170 175
 Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala
 180 185 190
 Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro
 195 200 205
 Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu
 210 215 220
 Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu
 225 230 235 240
 Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe
 245 250 255
 Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu
 260 265 270
 Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser
 275 280 285
 Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val
 290 295 300
 Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro
 305 310 315 320
 Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu
 325 330 335

gtc tcg cta acc aag cgt gat cga ttg tcc ggt gtg ttg gcg tcc atc 547
 Val Ser Leu Thr Lys Arg Asp Arg Leu Ser Gly Val Leu Ala Ser Ile
 135 140 145

gat gcc gct gtt gcc gct ggc ctt cac cca gtg aag atc aac gcc gtg 595
 Asp Ala Ala Val Ala Ala Gly Leu His Pro Val Lys Ile Asn Ala Val
 150 155 160 165

gtc atg cct ggg gtc aat gaa gta gat atc gtc ccc ctt gcg gaa tac 643
 Val Met Pro Gly Val Asn Glu Val Asp Ile Val Pro Leu Ala Glu Tyr
 170 175 180

tgc att tcc aaa ggc tcc caa ctg cga ttc atc gaa caa atg cca ctt 691
 Cys Ile Ser Lys Gly Ser Gln Leu Arg Phe Ile Glu Gln Met Pro Leu
 185 190 195

ggc ccg cgc gag cag tgg aaa cgc ggc gat atg gtc aca gcc gaa gaa 739
 Gly Pro Arg Glu Gln Trp Lys Arg Gly Asp Met Val Thr Ala Glu Glu
 200 205 210

atc ctg gcg cgc ctg gaa gaa aaa ttc acc tta tcc ccc gcc aag gaa 787
 Ile Leu Ala Arg Leu Glu Glu Lys Phe Thr Leu Ser Pro Ala Lys Glu
 215 220 225

ccc cga gga gct gca cct gct gcg ctg tgg aat gtg gta gat aaa tcc 835
 Pro Arg Gly Ala Ala Pro Ala Ala Leu Trp Asn Val Val Asp Lys Ser
 230 235 240 245

aac cct gat atc act gga caa atc ggc atc atc gcc tcg gtg acg cac 883
 Asn Pro Asp Ile Thr Gly Gln Ile Gly Ile Ile Ala Ser Val Thr His
 250 255 260

cca ttt tgc gga gat tgc gat cgc tcc cgc ctc acc acc gac ggc acc 931
 Pro Phe Cys Gly Asp Cys Asp Arg Ser Arg Leu Thr Thr Asp Gly Thr
 265 270 275

atc cga aac tgc ctt ttc tcc cgc act gaa act ccc cta cgt gac gcg 979
 Ile Arg Asn Cys Leu Phe Ser Arg Thr Glu Thr Pro Leu Arg Asp Ala
 280 285 290

ctt cgc gac ggc gcc tcc gac gat gag ctc gcg caa ctg tgg gca ggc 1027
 Leu Arg Asp Gly Ala Ser Asp Asp Glu Leu Ala Gln Leu Trp Ala Gly
 295 300 305

gcc atg tgg gag aag aaa ccc ggc cat ggc atc gac gat gaa ggc ttc 1075
 Ala Met Trp Glu Lys Lys Pro Gly His Gly Ile Asp Asp Glu Gly Phe
 310 315 320 325

ctc caa cca gat cgc ccc atg tct gcc atc ggg gct agc cca tac cag 1123
 Leu Gln Pro Asp Arg Pro Met Ser Ala Ile Gly Ala Ser Pro Tyr Gln
 330 335 340

<210> 758

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 758

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Gly Leu Glu Trp Leu Pro Thr Glu Gln Thr Leu Asn Asp Ala Glu Val	35	40	45
Leu Arg Leu Ile Arg Ile Ala Val Val Lys Leu Gly Ile Arg Gln Ile	50	55	60
Arg Phe Thr Gly Gly Glu Pro Leu Leu Arg Lys Asn Leu Glu Asp Ile	65	70	75
Ile Ala Gly Thr Ala Ala Leu Arg Thr Asp Glu Gly Glu Lys Val His	85	90	95
Ile Ala Leu Thr Thr Asn Gly Leu Gly Leu Asp Lys Arg Ile Ala Gly	100	105	110
Leu Lys Glu Ala Gly Leu Asp Arg Val Asn Ile Ser Leu Asp Thr Ile	115	120	125
Asp Ala Glu Arg Tyr Val Ser Leu Thr Lys Arg Asp Arg Leu Ser Gly	130	135	140
Val Leu Ala Ser Ile Asp Ala Ala Val Ala Ala Gly Leu His Pro Val	145	150	155
Lys Ile Asn Ala Val Val Met Pro Gly Val Asn Glu Val Asp Ile Val	165	170	175
Pro Leu Ala Glu Tyr Cys Ile Ser Lys Gly Ser Gln Leu Arg Phe Ile	180	185	190
Glu Gln Met Pro Leu Gly Pro Arg Glu Gln Trp Lys Arg Gly Asp Met	195	200	205
Val Thr Ala Glu Glu Ile Leu Ala Arg Leu Glu Glu Lys Phe Thr Leu	210	215	220
Ser Pro Ala Lys Glu Pro Arg Gly Ala Ala Pro Ala Ala Leu Trp Asn	225	230	235
Val Val Asp Lys Ser Asn Pro Asp Ile Thr Gly Gln Ile Gly Ile Ile	245	250	255
Ala Ser Val Thr His Pro Phe Cys Gly Asp Cys Asp Arg Ser Arg Leu	260	265	270
Thr Thr Asp Gly Thr Ile Arg Asn Cys Leu Phe Ser Arg Thr Glu Thr	275	280	285
Pro Leu Arg Asp Ala Leu Arg Asp Gly Ala Ser Asp Asp Glu Leu Ala	290	295	300
Gln Leu Trp Ala Gly Ala Met Trp Glu Lys Lys Pro Gly His Gly Ile	305	310	315
Asp Asp Glu Gly Phe Leu Gln Pro Asp Arg Pro Met Ser Ala Ile Gly	325	330	335

Ala Ser Pro Tyr Gln
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<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(634)

<223> RXN01734

<400> 759

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                                     Met Thr Asp Pro Ile
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Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala Met Arg Arg Asn Gly
                10                15                20

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Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe Arg Arg Pro Pro Ala
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Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly Arg Ala Ser Gly Leu
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Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala Glu Ser Leu Gly Ser
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Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp Gly Lys Asp Ile Ala
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ggc ggt tgg gtg acg tcc aac tgg gaa gag ctt gtt ggc gcg aag att 403
Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu Val Gly Ala Lys Ile
                90                95                100

gcg cag cat acg cgc gtg gaa atg atc aaa gat aag aag ctt ttt atc 451
Ala Gln His Thr Arg Val Glu Met Ile Lys Asp Lys Lys Leu Phe Ile
                105                110                115

act tgt gat tcc aca gcg tgg gcc acc aat ctg cgc atg atg cag cgg 499
Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu Arg Met Met Gln Arg
                120                125                130

caa atc ctg cag gta atc gct gaa aaa gtg ggt cca aat att att aca 547
Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly Pro Asn Ile Ile Thr
                135                140                145

gag ctg cgt att ttt ggg cct cag gcc cca agc tgg cgc aag ggg ccg 595
Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser Trp Arg Lys Gly Pro
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 35 40 45
 Arg Ala Ser Gly Leu Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala
 50 55 60
 Glu Ser Leu Gly Ser Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp
 65 70 75 80
 Gly Lys Asp Ile Ala Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu
 85 90 95
 Val Gly Ala Lys Ile Ala Gln His Thr Arg Val Glu Met Ile Lys Asp
 100 105 110
 Lys Lys Leu Phe Ile Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu
 115 120 125
 Arg Met Met Gln Arg Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly
 130 135 140
 Pro Asn Ile Ile Thr Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser
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 Trp Arg Lys Gly Pro Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr
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Tyr Gly

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Met Thr Asp Pro Ile
1 5

gag cag gca ttt gaa cgc atc cgc gcc gaa gcc atg cgc aga aat gga 163
Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala Met Arg Arg Asn Gly
10 15 20

tcc gtt ccc gac ctc aat aaa aac gat gct ttt cga cgc cca cct gcg 211
Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe Arg Arg Pro Pro Ala
25 30 35

ccg aaa ggg ggc gtc gaa aag cgc aaa aaa ggc cgt gca agc ggc cta 259
Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly Arg Ala Ser Gly Leu
40 45 50

gac ggc cgc cag aaa cga tat gtg cgc ggc gcg gag tcg ctg gga tcg 307
Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala Glu Ser Leu Gly Ser
55 60 65

gtg ctg aac aag gaa att cag cgt cgt ggc tgg ggc aaa gac att gcc 355
Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp Gly Lys Asp Ile Ala
70 75 80 85

ggc ggt tgg gtg acg tcc aac tgg gaa gag ctt gtt ggc gcg aag att 403
Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu Val Gly Ala Lys Ile
90 95 100

gcg cag cat acg cgc gtg gaa atg atc aaa gat aag aag ctt ttt atc 451
Ala Gln His Thr Arg Val Glu Met Ile Lys Asp Lys Lys Leu Phe Ile
105 110 115

act tgt gat tcc aca gcg tgg gcc acc aat ctg cgc atg atg cag cgg 499
Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu Arg Met Met Gln Arg
120 125 130

caa atc ctg cag gta atc gct gaa aaa gtg ggt cca aat att att aca 547
Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly Pro Asn Ile Ile Thr
135 140 145

gag ctg cgt att ttt ggg cct cag gcc cca agc tgg cgc aag ggg ccg 595
Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser Trp Arg Lys Gly Pro
150 155 160 165

ttg cac gta aaa gga cgc ggt ccg aga gac aca tac gga tagtttggtg 644
Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr Tyr Gly
170 175

ataaaaaccg tcg 657

<210> 762

<211> 178

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<400> 762

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Arg Arg Pro Pro Ala Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly	35	40	45
Arg Ala Ser Gly Leu Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala	50	55	60
Glu Ser Leu Gly Ser Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp	65	70	75
Gly Lys Asp Ile Ala Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu	85	90	95
Val Gly Ala Lys Ile Ala Gln His Thr Arg Val Glu Met Ile Lys Asp	100	105	110
Lys Lys Leu Phe Ile Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu	115	120	125
Arg Met Met Gln Arg Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly	130	135	140
Pro Asn Ile Ile Thr Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser	145	150	155
Trp Arg Lys Gly Pro Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr	165	170	175
Tyr Gly			

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 Met Gln Glu Lys Pro
 1 5
 gag atg cca gcg att gag gtc atc cgt tca gcg aaa cgc acc aaa act 163
 Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala Lys Arg Thr Lys Thr
 10 15 20
 gtt caa gct cga att gtg gac ggg caa atc cag gtg cgc atc cct gcg 211
 Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln Val Arg Ile Pro Ala
 25 30 35

cac gtg ccg gat tat gtg ttg gat gcg gtg ttg gtg cat gag ctg acg 499
 His Val Pro Asp Tyr Val Leu Asp Ala Val Leu Val His Glu Leu Thr
 120 125 130

cat acg ttt att gcg ggg cat tcg gcg gag ttt tgg gag tgg gca gac 547
 His Thr Phe Ile Ala Gly His Ser Ala Glu Phe Trp Glu Trp Ala Asp
 135 140 145

aaa acg ccc ctg gca gag agg gcc aag ggc tat ttg gag gcg tat cag 595
 Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr Leu Glu Ala Tyr Gln
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cgg tgg ggc tgaaggttta gttcttgtcg gag 627
 Arg Trp Gly

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 <211> 168
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 766
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Lys Arg Thr Lys Thr Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln
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Val Arg Ile Pro Ala Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val
 35 40 45

Gly Glu Ile Val Ala Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser
 50 55 60

Ser Asp Ala Asp Leu Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val
 65 70 75 80

Leu Glu Gly Arg Ala Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln
 85 90 95

Lys Gly Arg Trp Gly Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile
 100 105 110

Ser Asp Arg Leu Lys His Val Pro Asp Tyr Val Leu Asp Ala Val Leu
 115 120 125

Val His Glu Leu Thr His Thr Phe Ile Ala Gly His Ser Ala Glu Phe
 130 135 140

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 145 150 155 160

Leu Glu Ala Tyr Gln Arg Trp Gly
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 Val Lys Ile Lys Ser
 1 5

gta ttt ttg agc acc gct tta agc gct tcc tta ctg ctc gga atc acc 163
 Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu Leu Leu Gly Ile Thr
 10 15 20

cca ccc gtg ctg gga gca acg atc aac ccc agt ttg cct ctt tct gcg 211
 Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser Leu Pro Leu Ser Ala
 25 30 35

ttg agc tcc tcg gac gat atc gcc gta ccc aac ttc gcc aaa gaa tta 259
 Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn Phe Ala Lys Glu Leu
 40 45 50

ccg tta gct ttt gat gta cca gca ggc act gtt ccc caa agc ttg agt 307
 Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val Pro Gln Ser Leu Ser
 55 60 65

gga acg ctg cag att cct gcc gag ttt tct ggc ggc gtc gtg gag ttt 355
 Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly Gly Val Val Glu Phe
 70 75 80 85

tat gac ggt gac cgg ctc ttt cac acc ctg cgc cta gaa gtt aat gat 403
 Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg Leu Glu Val Asn Asp
 90 95 100

tcc cga gca cac att gag gtt ccg ctg caa agc gtt cct gtc gaa gac 451
 Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser Val Pro Val Glu Asp
 105 110 115

ggc cgc gcc acc ttt tgg ttg cgc gcc atg ttg gat cct gta aac aac 499
 Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu Asp Pro Val Asn Asn
 120 125 130

cag tgg tgc tac gag gag cag gaa gtc cgc ttc tta gac gga aac gtc 547
 Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe Leu Asp Gly Asn Val
 135 140 145

acc ttt gaa ggg gcg acg att aac cca gct gtg gtg gct gat tac ttc 595
 Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val Val Ala Asp Tyr Phe
 150 155 160 165

ccg tca gtg ctg cgc gcg ttg aca att tac gtc ccg gaa aac ccc tct 643
 Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val Pro Glu Asn Pro Ser
 170 175 180

gag gca gta caa gaa gcc acg tta gag gtt gcg acc tcc ctg gat tcg 691
 Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala Thr Ser Leu Asp Ser
 185 190 195

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Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val Glu Thr Leu Pro Thr	
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Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp Phe Glu Arg Gln Ile	
215 220 225	
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Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr Gln Lys Thr Glu Leu	
230 235 240 245	
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Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg Leu Asn Gly Asn Ala	
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gac gag ctt tac gat caa gcg cgc ttg ctt acc gac gca acc ctg cca	931
Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr Asp Ala Thr Leu Pro	
265 270 275	
ctt gcc gta gac acc gaa gta acg gcc tca ggt ttt ggt gat gtg ccc	979
Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly Phe Gly Asp Val Pro	
280 285 290	
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Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu Leu Gly Ile Thr Gln	
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Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val Thr Leu Gly Ile Glu	
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Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met Asp Leu His Ile Thr	
330 335 340	
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Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr Thr Asp Asp Thr Gly	
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atc att gac cgt gag ttc aac gtt cct gga gac ttg gtc aac cgc tac	1267
Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp Leu Val Asn Arg Tyr	
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Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly Asp Val Asn Cys Gly	
390 395 400 405	
gtc acc cag ccc gta ggc ctc aac att gat tcc gac agc ctt gtc acc	1363
Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser Asp Ser Leu Val Thr	
410 415 420	
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Ser Gln His Ser Asp Val Pro Val Leu Asn Gly Phe Arg Ser Leu Pro	
425 430 435	
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Gln	Ser	Phe	Gln	Pro	Arg	Val	Asp	Val	Ala	Phe	Ala	Asp	Pro	Ser	Val	
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Gln	Glu	Leu	Ser	Arg	Ala	Val	Ser	Val	Val	Leu	Gly	Ile	Gln	Ser	Met	
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agc	tcc	cag	cgc	atc	cgc	cca	cac	ctg	gtt	aac	tgg	gat	gaa	gcc	gta	1555
Ser	Ser	Gln	Arg	Ile	Arg	Pro	His	Leu	Val	Asn	Trp	Asp	Glu	Ala	Val	
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Leu	Gln	Thr	Asn	Ala	Ala	Leu	Val	Val	Gly	Ser	Ile	Gln	Ala	Val	Trp	
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Asp	Ala	Asp	Lys	Lys	Arg	Thr	Val	Ile	Val	Ala	Ser	Ser	Gln	Asp	Asn	
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Pro	Pro	Asp	Leu	Asp	Ala	Leu	Ile	Ser	Trp	Met	Gly	Glu	Asp	Arg	Glu	
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cgc	tgg	agt	gat	ctc	aac	ggc	gac	ctg	att	gtc	aaa	gtc	cga	gac	cgc	1891
Arg	Trp	Ser	Asp	Leu	Asn	Gly	Asp	Leu	Ile	Val	Lys	Val	Arg	Asp	Arg	
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Ser	Ala	Thr	Ala	Phe	Ile	Ala	Ile	Gly	Val	Ser	Leu	Val	Val	Ile	Ala	
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Leu	Ile	Val	Ala	Ala	Val	Val	Ser	Val	Ser	Arg	Arg	Ser	Gln	Lys	Gly	
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Tyr	Lys															

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<212> PRT

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Phe Ala Lys Glu Leu Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val
50 55 60
Pro Gln Ser Leu Ser Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly
65 70 75 80
Gly Val Val Glu Phe Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg
85 90 95
Leu Glu Val Asn Asp Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser
100 105 110
Val Pro Val Glu Asp Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu
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Asp Pro Val Asn Asn Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe
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Leu Asp Gly Asn Val Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val
145 150 155 160
Val Ala Asp Tyr Phe Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val
165 170 175
Pro Glu Asn Pro Ser Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala
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Thr Ser Leu Asp Ser Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val
195 200 205
Glu Thr Leu Pro Thr Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp
210 215 220
Phe Glu Arg Gln Ile Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr
225 230 235 240
Gln Lys Thr Glu Leu Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg
245 250 255
Leu Asn Gly Asn Ala Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr
260 265 270
Asp Ala Thr Leu Pro Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly
275 280 285
Phe Gly Asp Val Pro Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu
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305 310 315 320

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325 330 335

Asp Leu His Ile Thr Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala
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355 360 365

Thr Asp Asp Thr Gly Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp
370 375 380

Leu Val Asn Arg Tyr Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly
385 390 395 400

Asp Val Asn Cys Gly Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser
405 410 415

Asp Ser Leu Val Thr Ser Gln His Ser Asp Val Pro Val Leu Asn Gly
420 425 430

Phe Arg Ser Leu Pro Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe
435 440 445

Ala Asp Pro Ser Val Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu
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Gly Ile Gln Ser Met Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn
465 470 475 480

Trp Asp Glu Ala Val Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala
485 490 495

Ala Gly Ala Lys Thr Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly
500 505 510

Gln Thr Leu Glu Ile Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu
515 520 525

Gln Leu Thr Arg Ser Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser
530 535 540

Ile Gln Ala Val Trp Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala
545 550 555 560

Ser Ser Gln Asp Asn Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met
565 570 575

Gly Glu Asp Arg Glu Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val
580 585 590

Lys Val Arg Asp Arg Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro
595 600 605

Asp Gln Pro Gly Arg Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser
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Arg Ser Gln Lys Gly Tyr Lys

645

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                                   Val Lys Ile Lys Ser
                                   1 5
gta ttt ttg agc acc gct tta agc gct tcc tta ctg ctc gga atc acc 163
Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu Leu Leu Gly Ile Thr
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cca ccc gtg ctg gga gca acg atc aac ccc agt ttg cct ctt tct gcg 211
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Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg Leu Glu Val Asn Asp
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Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser Val Pro Val Glu Asp
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Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val Glu Thr Leu Pro Thr	
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Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp Phe Glu Arg Gln Ile	
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Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr Gln Lys Thr Glu Leu	
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Pro Gln Ser Leu Ser Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly
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Gly Val Val Glu Phe Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg
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Leu Glu Val Asn Asp Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser
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Val Pro Val Glu Asp Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu
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Leu Asp Gly Asn Val Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val
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Val Ala Asp Tyr Phe Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val
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Pro Glu Asn Pro Ser Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala
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Thr Ser Leu Asp Ser Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val
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Glu Thr Leu Pro Thr Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp
210 215 220

Phe Glu Arg Gln Ile Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr
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Gln Lys Thr Glu Leu Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg
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Leu Asn Gly Asn Ala Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr
260 265 270

Asp Ala Thr Leu Pro Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly
275 280 285

Phe Gly Asp Val Pro Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu
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 Leu Gly Ile Thr Gln Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val
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 Thr Leu Gly Ile Glu Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met
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 Asp Leu His Ile Thr Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala
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 Gly Gln Ile Thr Phe Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr
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 Thr Asp Asp Thr Gly Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp
 370 375 380
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 Asp Ser Leu Val Thr Ser Gln His Ser Asp Val Pro Val Leu Asn Gly
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 Gly Ile Gln Ser Met Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn
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 Trp Asp Glu Ala Val Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala
 485 490 495
 Ala Gly Ala Lys Thr Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly
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 Gln Thr Leu Glu Ile Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu
 515 520 525
 Gln Leu Thr Arg Ser Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser
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 Ile Gln Ala Val Trp Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala
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 Ser Ser Gln Asp Asn Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met
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 Lys Val Arg Asp Arg Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro
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Asp Gln Pro Gly Arg Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser
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Val Thr Ala Thr Val
1 5

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10 15 20

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Ile Ala Arg Met Glu Leu Lys His Asn Arg His Lys Thr Trp Arg Arg
25 30 35

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Arg Thr Met Ala Val Val Met Thr Leu Leu Ile Ser Val Gly Leu Ser
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Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu Lys Cys Leu Glu Ala
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Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr Ser Met Tyr Arg Met

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Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu Asp Ser Glu Asp Ala			
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Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys Ala Ala Asn Gly Gly			
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aat gtc ctt ggt tat gct gac gcg aaa cac aac gag gac tct ggt tgg			739
Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn Glu Asp Ser Gly Trp			
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Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys Thr Tyr Ser Tyr Asp			
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Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser Ser Lys Ala Glu Asp			
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Ile Ala Tyr Ile Ile Ser Gly Gly Ile Asp Leu Val Phe Asn Thr Val			
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Leu Asn Ile Leu Ser Thr Ile Asn Pro Phe Arg Leu Leu Val Gly Pro			
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Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile Arg Val Val Tyr Gly			
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Ala Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp	
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Leu Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser				
	1130	1135	1140	
agt tcc gat cag gcc atg aat gac gca gct ctt cag att gca gcg tct				3571
Ser Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser				
	1145	1150	1155	
cag ggt ctt gca cca gca ggt tcc ata gct ggt atg gag caa ctt agt				3619
Gln Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser				
	1160	1165	1170	
gct caa gcc act gaa gca cct gct gga aag gcc gcc aag cag ctt ggc				3667
Ala Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly				
	1175	1180	1185	
gat ctt tct ggc tca gcg ctc aat act cag ctg gcg tcc atg gga cag				3715
Asp Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln				
	1190	1195	1200	1205
cag gta ggt gac agt gtg aac agc gct tat gct gca gcc ggt atg ggt				3763
Gln Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly				
	1210	1215	1220	
ggt gtt gat gtg gct gcc aag gtc acc gag gca gca cag cac ttg tct				3811
Gly Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser				
	1225	1230	1235	
cag gtt cca ggt cag att cag aat gct gtg acc aat gcg gat gct ggt				3859
Gln Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly				
	1240	1245	1250	
tcc tct ggc gca agc ttt ggt cag atg gca cag ggg gca gct ggt att				3907
Ser Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile				
	1255	1260	1265	
gcc ggt gtc gca ggt gtg atc ggt gca gcg gcc gca gca agc tct gca				3955
Ala Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala				
	1270	1275	1280	1285
gca caa gcc gca ggt act gtc cag ggt gcg atg ggt aat gct gca gct				4003
Ala Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala				
	1290	1295	1300	
ggt gcg gga atg atc aac aac gct gtt tcc ggt gga gct act gcc tca				4051
Gly Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser				
	1305	1310	1315	
aca ggt gcc gca cat gtg gtc aat gca tca cat gga cca gtg gcg cct				4099
Thr Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro				
	1320	1325	1330	
ggt cag gct cac tac caa gag tct ggt cat gca caa gca ttt gtg cag				4147
Gly Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln				
	1335	1340	1345	
aac aac cag gcc aac acc gcg cac aca gca aac acg cgt gca ccg tca				4195
Asn Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser				
	1350	1355	1360	1365

tca gct caa att atg ggc gcg aac gtt gct ggc tca ctg gca tca cag 4243
 Ser Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln
 1370 1375 1380

gct gta cga gga atc ggt cag cct ggt cag atg ggt gct aat gtt cgc 4291
 Ala Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg
 1385 1390 1395

gac gcg atg ggt ggc agc gga cgc tct ggt ggc cgt ggt gga gca act 4339
 Asp Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr
 1400 1405 1410

caa ggc ggt cga ggc gca cag cgc agc ggt gtc agt gct aag aac ggt 4387
 Gln Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly
 1415 1420 1425

atc cgt gca cag cga ggt cag aag cct tct gtg acc ggc cag gcg atg 4435
 Ile Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met
 1430 1435 1440 1445

aat gca gca atg cgt tca gca gcg gta agc ggt cgc atg gca aac atg 4483
 Asn Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met
 1450 1455 1460

gac ggc aac agt gta ggt ggc act gaa gca gat cca cag cag ggg agt 4531
 Asp Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser
 1465 1470 1475

ggc gta acc gag aag ggt gat aaa ggc gtt aaa tagcgtgtaa aacacaatga 4584
 Gly Val Thr Glu Lys Gly Asp Lys Gly Val Lys
 1480 1485

ccg 4587

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<211> 1488

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

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Asp Val Asp Ala Glu Ile Ala Arg Met Glu Leu Lys His Asn Arg His
 20 25 30

Lys Thr Trp Arg Arg Arg Thr Met Ala Val Val Met Thr Leu Leu Ile
 35 40 45

Ser Val Gly Leu Ser Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala
 50 55 60

Asn Ala Phe Ala Ser Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly
 65 70 75 80

Glu Val Ala Phe Glu Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met
 85 90 95

Leu Leu Lys Cys Ile Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu

100					105					110					
Lys	Cys	Leu	Glu	Ala	Glu	Asp	Val	Leu	Lys	Cys	Phe	Tyr	Asp	Ala	Lys
	115						120					125			
Asn	Glu	Glu	Gln	Arg	Lys	Glu	Gln	Asn	Leu	Asp	Lys	Ala	Pro	Asp	Tyr
	130					135					140				
Ser	Met	Tyr	Arg	Met	Ala	Ser	Ala	Met	Ala	Ser	Phe	Tyr	Gly	Asn	Gly
145					150					155					160
Arg	Ala	Ala	Thr	Ala	Gly	Val	Glu	Glu	Gly	Gly	Pro	Asn	Glu	Phe	Leu
				165					170					175	
Asp	Ser	Glu	Asp	Ala	Gly	Leu	Lys	Val	Trp	Glu	Gly	Ile	Leu	Ser	Lys
			180					185					190		
Ala	Ala	Asn	Gly	Gly	Asn	Val	Leu	Gly	Tyr	Ala	Asp	Ala	Lys	His	Asn
		195					200					205			
Glu	Asp	Ser	Gly	Trp	Phe	Phe	Gly	Asn	Gly	Val	Ala	Asn	Asn	Glu	Lys
	210					215					220				
Thr	Tyr	Ser	Tyr	Asp	Ser	Leu	Ala	Asp	His	Ala	Phe	Gln	Gly	Pro	Tyr
225					230					235					240
His	Phe	Ala	Leu	Phe	Gly	Ala	Thr	Leu	Ser	Gly	Leu	Gly	Phe	Asp	Ser
				245					250					255	
Ser	Lys	Ala	Glu	Asp	Ser	Gln	Thr	Asp	Phe	Ala	Gln	Arg	Lys	Gly	Met
			260					265					270		
Gly	Tyr	Ala	Met	Met	Ile	Ala	Tyr	Ile	Ile	Ser	Gly	Gly	Ile	Asp	Leu
		275					280					285			
Val	Phe	Asn	Thr	Val	Leu	Asn	Ile	Leu	Ser	Thr	Ile	Asn	Pro	Phe	Arg
	290					295					300				
Leu	Leu	Val	Gly	Pro	Val	Ser	Gln	Asn	Thr	Asn	Lys	Thr	Phe	Thr	Glu
305					310					315					320
Asn	Met	Ala	Gly	Gly	Gln	Thr	Thr	Glu	Gly	Thr	Pro	Phe	Glu	Gly	Met
				325					330					335	
Thr	Asp	Phe	Phe	Gly	Leu	Ile	Tyr	Asn	Trp	Ser	Val	Thr	Val	Gly	Trp
				340				345						350	
Leu	Ile	Gly	Ile	Pro	Val	Ser	Ile	Gly	Leu	Phe	Met	Met	Gly	Ala	Leu
		355					360					365			
Met	Phe	Arg	Arg	Met	Asp	Lys	Gly	Ser	Ala	Phe	Lys	Lys	Val	Val	Ile
						375					380				
Arg	Val	Val	Tyr	Gly	Val	Val	Gly	Leu	Pro	Leu	Leu	Gly	Val	Ser	Tyr
385					390					395					400
Thr	Gly	Ala	Leu	Asp	Ser	Phe	Leu	Asp	Ser	Gly	Ser	Ser	Thr	Ser	Ala
				405					410					415	
Gly	Ser	Asn	Ala	Thr	Lys	Ile	Val	Leu	Ser	Thr	Tyr	Val	Asp	Phe	Gln
			420					425					430		

Ser Trp Ala Glu Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu
 435 440 445
 Ala Trp Ser Leu Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met
 450 455 460
 Val Arg Asn Ser Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe
 465 470 475 480
 Thr Thr Phe Lys Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp
 485 490 495
 Trp Met Glu Lys Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr
 500 505 510
 Ser Ser Ser Ser Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu
 515 520 525
 Ser Arg Tyr Ile Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr
 530 535 540
 Ser Ile Arg Ser Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly
 545 550 555 560
 Glu Ala Val Ala Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn
 565 570 575
 Thr Ala Ser Gly Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala
 580 585 590
 Asn Asn Pro Leu Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg
 595 600 605
 Pro Ile Asp Arg Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala
 610 615 620
 Ser Cys Asn Asn Ser Val Val Thr Gly Ser Arg Ala Val Val Gly Asp
 625 630 635 640
 Tyr Arg Ser Asp Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu
 645 650 655
 Asn Thr Ser Phe His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr
 660 665 670
 Ser Ala Ser Ser Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile
 675 680 685
 Gly Ser Gly Ala Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu
 690 695 700
 Met Gly Ser Phe Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu
 705 710 715 720
 Phe Asn Thr Ile Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe
 725 730 735
 Ala Ala Met Gly Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr
 740 745 750

Ile Ala Met Leu Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu
755 760 765

Ile Thr Arg Phe Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu
770 775 780

Ala Asp Ser Leu Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala
785 790 795 800

Gly Met Gly Leu Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala
805 810 815

Ile Ala Gly Met Val Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile
820 825 830

Phe Thr Ile Ile Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly Val
835 840 845

Asp Glu Thr Val Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val
850 855 860

Ser Ser Ala Gly Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala
865 870 875 880

Ala Thr Gly Leu Gly Ile Gly Ala Thr His Met Val Leu Asn Arg Asp
885 890 895

Gly Asp Gly Gly Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Gly
900 905 910

Ser Asp Ser Gly Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val
915 920 925

Thr Thr Val Ala Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala
930 935 940

Leu Asp Asn Tyr Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala
945 950 955 960

Phe Ala Ala Gly Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp
965 970 975

Gly Asp Ala Ile Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly
980 985 990

Val Val Asp Gly Ala Gly Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser
995 1000 1005

Ser Asp Gly Thr Thr Leu Asp Gly Glu Gly Ala Ser Val Asp Ala Gln
1010 1015 1020

Gly Asn Pro Leu His Ala Asp Gly Thr Pro Met Ser Ala Ala Glu Ala
1025 1030 1035 1040

Glu Met Lys Met Ala Gly Leu Ser Ser Ser Gly Thr Met Met Glu Lys
1045 1050 1055

Ser Gly Val Lys Ser Ser Gly Ile Thr Thr Ala Ala Asp Val Met Asp
1060 1065 1070

Asp Gln Ser Leu Ala Ser Ser Val Thr Glu Ser Gly Leu Ser Lys Ile

1075	1080	1085
Pro Asp Thr Tyr Gly Ala	Asp Val Ser Gly Ala	Ala Gly Thr Val Gly
1090	1095	1100
Thr Thr Gly Ala Asp	Tyr Ser Ala Thr Asp	Ser Ser Ala Gly Leu Asn
1105	1110	1115 1120
Met Ser Glu Ala Ala	Leu Gln Ser Gly Thr	Pro Met Gly Ala Leu Ala
1125	1130	1135
Gly Gly Ser Val Ser	Ser Ser Asp Gln Ala	Met Asn Asp Ala Ala Leu
1140	1145	1150
Gln Ile Ala Ala Ser	Gln Gly Leu Ala Pro	Ala Gly Ser Ile Ala Gly
1155	1160	1165
Met Glu Gln Leu Ser	Ala Gln Ala Thr Glu	Ala Pro Ala Gly Lys Ala
1170	1175	1180
Gly Lys Gln Leu Gly	Asp Leu Ser Gly Ser	Ala Leu Asn Thr Gln Leu
1185	1190	1195 1200
Ala Ser Met Gly Gln	Gln Val Gly Asp Ser	Val Asn Ser Ala Tyr Ala
1205	1210	1215
Ala Gly Gly Met Gly	Gly Val Asp Val Ala	Gly Lys Val Thr Glu Ala
1220	1225	1230
Ala Gln His Leu Ser	Gln Val Pro Gly Gln	Ile Gln Asn Ala Val Thr
1235	1240	1245
Asn Ala Asp Ala Gly	Ser Ser Gly Ala Ser	Phe Gly Gln Met Ala Gln
1250	1255	1260
Gly Ala Ala Gly Ile	Ala Gly Val Ala Gly	Val Ile Gly Ala Ala Gly
1265	1270	1275 1280
Ala Ala Ser Ser Ala	Ala Gln Gly Ala Gly	Thr Val Gln Gly Ala Met
1285	1290	1295
Gly Asn Ala Ala Ala	Gly Ala Gly Met Ile	Asn Asn Ala Val Ser Gly
1300	1305	1310
Gly Ala Thr Gly Ser	Thr Gly Ala Ala His	Val Val Asn Ala Ser His
1315	1320	1325
Gly Pro Val Ala Pro	Gly Gln Ala His Tyr	Gln Glu Ser Gly His Ala
1330	1335	1340
Gln Ala Phe Val Gln	Asn Asn Gln Ala Asn	Thr Ala His Thr Ala Asn
1345	1350	1355 1360
Thr Arg Ala Pro Ser	Ser Ala Gln Ile Met	Gly Ala Asn Val Ala Gly
1365	1370	1375
Ser Leu Ala Ser Gln	Ala Val Arg Gly Ile	Gly Gln Pro Gly Gln Met
1380	1385	1390
Gly Ala Asn Val Arg	Asp Ala Met Gly Gly	Ser Gly Arg Ser Gly Gly
1395	1400	1405

Arg Gly Gly Ala Thr Gln Gly Gly Arg Gly Ala Gln Arg Ser Gly Val
 1410 1415 1420

Ser Ala Lys Asn Gly Ile Arg Ala Gln Arg Gly Gln Lys Pro Ser Val
 1425 1430 1435 1440

Thr Gly Gln Ala Met Asn Ala Ala Met Arg Ser Ala Ala Val Ser Gly
 1445 1450 1455

Arg Met Ala Asn Met Asp Gly Asn Ser Val Gly Gly Thr Glu Ala Asp
 1460 1465 1470

Pro Gln Gln Gly Ser Gly Val Thr Glu Lys Gly Asp Lys Gly Val Lys
 1475 1480 1485

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 <213> Corynebacterium glutamicum

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 <222> (101)..(916)
 <223> FRXA00739

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agcaattggt taaaacgaat attgaggggg tggcgggcaa gtg act gcg aca gtt 115
 Val Thr Ala Thr Val
 1 5

tta gaa ccg caa cct gta cag ctt agt gag cag gac gta gat gct gag 163
 Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln Asp Val Asp Ala Glu
 10 15 20

att gcg cgc atg gag ctt aaa cac aac cga cac aag acg tgg cga cgc 211
 Ile Ala Arg Met Glu Leu Lys His Asn Arg His Lys Thr Trp Arg Arg
 25 30 35

cga acg atg gct gtt gtc atg acg ctc ttg atc tca gtg ggt ttg agc 259
 Arg Thr Met Ala Val Val Met Thr Leu Leu Ile Ser Val Gly Leu Ser
 40 45 50

ttt ggt gcg ttt ggt aac aag gaa cgt gaa gct aat gct ttc gcc agc 307
 Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala Asn Ala Phe Ala Ser
 55 60 65

gct att att gcc cag gtt gtc ggt gct atg ggc gag gtt gcc ttt gaa 355
 Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly Glu Val Ala Phe Glu
 70 75 80 85

gcg att tgt ccc agt gat ggt gac acc gag atg ctt ctt aag tgc atc 403
 Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met Leu Leu Lys Cys Ile
 90 95 100

acc gag aac tta ggt gaa atg cac att atc gag aag tgt ctc gaa gca 451
 Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu Lys Cys Leu Glu Ala
 105 110 115

gaa gat gtc ttg aag tgc ttc tac gat gcg aaa aac gaa gag caa cgt 499
 Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys Asn Glu Glu Gln Arg
 120 125 130
 aaa gaa cag aac ctt gat aaa gcc cct gat tac tcc atg tac cgt atg 547
 Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr Ser Met Tyr Arg Met
 135 140 145
 gcc tct gcg atg gca tcg ttc tat gcc aat ggt cgg gca gct act gcc 595
 Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly Arg Ala Ala Thr Ala
 150 155 160 165
 ggt gta gag gaa ggc gga ccg aac gag ttc ctc gat tct gag gac gcc 643
 Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu Asp Ser Glu Asp Ala
 170 175 180
 ggt ctt aag gtg tgg gag ggc att ctc agt aag gcc gcc aac gga ggc 691
 Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys Ala Ala Asn Gly Gly
 185 190 195
 aat gtc ctt ggt tat gct gac gcg aaa cac aac gag gac tct ggt tgg 739
 Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn Glu Asp Ser Gly Trp
 200 205 210
 ttc ttt ggt aat ggt gtt gcc aac aac gag aaa acg tac tcc tat gat 787
 Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys Thr Tyr Ser Tyr Asp
 215 220 225
 tct cta gct gat cat gcc ttt caa ggg cct tat cac ttt gca tta ttt 835
 Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr His Phe Ala Leu Phe
 230 235 240 245
 ggc gcg aca ctg agt ggc tta ggc ttt gat agc tca aag gcg gag gat 883
 Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser Ser Lys Ala Glu Asp
 250 255 260
 tcg cag act gat ttt gct cag cgt aag ggc atg 916
 Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
 265 270

<210> 774

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 774

Val Thr Ala Thr Val Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln
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 Asp Val Asp Ala Glu Ile Ala Arg Met Glu Leu Lys His Asn Arg His
 20 25 30
 Lys Thr Trp Arg Arg Arg Thr Met Ala Val Val Met Thr Leu Leu Ile
 35 40 45
 Ser Val Gly Leu Ser Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala
 50 55 60
 Asn Ala Phe Ala Ser Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly

65	70	75	80
Glu Val Ala Phe Glu Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met	85	90	95
Leu Leu Lys Cys Ile Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu	100	105	110
Lys Cys Leu Glu Ala Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys	115	120	125
Asn Glu Glu Gln Arg Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr	130	135	140
Ser Met Tyr Arg Met Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly	145	150	155
Arg Ala Ala Thr Ala Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu	165	170	175
Asp Ser Glu Asp Ala Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys	180	185	190
Ala Ala Asn Gly Gly Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn	195	200	205
Glu Asp Ser Gly Trp Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys	210	215	220
Thr Tyr Ser Tyr Asp Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr	225	230	235
His Phe Ala Leu Phe Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser	245	250	255
Ser Lys Ala Glu Asp Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met	260	265	270

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 <223> FRXA01587

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 Met Thr Asp Phe Phe
 1 5
 ggg ttg atc tat aac tgg tca gtg act gtg ggc tgg ctc atc ggt att 163
 Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp Leu Ile Gly Ile
 10 15 20
 cct gtc tcc att ggt ctg ttt atg atg ggt gcg ttg atg ttt cga cgc 211

Pro	Val	Ser	Ile	Gly	Leu	Phe	Met	Met	Gly	Ala	Leu	Met	Phe	Arg	Arg		
			25					30					35				
atg	gac	aag	gga	tca	gcg	ttt	aaa	aag	gtt	gtt	atc	cgc	gtc	gtg	tac	259	
Met	Asp	Lys	Gly	Ser	Ala	Phe	Lys	Lys	Val	Val	Ile	Arg	Val	Val	Tyr		
		40					45					50					
ggg	gtc	gtt	ggc	ctg	cca	ctg	ctt	ggg	gtc	tct	tat	acc	ggg	gcg	ctg	307	
Gly	Val	Val	Gly	Leu	Pro	Leu	Leu	Gly	Val	Ser	Tyr	Thr	Gly	Ala	Leu		
	55					60					65						
gat	tcc	ttc	ctc	gac	agc	ggg	agt	tcc	aca	agt	gct	gga	tca	aat	gcg	355	
Asp	Ser	Phe	Leu	Asp	Ser	Gly	Ser	Ser	Thr	Ser	Ala	Gly	Ser	Asn	Ala		
	70				75				80						85		
aca	aag	att	gtg	ttg	tcc	acc	tac	gtg	gat	ttc	caa	tca	tgg	gca	gaa	403	
Thr	Lys	Ile	Val	Leu	Ser	Thr	Tyr	Val	Asp	Phe	Gln	Ser	Trp	Ala	Glu		
			90					95						100			
aac	acc	cgt	atg	cgt	gtt	cct	gac	aaa	gta	aca	ctg	gcg	tgg	agt	ctg	451	
Asn	Thr	Arg	Met	Arg	Val	Pro	Asp	Lys	Val	Thr	Leu	Ala	Trp	Ser	Leu		
			105					110					115				
gag	gat	cag	gcg	cca	aca	ggg	cag	tcc	atg	cgg	atg	gta	cgc	aat	tcg	499	
Glu	Asp	Gln	Ala	Pro	Thr	Gly	Gln	Ser	Met	Arg	Met	Val	Arg	Asn	Ser		
		120					125					130					
gcg	ttg	gaa	att	aat	gct	caa	tca	aat	gag	agt	ttt	act	act	ttt	aag	547	
Ala	Leu	Glu	Ile	Asn	Ala	Gln	Ser	Asn	Glu	Ser	Phe	Thr	Thr	Phe	Lys		
	135					140					145						
aat	cca	ggg	tcc	atg	gat	cta	ggc	tat	agc	atg	gac	tgg	atg	gaa	aag	595	
Asn	Pro	Gly	Ser	Met	Asp	Leu	Gly	Tyr	Ser	Met	Asp	Trp	Met	Glu	Lys		
	150				155				160					165			
atg	gcg	gat	cca	gcc	aat	tct	ggc	acc	gat	ggg	acc	tca	tca	agt	tcg	643	
Met	Ala	Asp	Pro	Ala	Asn	Ser	Gly	Thr	Asp	Gly	Thr	Ser	Ser	Ser	Ser		
			170					175						180			
gcg	acg	act	att	ttc	cag	gga	acc	atc	gcg	cta	ctg	agt	cgt	tat	atc	691	
Ala	Thr	Thr	Ile	Phe	Gln	Gly	Thr	Ile	Ala	Leu	Leu	Ser	Arg	Tyr	Ile		
			185					190					195				
gac	aac	gac	agt	atc	tcc	tct	ggc	agt	ttc	gaa	acc	tct	att	cga	agt	739	
Asp	Asn	Asp	Ser	Ile	Ser	Ser	Gly	Ser	Phe	Glu	Thr	Ser	Ile	Arg	Ser		
		200					205					210					
gcg	atg	gaa	tct	ttg	acc	tcg	aaa	gag	gga	agt	ggc	gaa	gct	gtt	gcc	787	
Ala	Met	Glu	Ser	Leu	Thr	Ser	Lys	Glu	Gly	Ser	Gly	Glu	Ala	Val	Ala		
	215					220					225						
ggg	ggg	gat	gta	atg	gcc	tgg	gtt	act	ggg	tac	aac	aca	gcc	tct	ggg	835	
Gly	Gly	Asp	Val	Met	Ala	Trp	Val	Thr	Gly	Tyr	Asn	Thr	Ala	Ser	Gly		
	230				235				240				245				
ctt	aat	gag	atc	act	gct	gct	gaa	tta	gct	gat	gcg	aac	aat	cca	ttg	883	
Leu	Asn	Glu	Ile	Thr	Ala	Ala	Glu	Leu	Ala	Asp	Ala	Asn	Asn	Pro	Leu		
			250					255						260			
ctt	gag	gtc	agc	gac	tca	gct	ggg	ctg	cag	gga	cga	cct	att	gac	cgc	931	
Leu	Glu	Val	Ser	Asp	Ser	Ala	Gly	Leu	Gln	Gly	Arg	Pro	Ile	Asp	Arg		

265					270					275					
aat gcg gtg tca ttt aaa tct ggt gat gcg aca gcg tca tgc aac aac	979														
Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala Ser Cys Asn Asn															
280	285	290													
tca gtc gtg aca ggt tct cgt gct gtg gtc ggg gac tac cga agt gac	1027														
Ser Val Val Thr Gly Ser Arg Ala Val Val Gly Asp Tyr Arg Ser Asp															
295	300	305													
tgc aat atg tcg ccc ttg acg atg tac aac ttc ctc aac acc tca ttc	1075														
Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu Asn Thr Ser Phe															
310	315	320	325												
cat cca gct gat gca agt gtc ttt tct acg tcc act tct gcg tca agc	1123														
His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr Ser Ala Ser Ser															
330	335	340													
tac acc cgt gca tcg cat agc gca gtg agt ctt atc ggt tct ggt gcc	1171														
Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile Gly Ser Gly Ala															
345	350	355													
atg aac ttt gtg tac tgg ttc tct gca atg tcc ctg atg ggt agc ttc	1219														
Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu Met Gly Ser Phe															
360	365	370													
atc gtg atc ggt atc ggt tac gcc ggt gcc atg ctg ttt aat acg att	1267														
Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu Phe Asn Thr Ile															
375	380	385													
cga cgc acg ctg tcg ctc att ggt gcc gtt cct ttt gct gcg atg ggc	1315														
Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe Ala Ala Met Gly															
390	395	400	405												
ttt att gct ggt gtt gcc aag gtc att gtg tac acc atc gct atg ctc	1363														
Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr Ile Ala Met Leu															
410	415	420													
gta gag gtt atc gga acg atc att ttg tac cag ctc att acc cgg ttc	1411														
Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu Ile Thr Arg Phe															
425	430	435													
ttg atg gct gta cca gca ctc ttt gaa caa cct ttg gct gat tcc tta	1459														
Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu Ala Asp Ser Leu															
440	445	450													
agt agt aac gag agt gct gag ctg gtt gcc ggt gct ggt atg ggg cta	1507														
Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala Gly Met Gly Leu															
455	460	465													
gtc ggt atg gca cta gct acc tca ggc aac tgg gcg att gcc ggc atg	1555														
Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala Ile Ala Gly Met															
470	475	480	485												
gtg atc aca gtg gcc tca tcc atg ggg gtc atc atc ttc acg att att	1603														
Val Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile Phe Thr Ile Ile															
490	495	500													
gcg atg aag gtg cgc gga tct ttg gta tca ggt gtc gat gaa acc gtg	1651														
Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly Val Asp Glu Thr Val															
505	510	515													

acc agt gtt att aac cgc ttc ttg gat aca cag gtc tct tct gca ggt 1699
 Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val Ser Ser Ala Gly
 520 525 530

gct acc tct ggt gac ggc atg atg cgt cgt gca gcc gca acg ggt ctt 1747
 Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala Ala Thr Gly Leu
 535 540 545

ggt att ggt gcg aca cat atg gta ctc aac cgt gat ggt gac ggt ggt 1795
 Gly Ile Gly Ala Thr His Met Val Leu Asn Arg Asp Gly Asp Gly Gly
 550 555 560 565

gga tct gat tca ggc tct ggt gga tca ggt ggc ggt agc gat tca ggc 1843
 Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Ser Asp Ser Gly
 570 575 580

ttg ggt gag aag gct gct ggt ctg gcg aag gtt gtc aca act gtg gct 1891
 Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val Thr Thr Val Ala
 585 590 595

ggt gcc gga tta gtc ggt aag tat gct acg gat gcg ctc gat aat tat 1939
 Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala Leu Asp Asn Tyr
 600 605 610

gca gat ggc gtt atc aac ggc gac ggt gat ggt gcg ttc gca gca ggt 1987
 Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala Phe Ala Ala Gly
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ggt gac gct acc gtt gat ggc gac tat gta gca gat gga gat gca att 2035
 Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp Gly Asp Ala Ile
 630 635 640 645

gct tct gct gat gct aac gct gat ttt gta gac ggg gtt gct gat ggt 2083
 Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Ala Asp Gly
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<211> 661

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

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Trp Leu Ile Gly Ile Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala
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Leu Met Phe Arg Arg Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val
 35 40 45

Ile Arg Val Val Tyr Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser
 50 55 60

Tyr Thr Gly Ala Leu Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser
 65 70 75 80

Ala Gly Ser Asn Ala Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe
 85 90 95

Gln Ser Trp Ala Glu Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr
 100 105 110
 Leu Ala Trp Ser Leu Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg
 115 120 125
 Met Val Arg Asn Ser Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser
 130 135 140
 Phe Thr Thr Phe Lys Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met
 145 150 155 160
 Asp Trp Met Glu Lys Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly
 165 170 175
 Thr Ser Ser Ser Ser Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu
 180 185 190
 Leu Ser Arg Tyr Ile Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu
 195 200 205
 Thr Ser Ile Arg Ser Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser
 210 215 220
 Gly Glu Ala Val Ala Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr
 225 230 235 240
 Asn Thr Ala Ser Gly Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp
 245 250 255
 Ala Asn Asn Pro Leu Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly
 260 265 270
 Arg Pro Ile Asp Arg Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr
 275 280 285
 Ala Ser Cys Asn Asn Ser Val Val Thr Gly Ser Arg Ala Val Val Gly
 290 295 300
 Asp Tyr Arg Ser Asp Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe
 305 310 315 320
 Leu Asn Thr Ser Phe His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser
 325 330 335
 Thr Ser Ala Ser Ser Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu
 340 345 350
 Ile Gly Ser Gly Ala Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser
 355 360 365
 Leu Met Gly Ser Phe Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met
 370 375 380
 Leu Phe Asn Thr Ile Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro
 385 390 395 400
 Phe Ala Ala Met Gly Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr
 405 410 415

Thr Ile Ala Met Leu Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln
420 425 430

Leu Ile Thr Arg Phe Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro
435 440 445

Leu Ala Asp Ser Leu Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly
450 455 460

Ala Gly Met Gly Leu Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp
465 470 475 480

Ala Ile Ala Gly Met Val Ile Thr Val Ala Ser Ser Met Gly Val Ile
485 490 495

Ile Phe Thr Ile Ile Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly
500 505 510

Val Asp Glu Thr Val Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln
515 520 525

Val Ser Ser Ala Gly Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala
530 535 540

Ala Ala Thr Gly Leu Gly Ile Gly Ala Thr His Met Val Leu Asn Arg
545 550 555 560

Asp Gly Asp Gly Gly Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly
565 570 575

Gly Ser Asp Ser Gly Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val
580 585 590

Val Thr Thr Val Ala Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp
595 600 605

Ala Leu Asp Asn Tyr Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly
610 615 620

Ala Phe Ala Ala Gly Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala
625 630 635 640

Asp Gly Asp Ala Ile Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp
645 650 655

Gly Val Ala Asp Gly
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> FRXA01761

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cgc	gcg	tca	ttt	agc	aat	gct	gcg	tat	agc	tcc	gat	gga	acc	act	ctc	96	
Arg	Ala	Ser	Phe	Ser	Asn	Ala	Ala	Tyr	Ser	Ser	Asp	Gly	Thr	Thr	Leu		
			20					25					30				
gac	ggg	gag	ggg	gcg	agc	gtt	gat	gca	cag	ggg	aac	ccg	ctt	cat	gct	144	
Asp	Gly	Glu	Gly	Ala	Ser	Val	Asp	Ala	Gln	Gly	Asn	Pro	Leu	His	Ala		
		35					40					45					
gat	ggc	aca	cca	atg	agt	gct	gct	gaa	gct	gaa	atg	aag	atg	gct	ggg	192	
Asp	Gly	Thr	Pro	Met	Ser	Ala	Ala	Glu	Ala	Glu	Met	Lys	Met	Ala	Gly		
	50					55					60						
ctg	agc	tcg	tca	gga	acc	atg	atg	gag	aaa	tct	ggg	gtg	aaa	tcg	agt	240	
Leu	Ser	Ser	Ser	Gly	Thr	Met	Met	Glu	Lys	Ser	Gly	Val	Lys	Ser	Ser		
65					70				75						80		
ggc	att	acc	act	gca	gcg	gat	gtc	atg	gac	gat	cag	tct	ctg	gca	agc	288	
Gly	Ile	Thr	Thr	Ala	Ala	Asp	Val	Met	Asp	Asp	Gln	Ser	Leu	Ala	Ser		
				85					90					95			
agt	gtc	act	gag	tct	ggg	ctg	tcc	aag	att	cca	gac	acc	tat	ggg	gca	336	
Ser	Val	Thr	Glu	Ser	Gly	Leu	Ser	Lys	Ile	Pro	Asp	Thr	Tyr	Gly	Ala		
			100					105					110				
gat	gtc	tcg	ggg	gct	gcg	ggc	aca	gtc	gga	act	acc	ggg	gct	gat	tac	384	
Asp	Val	Ser	Gly	Ala	Ala	Gly	Thr	Val	Gly	Thr	Thr	Gly	Ala	Asp	Tyr		
		115					120					125					
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Ser	Ala	Thr	Asp	Ser	Ser	Ala	Gly	Leu	Asn	Met	Ser	Glu	Ala	Ala	Leu		
	130					135					140						
cag	agt	ggc	acc	cca	atg	ggc	gct	ctc	gct	ggg	gga	tct	gtg	tcg	agt	480	
Gln	Ser	Gly	Thr	Pro	Met	Gly	Ala	Leu	Ala	Gly	Gly	Ser	Val	Ser	Ser		
145					150					155					160		
tcc	gat	cag	gcc	atg	aat	gac	gca	gct	ctt	cag	att	gca	gcg	tct	cag	528	
Ser	Asp	Gln	Ala	Met	Asn	Asp	Ala	Ala	Leu	Gln	Ile	Ala	Ala	Ser	Gln		
				165					170					175			
ggg	ctt	gca	cca	gca	ggg	tcc	ata	gct	ggg	atg	gag	caa	ctt	agt	gct	576	
Gly	Leu	Ala	Pro	Ala	Gly	Ser	Ile	Ala	Gly	Met	Glu	Gln	Leu	Ser	Ala		
			180				185						190				
caa	gcc	act	gaa	gca	cct	gct	gga	aag	gcc	ggc	aag	cag	ctt	ggc	gat	624	
Gln	Ala	Thr	Glu	Ala	Pro	Ala	Gly	Lys	Ala	Gly	Lys	Gln	Leu	Gly	Asp		
		195					200					205					
ctt	tct	ggc	tca	gcg	ctc	aat	act	cag	ctg	gcg	tcc	atg	gga	cag	cag	672	
Leu	Ser	Gly	Ser	Ala	Leu	Asn	Thr	Gln	Leu	Ala	Ser	Met	Gly	Gln	Gln		
	210					215					220						
gta	ggg	gac	agt	gtg	aac	agc	gct	tat	gct	gca	ggc	ggg	atg	ggg	ggg	720	
Val	Gly	Asp	Ser	Val	Asn	Ser	Ala	Tyr	Ala	Ala	Gly	Gly	Met	Gly	Gly		
225					230				235						240		
gtt	gat	gtg	gct	ggc	aag	gtc	acc	gag	gca	gca	cag	cac	ttg	tct	cag	768	
Val	Asp	Val	Ala	Gly	Lys	Val	Thr	Glu	Ala	Ala	Gln	His	Leu	Ser	Gln		

245										250					255					
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Val	Pro	Gly	Gln	Ile	Gln	Asn	Ala	Val	Thr	Asn	Ala	Asp	Ala	Gly	Ser					
260					265					270										
tct	ggc	gca	agc	ttt	ggt	cag	atg	gca	cag	ggg	gca	gct	ggt	att	gcc	864				
Ser	Gly	Ala	Ser	Phe	Gly	Gln	Met	Ala	Gln	Gly	Ala	Ala	Gly	Ile	Ala					
275					280					285										
ggt	gtc	gca	ggt	gtg	atc	ggt	gca	gcg	ggc	gca	gca	agc	tct	gca	gca	912				
Gly	Val	Ala	Gly	Val	Ile	Gly	Ala	Ala	Gly	Ala	Ala	Ser	Ser	Ala	Ala					
290					295					300										
caa	ggc	gca	ggt	act	gtc	cag	ggt	gcg	atg	ggt	aat	gct	gca	gct	ggt	960				
Gln	Gly	Ala	Gly	Thr	Val	Gln	Gly	Ala	Met	Gly	Asn	Ala	Ala	Ala	Gly					
305					310					315					320					
gcg	gga	atg	atc	aac	aac	gct	gtt	tcc	ggt	gga	gct	act	ggc	tca	aca	1008				
Ala	Gly	Met	Ile	Asn	Asn	Ala	Val	Ser	Gly	Gly	Ala	Thr	Gly	Ser	Thr					
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ggt	gcc	gca	cat	gtg	gtc	aat	gca	tca	cat	gga	cca	gtg	gcg	cct	ggt	1056				
Gly	Ala	Ala	His	Val	Val	Asn	Ala	Ser	His	Gly	Pro	Val	Ala	Pro	Gly					
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cag	gct	cac	tac	caa	gag	tct	ggt	cat	gca	caa	gca	ttt	gtg	cag	aac	1104				
Gln	Ala	His	Tyr	Gln	Glu	Ser	Gly	His	Ala	Gln	Ala	Phe	Val	Gln	Asn					
355					360					365										
aac	cag	gcc	aac	acc	gcg	cac	aca	gca	aac	acg	cgt	gca	ccg	tca	tca	1152				
Asn	Gln	Ala	Asn	Thr	Ala	His	Thr	Ala	Asn	Thr	Arg	Ala	Pro	Ser	Ser					
370					375					380										
gct	caa	att	atg	ggc	gcg	aac	gtt	gct	ggc	tca	ctg	gca	tca	cag	gct	1200				
Ala	Gln	Ile	Met	Gly	Ala	Asn	Val	Ala	Gly	Ser	Leu	Ala	Ser	Gln	Ala					
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gta	cga	gga	atc	ggt	cag	cct	ggt	cag	atg	ggt	gct	aat	gtt	cgc	gac	1248				
Val	Arg	Gly	Ile	Gly	Gln	Pro	Gly	Gln	Met	Gly	Ala	Asn	Val	Arg	Asp					
405					410					415										
gcg	atg	ggt	ggc	agc	gga	cgc	tct	ggt	ggc	cgt	ggt	gga	gca	act	caa	1296				
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435					440					445										
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Arg	Ala	Gln	Arg	Gly	Gln	Lys	Pro	Ser	Val	Thr	Gly	Gln	Ala	Met	Asn					
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gca	gca	atg	cgt	tca	gca	gcg	gta	agc	ggt	cgc	atg	gca	aac	atg	gac	1440				
Ala	Ala	Met	Arg	Ser	Ala	Ala	Val	Ser	Gly	Arg	Met	Ala	Asn	Met	Asp					
465					470					475					480					
ggc	aac	agt	gta	ggt	ggc	act	gaa	gca	gat	cca	cag	cag	ggg	agt	ggc	1488				
Gly	Asn	Ser	Val	Gly	Gly	Thr	Glu	Ala	Asp	Pro	Gln	Gln	Gly	Ser	Gly					
485					490					495										

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 Val Thr Glu Lys Gly Asp Lys Gly Val Lys
 500 505

ccg 1541

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 <212> PRT
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<400> 778
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 Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His Ala
 35 40 45
 Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala Gly
 50 55 60
 Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser Ser
 65 70 75 80
 Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala Ser
 85 90 95
 Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly Ala
 100 105 110
 Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp Tyr
 115 120 125
 Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala Leu
 130 135 140
 Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser Ser
 145 150 155 160
 Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser Gln
 165 170 175
 Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser Ala
 180 185 190
 Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly Asp
 195 200 205
 Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln Gln
 210 215 220
 Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly Gly
 225 230 235 240
 Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser Gln
 245 250 255

Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly Ser
260 265 270

Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile Ala
275 280 285

Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala Ala
290 295 300

Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala Gly
305 310 315 320

Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser Thr
325 330 335

Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro Gly
340 345 350

Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln Asn
355 360 365

Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser Ser
370 375 380

Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln Ala
385 390 395 400

Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg Asp
405 410 415

Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr Gln
420 425 430

Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly Ile
435 440 445

Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met Asn
450 455 460

Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met Asp
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Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser Gly
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Val Thr Glu Lys Gly Asp Lys Gly Val Lys
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<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXN01765

<400> 779

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Met Ser Asn Asn Val
1 5

gtg aaa tat gag tgc gcg gtc gac gcc gac aac att gtc gca gtc gat 163
Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn Ile Val Ala Val Asp
10 15 20

atg cat gtg cac ttg gaa gtc gac agc tgc gga cac aaa tcg atg ccg 211
Met His Val His Leu Glu Val Asp Ser Cys Gly His Lys Ser Met Pro
25 30 35

gca gac atc atg gcg gca tcc tcg aag tac ttt aag acc gcg gaa cga 259
Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe Lys Thr Ala Glu Arg
40 45 50

act ccc tca gca gat gcc att gct gat att tat agg gaa cac aag atg 307
Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr Arg Glu His Lys Met
55 60 65

gcg gcg gtg gtt ttc acc atc gat gcg cgg acc caa atg ggg cat ctg 355
Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr Gln Met Gly His Leu
70 75 80 85

ccg aac tcg att gat gat ttg gtg gca agc tgt gcc cgc aac aat gac 403
Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys Ala Arg Asn Asn Asp
90 95 100

gtg ctg atc cct ttt ggc agt gtg gat cct cgt acc ggc gag gac gcg 451
Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg Thr Gly Glu Asp Ala
105 110 115

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Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu Gly Val Arg Gly Phe
120 125 130

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Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro Ser Ala Pro Glu Phe
135 140 145

tac cca ctg tgg gaa ttg ctc gaa agt ttt gga ttg cca tgc gtg ttc 595
Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly Leu Pro Cys Val Phe
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cat acc gga caa aac ggc atg ggt gca ggt ctt cca ggt ggt cga ggc 643
His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu Pro Gly Gly Arg Gly
170 175 180

att aag ctg cgc ttc tcc aac cca atg ttg ctt gat gat gtt gcg gcg 691
Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu Asp Asp Val Ala Ala
185 190 195

gac ttc ccg aac ctg acc atc atc atg gcg cac cct tct gtt cct tgg 739
Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His Pro Ser Val Pro Trp
200 205 210

cag gat gag gct aac tcg att gcc acc cac aag gcc aat gtg ttc att 787
Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys Ala Asn Val Phe Ile
215 220 225

gat ctt tcc ggc tgg tcg ccg aag tat ttc cca gag tct ttg gtc aga 835
Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro Glu Ser Leu Val Arg
230 235 240 245
cag tcc aat aac gtg cta tcc aag aag gtg ctg ttt ggc acg gac ttc 883
Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu Phe Gly Thr Asp Phe
250 255 260
ccg ctg att acc cca gag aaa tgg ctt gcg gct ttc gcg aat ctg cca 931
Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala Phe Ala Asn Leu Pro
265 270 275
ctg aag gat gag gtt cgt ccg gga atc ctc aaa gac aat gcg gtg aag 979
Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys Asp Asn Ala Val Lys
280 285 290
gta ctt ggc cta gcc gct agc act gag cgc gga tct caa gca gaa aag 1027
Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly Ser Gln Ala Glu Lys
295 300 305
gtc gtg caa cat gcg tgatccatt caaggtgctg tta 1065
Val Val Gln His Ala
310

<210> 780
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 780
Met Ser Asn Asn Val Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn
1 5 10 15
Ile Val Ala Val Asp Met His Val His Leu Glu Val Asp Ser Cys Gly
20 25 30
His Lys Ser Met Pro Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe
35 40 45
Lys Thr Ala Glu Arg Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr
50 55 60
Arg Glu His Lys Met Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr
65 70 75 80
Gln Met Gly His Leu Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys
85 90 95
Ala Arg Asn Asn Asp Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg
100 105 110
Thr Gly Glu Asp Ala Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu
115 120 125
Gly Val Arg Gly Phe Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro
130 135 140
Ser Ala Pro Glu Phe Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly
145 150 155 160

Leu Pro Cys Val Phe His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu
 165 170 175
 Pro Gly Gly Arg Gly Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu
 180 185 190
 Asp Asp Val Ala Ala Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His
 195 200 205
 Pro Ser Val Pro Trp Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys
 210 215 220
 Ala Asn Val Phe Ile Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro
 225 230 235 240
 Glu Ser Leu Val Arg Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu
 245 250 255
 Phe Gly Thr Asp Phe Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala
 260 265 270
 Phe Ala Asn Leu Pro Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys
 275 280 285
 Asp Asn Ala Val Lys Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly
 290 295 300
 Ser Gln Ala Glu Lys Val Val Gln His Ala
 305 310

<210> 781
 <211> 1065
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1042)
 <223> FRXA01765

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 caaggcataa caccgcacac caagaatddd aggaggggtc atg agc aac aac gta 115
 Met Ser Asn Asn Val
 1 5
 gtg aaa tat gag tgc gcg gtc gac gcc gac aac att gtc gca gtc gat 163
 Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn Ile Val Ala Val Asp
 10 15 20
 atg cat gtg cac ttg gaa gtc gac agc tgc gga cac aaa tcg atg ccg 211
 Met His Val His Leu Glu Val Asp Ser Cys Gly His Lys Ser Met Pro
 25 30 35
 gca gac atc atg gcg gca tcc tcg aag tac ttt aag acc gcg gaa cga 259
 Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe Lys Thr Ala Glu Arg
 40 45 50

act ccc tca gca gat gcc att gct gat att tat agg gaa cac aag atg	307
Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr Arg Glu His Lys Met	
55 60 65	
gcg gcg gtg gtt ttc acc atc gat gcg cgg acc caa atg ggg cat ctg	355
Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr Gln Met Gly His Leu	
70 75 80 85	
ccg aac tcg att gat gat ttg gtg gca agc tgt gcc cgc aac aat gac	403
Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys Ala Arg Asn Asn Asp	
90 95 100	
gtg ctg atc cct ttt ggc agt gtg gat cct cgt acc ggc gag gac gcg	451
Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg Thr Gly Glu Asp Ala	
105 110 115	
ctg gtg gaa gct cgc cga cag gtg gaa gaa ctc ggg gtg cga ggc ttc	499
Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu Gly Val Arg Gly Phe	
120 125 130	
aaa ttc cat cca tcg gtt caa gga ttc gac cca tcc gcg cca gag ttc	547
Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro Ser Ala Pro Glu Phe	
135 140 145	
tac cca ctg tgg gaa ttg ctc gaa agt ttt gga ttg cca tgc gtg ttc	595
Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly Leu Pro Cys Val Phe	
150 155 160 165	
cat acc gga caa aac ggc atg ggt gca ggt ctt cca ggt ggt cga ggc	643
His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu Pro Gly Gly Arg Gly	
170 175 180	
att aag ctg cgc ttc tcc aac cca atg ttg ctt gat gat gtt gcg gcg	691
Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu Asp Asp Val Ala Ala	
185 190 195	
gac ttc ccg aac ctg acc atc atc atg gcg cac cct tct gtt cct tgg	739
Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His Pro Ser Val Pro Trp	
200 205 210	
cag gat gag gct aac tcg att gcc acc cac aag gcc aat gtg ttc att	787
Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys Ala Asn Val Phe Ile	
215 220 225	
gat ctt tcc ggc tgg tcg ccg aag tat ttc cca gag tct ttg gtc aga	835
Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro Glu Ser Leu Val Arg	
230 235 240 245	
cag tcc aat aac gtg cta tcc aag aag gtg ctg ttt ggc acg gac ttc	883
Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu Phe Gly Thr Asp Phe	
250 255 260	
ccg ctg att acc cca gag aaa tgg ctt gcg gct ttc gcg aat ctg cca	931
Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala Phe Ala Asn Leu Pro	
265 270 275	
ctg aag gat gag gtt cgt ccg gga atc ctc aaa gac aat gcg gtg aag	979
Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys Asp Asn Ala Val Lys	
280 285 290	
gta ctt ggc cta gcc gct agc act gag cgc gga tct caa gca gaa aag	1027

Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly Ser Gln Ala Glu Lys
 295 300 305

gtc gtg caa cat gcg tgatccatt caaggtgctg tta

1065

Val Val Gln His Ala

310

<210> 782

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

Met Ser Asn Asn Val Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn
 1 5 10 15

Ile Val Ala Val Asp Met His Val His Leu Glu Val Asp Ser Cys Gly
 20 25 30

His Lys Ser Met Pro Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe
 35 40 45

Lys Thr Ala Glu Arg Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr
 50 55 60

Arg Glu His Lys Met Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr
 65 70 75 80

Gln Met Gly His Leu Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys
 85 90 95

Ala Arg Asn Asn Asp Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg
 100 105 110

Thr Gly Glu Asp Ala Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu
 115 120 125

Gly Val Arg Gly Phe Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro
 130 135 140

Ser Ala Pro Glu Phe Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly
 145 150 155 160

Leu Pro Cys Val Phe His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu
 165 170 175

Pro Gly Gly Arg Gly Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu
 180 185 190

Asp Asp Val Ala Ala Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His
 195 200 205

Pro Ser Val Pro Trp Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys
 210 215 220

Ala Asn Val Phe Ile Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro
 225 230 235 240

Glu Ser Leu Val Arg Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu
 245 250 255

Phe Gly Thr Asp Phe Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala
 260 265 270

Phe Ala Asn Leu Pro Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys
 275 280 285

Asp Asn Ala Val Lys Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly
 290 295 300

Ser Gln Ala Glu Lys Val Val Gln His Ala
 305 310

<210> 783
 <211> 588
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(565)
 <223> RXN01767

<400> 783
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cctactcatc cccacataa gaaaaaaaga cgacaccacc atg att gac cat aaa 115
 Met Ile Asp His Lys
 1 5

ctg tgg ttt aac aca gta acc aac aac gcc tct gtc cga gaa gct gca 163
 Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser Val Arg Glu Ala Ala
 10 15 20

gga aaa tgc gac ata ccc atc aga acg ctc aac gag cag ctt aac cgt 211
 Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn Glu Gln Leu Asn Arg
 25 30 35

cga ata ctc cct gaa aag acc gtc atc gct cta gca cgc gct tat gat 259
 Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu Ala Arg Ala Tyr Asp
 40 45 50

ctc tca cct gtt gat gcg ctc gtt cgc acc gga cac ctc acc gaa gaa 307
 Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly His Leu Thr Glu Glu
 55 60 65

gag gct ggt agt cgt gaa gaa gat gcc agc cca gat tca gct gac gac 355
 Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro Asp Ser Ala Asp Asp
 70 75 80 85

tac cct acc tgg gca ctg aac tcg cac ctt gac tat ggc att ctc gga 403
 Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp Tyr Gly Ile Leu Gly
 90 95 100

gct ttt ggc gac atc gct gaa gaa gta aac agc gaa aga gtt aac cgc 451
 Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser Glu Arg Val Asn Arg
 105 110 115

gac aac gcc ata gag caa att cgc gca tgg ctc gac gag ctt cca ggc 499
 Asp Asn Ala Ile Glu Gln Ile Arg Ala Trp Leu Asp Glu Leu Pro Gly

120 125 130
agc cta ttc aac aac ctc cgc agc act aaa aca ggc tac atc gaa cta 547
Ser Leu Phe Asn Asn Leu Arg Ser Thr Lys Thr Gly Tyr Ile Glu Leu
135 140 145
ttc gag acc tat ctc gat taaacccaac cagcacaaca ata 588
Phe Glu Thr Tyr Leu Asp
150 155

<210> 784
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 784
Met Ile Asp His Lys Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser
1 5 10 15
Val Arg Glu Ala Ala Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn
20 25 30
Glu Gln Leu Asn Arg Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu
35 40 45
Ala Arg Ala Tyr Asp Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly
50 55 60
His Leu Thr Glu Glu Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro
65 70 75 80
Asp Ser Ala Asp Asp Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp
85 90 95
Tyr Gly Ile Leu Gly Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
100 105 110
Glu Arg Val Asn Arg Asp Asn Ala Ile Glu Gln Ile Arg Ala Trp Leu
115 120 125
Asp Glu Leu Pro Gly Ser Leu Phe Asn Asn Leu Arg Ser Thr Lys Thr
130 135 140
Gly Tyr Ile Glu Leu Phe Glu Thr Tyr Leu Asp
145 150 155

<210> 785
<211> 436
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> FRXA01767

<400> 785
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cctactcatc cccacataa gaaaaaaga cgacaccacc atg att gac cat aaa 115
                                   Met Ile Asp His Lys
                                   1                               5

ctg tgg ttt aac aca gta acc aac aac gcc tct gtc cga gaa gct gca 163
Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser Val Arg Glu Ala Ala
                                   10                               15                               20

gga aaa tgc gac ata ccc atc aga acg ctc aac gag cag ctt aac cgt 211
Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn Glu Gln Leu Asn Arg
                                   25                               30                               35

cga ata ctc cct gaa aag acc gtc atc gct cta gca cgc gct tat gat 259
Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu Ala Arg Ala Tyr Asp
                                   40                               45                               50

ctc tca cct gtt gat gcg ctc gtt cgc acc gga cac ctc acc gaa gaa 307
Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly His Leu Thr Glu Glu
                                   55                               60                               65

gag gct ggt agt cgt gaa gaa gat gcc agc cca gat tca gct gac gac 355
Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro Asp Ser Ala Asp Asp
                                   70                               75                               80                               85

tac cct acc tgg gca ctg aac tcg cac ctt gac tat ggc att ctc gga 403
Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp Tyr Gly Ile Leu Gly
                                   90                               95                               100

gct ttt ggc gac atc gct gaa gaa gta aac agc 436
Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
                                   105                               110

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<210> 786

<211> 112

<212> PRT

<213> Corynebacterium glutamicum

<400> 786

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Met Ile Asp His Lys Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser
 1                               5                               10                               15

Val Arg Glu Ala Ala Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn
                20                               25                               30

Glu Gln Leu Asn Arg Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu
    35                               40                               45

Ala Arg Ala Tyr Asp Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly
    50                               55                               60

His Leu Thr Glu Glu Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro
    65                               70                               75                               80

Asp Ser Ala Asp Asp Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp
    85                               90                               95

Tyr Gly Ile Leu Gly Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
    100                               105                               110

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<210> 787
 <211> 564
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)
 <223> RXN01769

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 cacaacccccg ttgcagcacc agcataaatac tatattcgct gtg acg ggg ttg ttg 115
 Val Thr Gly Leu Leu
 1 5
 ggg cgc gcc cca cat tca ctc ttt ttc ccg att ggt ttc tac tac aca 163
 Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr Thr
 10 15 20
 ccc atg acc tct att act act acc gat acc ccg cta tat aca gca ctg 211
 Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala Leu
 25 30 35
 ccc cat acc cgt atc tct gat gcg gaa ttg ttg aca cca aca aca act 259
 Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr Thr
 40 45 50
 gtg cac gag att ctc gtt tac gga ccg gct gag tgc cca ggg tgt aca 307
 Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys Thr
 55 60 65
 gca acg ctt gac ttc ttt gca cgc aaa aac atg ccg gcc acc aaa gtc 355
 Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys Val
 70 75 80 85
 act gta gct gcc ggt gat gta gca cat acc tac atc acc caa gac tta 403
 Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp Leu
 90 95 100
 ggt tat ctc caa gca ccg att gtc act gtc cgt atc agt tcc tct gct 451
 Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser Ala
 105 110 115
 tct aac cac gac aac gaa cac aac acc cag atc ctg cac tgg tcc ggc 499
 Ser Asn His Asp Asn Glu His Asn Thr Gln Ile Leu His Trp Ser Gly
 120 125 130
 gtt aat cgc tac ctc atg cag gca ctc tcc cgt act cat ttc 541
 Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg Thr His Phe
 135 140 145
 tagaaagggtt tttcccgctca tgt 564

<210> 788
 <211> 147
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 788

Val Thr Gly Leu Leu Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile
 1 5 10 15
 Gly Phe Tyr Tyr Thr Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro
 20 25 30
 Leu Tyr Thr Ala Leu Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu
 35 40 45
 Thr Pro Thr Thr Thr Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu
 50 55 60
 Cys Pro Gly Cys Thr Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met
 65 70 75 80
 Pro Ala Thr Lys Val Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr
 85 90 95
 Ile Thr Gln Asp Leu Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg
 100 105 110
 Ile Ser Ser Ser Ala Ser Asn His Asp Asn Glu His Asn Thr Gln Ile
 115 120 125
 Leu His Trp Ser Gly Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg
 130 135 140
 Thr His Phe
 145

<210> 789

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> FRXA01769

<400> 789

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 gcagcaccag cataaatcta tattcgctgt gacgggggtg ttg ggg cgc gcc cca 115
 Leu Gly Arg Ala Pro
 1 5
 cat tca ctc ttt ttc ccg att ggt ttc tac tac aca ccc atg acc tct 163
 His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr Thr Pro Met Thr Ser
 10 15 20
 att act act acc gat acc ccg cta tat aca gca ctg ccc cat acc cgt 211
 Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala Leu Pro His Thr Arg
 25 30 35
 atc tct gat gcg gaa ttg ttg aca cca aca aca act gtg cac gag att 259
 Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr Thr Val His Glu Ile
 40 45 50

ctc gtt tac gga ccg gct gag tgc cca ggg tgt aca gca acg ctt gac 307
 Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys Thr Ala Thr Leu Asp
 55 60 65

ttc ttt gca cgc aaa aac atg ccg gcc acc aaa gtc act gta gct gcc 355
 Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys Val Thr Val Ala Ala
 70 75 80 85

ggg gat gta gca cat acc tac atc acc caa gac tta ggt tat ctc caa 403
 Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp Leu Gly Tyr Leu Gln
 90 95 100

gca ccg att gtc act gtc cgt atc agt tcc tct gct tct aac cac gac 451
 Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser Ala Ser Asn His Asp
 105 110 115

aac gaa cac aac acc cag atc ctg cac tgg tcc ggc gtt aat cgc tac 499
 Asn Glu His Asn Thr Gln Ile Leu His Trp Ser Gly Val Asn Arg Tyr
 120 125 130

ctc atg cag gca ctc tcc cgt act cat ttc tagaaagggtt tttcccgta 549
 Leu Met Gln Ala Leu Ser Arg Thr His Phe
 135 140

tgt 552

<210> 790

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 790

Leu Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr
 1 5 10 15

Thr Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala
 20 25 30

Leu Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr
 35 40 45

Thr Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys
 50 55 60

Thr Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys
 65 70 75 80

Val Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp
 85 90 95

Leu Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser
 100 105 110

Ala Ser Asn His Asp Asn Glu His Asn Thr Gln Ile Leu His Trp Ser
 115 120 125

Gly Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg Thr His Phe
 130 135 140

tac tcg gga gcg ttg cag gaa tcg atc gtt gcg aaa att caa gcc gaa 643
 Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala Lys Ile Gln Ala Glu
 170 175 180

act gat ctg gaa cgt gca cga aat gaa gtg aaa act acc cgt gct cga 691
 Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys Thr Thr Arg Ala Arg
 185 195 195

ctt gcc agc gcg aaa gtg ttg gag caa aat ccg att ctt gcc aaa att 739
 Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro Ile Leu Ala Lys Ile
 200 205 210

cgg atg att gaa gcg ctc cca ccg gga tcc aca att gag gtt cgg gag 787
 Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr Ile Glu Val Arg Glu
 215 220 225

ggt gac tca aag gca taaagttgcc catttcggtg ccc 825
 Gly Asp Ser Lys Ala
 230

<210> 792
 <211> 234
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 792
 Met His Gln Ala Gly Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp
 1 5 10 15

Arg Thr Ser Ala Leu Arg Ser Pro Val Ala Arg Val Gly His Ala Val
 20 25 30

Leu Arg Gln Arg Ala Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe
 35 40 45

Ser Arg Pro Gly Asp Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu
 50 55 60

Ile Gln Val His Pro Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val
 65 70 75 80

Thr Ile Thr Met Ala Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe
 85 90 95

Val Ala Asp Ser Gln Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln
 100 105 110

Ile Ala Leu Arg Glu Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile
 115 120 125

Gly Val Arg Ile Asp Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala
 130 135 140

Ala Lys Asn Val Gly Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu
 145 150 155 160

Asn Leu Pro Gln Glu Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala
 165 170 175

Lys Ile Gln Ala Glu Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys
 180 185 190

Thr Thr Arg Ala Arg Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro
 195 200 205

Ile Leu Ala Lys Ile Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr
 210 215 220

Ile Glu Val Arg Glu Gly Asp Ser Lys Ala
 225 230

<210> 793
 <211> 825
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(802)
 <223> FRXA01771

<400> 793
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 gggatattttc aggtcgcggt cgcaggattt tgggtggagc atg cac cag gct ggc 115
 Met His Gln Ala Gly
 1 5
 cag ctc atc aat gat ccc agt cag ggt ctg tgg cgc act tct gcc ctg 163
 Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp Arg Thr Ser Ala Leu
 10 15 20
 cgc tcg ccg gtt gct cgg gtt gga cat gcc gtg ttg cgc cag cgt gcc 211
 Arg Ser Pro Val Ala Arg Val Gly His Ala Val Leu Arg Gln Arg Ala
 25 30 35
 ggt gag atc tcg cgc atg caa ggt cgt gag ttt tct cgc cct ggg gat 259
 Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe Ser Arg Pro Gly Asp
 40 45 50
 cag ttc cga cag gta gat ttg cgc agg cga ctg att cag gtc cat ccc 307
 Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu Ile Gln Val His Pro
 55 60 65
 caa tca att cct aca gcg gat gcg atg gcc gta acc atc acc atg gcg 355
 Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val Thr Ile Thr Met Ala
 70 75 80 85
 ctc acc gct gcc acg att gat ccg gtg aag ttc gtc gcg gat tca cag 403
 Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe Val Ala Asp Ser Gln
 90 95 100
 aac ccg gat gaa gag att tat ttg gca gct cag atc gca ttg cgg gaa 451
 Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln Ile Ala Leu Arg Glu
 105 110 115
 atg gtt atc gct atg cct ttg gag gat ttc atc ggg gtg cgc att gat 499
 Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile Gly Val Arg Ile Asp
 120 125 130
 cta gag cct gtt ttg gtg gct gct caa gct gct gcg aag aat gtg ggc 547
 Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala Ala Lys Asn Val Gly
 135 140 145

gtg gaa gtc tcg tca atc ttg ctg aag gat ctg aat ctt ccc cag gag 595
Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu Asn Leu Pro Gln Glu
150 155 160 165

tac tcg gga gcg ttg cag gaa tcg atc gtt gcg aaa att caa gcc gaa 643
Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala Lys Ile Gln Ala Glu
170 175 180

act gat ctg gaa cgt gca cga aat gaa gtg aaa act acc cgt gct cga 691
Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys Thr Thr Arg Ala Arg
185 190 195

ctt gcc agc gcg aaa gtg ttg gag caa aat ccg att ctt gcc aaa att 739
Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro Ile Leu Ala Lys Ile
200 205 210

cgg atg att gaa gcg ctc cca ccg gga tcc aca att gag gtt cgg gag 787
Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr Ile Glu Val Arg Glu
215 220 225

ggt gac tca aag gca taaagttgcc catttcggtg ccc 825
Gly Asp Ser Lys Ala
230

<210> 794
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 794
Met His Gln Ala Gly Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp
1 5 10 15

Arg Thr Ser Ala Leu Arg Ser Pro Val Ala Arg Val Gly His Ala Val
20 25 30

Leu Arg Gln Arg Ala Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe
35 40 45

Ser Arg Pro Gly Asp Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu
50 55 60

Ile Gln Val His Pro Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val
65 70 75 80

Thr Ile Thr Met Ala Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe
85 90 95

Val Ala Asp Ser Gln Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln
100 105 110

Ile Ala Leu Arg Glu Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile
115 120 125

Gly Val Arg Ile Asp Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala
130 135 140

Ala Lys Asn Val Gly Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu
145 150 155 160

Asn Leu Pro Gln Glu Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala
 165 170 175

Lys Ile Gln Ala Glu Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys
 180 185 190

Thr Thr Arg Ala Arg Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro
 195 200 205

Ile Leu Ala Lys Ile Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr
 210 215 220

Ile Glu Val Arg Glu Gly Asp Ser Lys Ala
 225 230

<210> 795

<211> 849

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(826)

<223> RXN01774

<400> 795

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cacacaccac tcttcctgag agaatcctga ggtcatcacc atg tca ccg aac ttc 115
 Met Ser Pro Asn Phe
 1 5

caa gct cgc ggt act act gcg ccc act gtt gct ttg tcc atg cgc cag 163
 Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala Leu Ser Met Arg Gln
 10 15 20

atc gcg cac atc cgt gaa gaa att aag aaa tca cca ctc gct gct tcc 211
 Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser Pro Leu Ala Ala Ser
 25 30 35

gtt ttc atc aca ccc acc acc aaa caa atg gtt gtc cga gat cta gaa 259
 Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val Val Arg Asp Leu Glu
 40 45 50

tca ctg ttc cag cag ctc tac cac aca gat cta cct gaa cca tcc atc 307
 Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu Pro Glu Pro Ser Ile
 55 60 65

aaa gac agt ggt ctt atc agt gct atc ggc tct agc gcc ggc aat acc 355
 Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser Ser Ala Gly Asn Thr
 70 75 80 85

aat aat cca gca ctc gcc cta gaa act cag atg gct tac cac ctg gtg 403
 Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met Ala Tyr His Leu Val
 90 95 100

ctt gct atg cac cac acc gat gtt gct acc tgg cac aag gtg gtg acc 451
 Leu Ala Met His His Thr Asp Val Ala Thr Trp His Lys Val Val Thr
 105 110 115

aaa aac atc acc gaa tct gct gct gca caa gat gct gcg gtc gag cac 499
 Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp Ala Ala Val Glu His
 120 125 130

agt gct aaa tac gat gct gtg tac gat gcc gca caa ctt atg ggc atc 547
 Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala Gln Leu Met Gly Ile
 135 140 145

act gtt gag gaa ggt aat gtc ggt agc atc gct att gcc ttt agc aca 595
 Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala Ile Ala Phe Ser Thr
 150 155 160 165

gca cgt gca gac ggt aaa tct gat tgg tgt gtt tcc ggc atc agc cgc 643
 Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val Ser Gly Ile Ser Arg
 170 175 180

tac atc gag gtc acc gaa gcc ttg gat gct gcg cga gct gtc act aaa 691
 Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala Arg Ala Val Thr Lys
 185 190 195

aat act gat gcg ctc aat aaa act gct cta cca gac gtg cag ccg gcg 739
 Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro Asp Val Gln Pro Ala
 200 205 210

ccg gtt gtg cat tca gca cag ttc atg aac aag tcc gca cac gat cat 787
 Pro Val Val His Ser Ala Gln Phe Met Asn Lys Ser Ala His Asp His
 215 220 225

ggg gtt aat act gcg gaa aaa gat caa cca acc ctg ttt taaaagactg 836
 Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr Leu Phe
 230 235 240

tccatttaac aac 849

<210> 796
 <211> 242
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 796
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Leu Ser Met Arg Gln Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser
 20 25 30

Pro Leu Ala Ala Ser Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val
 35 40 45

Val Arg Asp Leu Glu Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu
 50 55 60

Pro Glu Pro Ser Ile Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser
 65 70 75 80

Ser Ala Gly Asn Thr Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met
 85 90 95

Ala Tyr His Leu Val Leu Ala Met His His Thr Asp Val Ala Thr Trp
 100 105 110

His Lys Val Val Thr Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp
 115 120 125
 Ala Ala Val Glu His Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala
 130 135 140
 Gln Leu Met Gly Ile Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala
 145 150 155 160
 Ile Ala Phe Ser Thr Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val
 165 170 175
 Ser Gly Ile Ser Arg Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala
 180 185 190
 Arg Ala Val Thr Lys Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro
 195 200 205
 Asp Val Gln Pro Ala Pro Val Val His Ser Ala Gln Phe Met Asn Lys
 210 215 220
 Ser Ala His Asp His Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr
 225 230 235 240
 Leu Phe

<210> 797
 <211> 883
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(883)
 <223> FRXA01774

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 Met Ser Pro Asn Phe
 1 5
 caa gct cgc ggt act act gcg ccc act gtt gct ttg tcc atg cgc cag 163
 Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala Leu Ser Met Arg Gln
 10 15 20
 atc gcg cac atc cgt gaa gaa att aag aaa tca cca ctc gct gct tcc 211
 Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser Pro Leu Ala Ala Ser
 25 30 35
 gtt ttc atc aca ccc acc acc aaa caa atg gtt gtc cga gat cta gaa 259
 Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val Val Arg Asp Leu Glu
 40 45 50
 tca ctg ttc cag cag ctc tac cac aca gat cta cct gaa cca tcc atc 307
 Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu Pro Glu Pro Ser Ile
 55 60 65

aaa gac agt ggt ctt atc agt gct atc ggc tct agc gcc ggc aat acc 355
 Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser Ser Ala Gly Asn Thr
 70 75 80 85

aat aat cca gca ctc gcc cta gaa act cag atg gct tac cac ctg gtg 403
 Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met Ala Tyr His Leu Val
 90 95 100

ctt gct atg cac cac acc gat gtt gct acc tgg cac aag gtg gtg acc 451
 Leu Ala Met His His Thr Asp Val Ala Thr Trp His Lys Val Val Thr
 105 110 115

aaa aac atc acc gaa tct gct gct gca caa gat gct gcg gtc gag cac 499
 Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp Ala Ala Val Glu His
 120 125 130

agt gct aaa tac gat gct gtg tac gat gcc gca caa ctt atg ggc atc 547
 Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala Gln Leu Met Gly Ile
 135 140 145

act gtt gag gaa ggt aat gtc ggt agc atc gct att gcc ttt agc aca 595
 Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala Ile Ala Phe Ser Thr
 150 155 160 165

gca cgt gca gac ggt aaa tct gat tgg tgt gtt tcc ggc atc agc cgc 643
 Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val Ser Gly Ile Ser Arg
 170 175 180

tac atc gag gtc acc gaa gcc ttg gat gct gcg cga gct gtc act aaa 691
 Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala Arg Ala Val Thr Lys
 185 190 195

aat act gat gcg ctc aat aaa act gct cta cca gac gtg cag ccg gcg 739
 Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro Asp Val Gln Pro Ala
 200 205 210

ccg gtt gtg cat tca gca cag ttc atg aac aag tcc gca cac gat cat 787
 Pro Val Val His Ser Ala Gln Phe Met Asn Lys Ser Ala His Asp His
 215 220 225

ggg gtt aat act gcg gaa aaa gat caa cca acc tgt tta aag act gtg 835
 Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr Cys Leu Lys Thr Val
 230 235 240 245

cat tta caa cca cat cgt tac ccc cga aca ggc ttt aag gct att caa 883
 His Leu Gln Pro His Arg Tyr Pro Arg Thr Gly Phe Lys Ala Ile Gln
 250 255 260

<210> 798
 <211> 261
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 798
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 20 25 30

Pro Leu Ala Ala Ser Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val
35 40 45
Val Arg Asp Leu Glu Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu
50 55 60
Pro Glu Pro Ser Ile Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser
65 70 75 80
Ser Ala Gly Asn Thr Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met
85 90 95
Ala Tyr His Leu Val Leu Ala Met His His Thr Asp Val Ala Thr Trp
100 105 110
His Lys Val Val Thr Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp
115 120 125
Ala Ala Val Glu His Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala
130 135 140
Gln Leu Met Gly Ile Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala
145 150 155 160
Ile Ala Phe Ser Thr Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val
165 170 175
Ser Gly Ile Ser Arg Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala
180 185 190
Arg Ala Val Thr Lys Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro
195 200 205
Asp Val Gln Pro Ala Pro Val Val His Ser Ala Gln Phe Met Asn Lys
210 215 220
Ser Ala His Asp His Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr
225 230 235 240
Cys Leu Lys Thr Val His Leu Gln Pro His Arg Tyr Pro Arg Thr Gly
245 250 255
Phe Lys Ala Ile Gln
260

<210> 799

<211> 816

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(793)

<223> RXN01787

<400> 799

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ttacacaccc cactccacac aactcgcaa aggattcatc atg agc aac aat gct 115

	Met	Ser	Asn	Asn	Ala	
	1				5	
ctt tta gta gca aac gaa gcc gac atc ggt ctc tac ctc cac tgg aat						163
Leu Leu Val Ala Asn Glu Ala Asp Ile Gly Leu Tyr Leu His Trp Asn						
	10			15	20	
ggt ggt cgc gac tcg att gag gcg ttt ctc gcc tac gcc gca tac gcg						211
Gly Gly Arg Asp Ser Ile Glu Ala Phe Leu Ala Tyr Ala Ala Tyr Ala						
	25		30		35	
cag tta cca ccc atc aac gaa aat aac gat tgg ttg cca ccg ttt att						259
Gln Leu Pro Pro Ile Asn Glu Asn Asn Asp Trp Leu Pro Pro Phe Ile						
	40		45		50	
act gtg ctg aag aac ttc ttc ggc aat gat ggt tct ggc gtc tac ctc						307
Thr Val Leu Lys Asn Phe Phe Gly Asn Asp Gly Ser Gly Val Tyr Leu						
	55		60		65	
gaa cct gtc aat cag gat tat ctc gac ggc atc gac tat gac aac ggt						355
Glu Pro Val Asn Gln Asp Tyr Leu Asp Gly Ile Asp Tyr Asp Asn Gly						
	70		75		80	85
gtt tac atg ctt gac gat tat gag atc act gag cgt att aat cca ccc						403
Val Tyr Met Leu Asp Asp Tyr Glu Ile Thr Glu Arg Ile Asn Pro Pro						
	90		95		100	
gct gtt gag caa gac tcc cac gat ctc cac gac atg ttg atc aaa att						451
Ala Val Glu Gln Asp Ser His Asp Leu His Asp Met Leu Ile Lys Ile						
	105		110		115	
gat aaa gct caa cca cct gtc gat caa ctc ggg agt ttt ctc cat ggc						499
Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser Phe Leu His Gly						
	120		125		130	
cta gag acc tct gtc gca gat ttg ggg gtt ggt gat cgc gta ttt ttg						547
Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp Arg Val Phe Leu						
	135		140		145	
cca cgt ttt agc acc ttt gat aag aaa ctc ggt cgc tac cgc atc cac						595
Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg Tyr Arg Ile His						
	150		155		160	165
act gtt ctc gga ttc gct gag aac gat ccg ttt aac cct atg acc agc						643
Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn Pro Met Thr Ser						
	170		175		180	
agc gag cga ttt aaa ggt aag ccc tat gtc gat atg ttc gac aat caa						691
Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met Phe Asp Asn Gln						
	185		190		195	
gac aac gcc ttt aac cca aat tcc tat atc act aca gat acc gtg cgc						739
Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr Asp Thr Val Arg						
	200		205		210	
atc gtt gtc gat cct gta ccg gaa act aat ccc gac gat gag aaa gca						787
Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp Asp Glu Lys Ala						
	215		220		225	
gga cgc tagccatgtc tcgcagctac ccc						816
Gly Arg						

230

<210> 800

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 800

Met Ser Asn Asn Ala Leu Leu Val Ala Asn Glu Ala Asp Ile Gly Leu
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Tyr Leu His Trp Asn Gly Gly Arg Asp Ser Ile Glu Ala Phe Leu Ala
20 25 30

Tyr Ala Ala Tyr Ala Gln Leu Pro Pro Ile Asn Glu Asn Asn Asp Trp
35 40 45

Leu Pro Pro Phe Ile Thr Val Leu Lys Asn Phe Phe Gly Asn Asp Gly
50 55 60

Ser Gly Val Tyr Leu Glu Pro Val Asn Gln Asp Tyr Leu Asp Gly Ile
65 70 75 80

Asp Tyr Asp Asn Gly Val Tyr Met Leu Asp Asp Tyr Glu Ile Thr Glu
85 90 95

Arg Ile Asn Pro Pro Ala Val Glu Gln Asp Ser His Asp Leu His Asp
100 105 110

Met Leu Ile Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly
115 120 125

Ser Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly
130 135 140

Asp Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly
145 150 155 160

Arg Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe
165 170 175

Asn Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp
180 185 190

Met Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr
195 200 205

Thr Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro
210 215 220

Asp Asp Glu Lys Ala Gly Arg
225 230

<210> 801

<211> 377

<212> DNA

<213> Corynebacterium glutamicum

<220>

<400> 801

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Phe	Leu	His	Gly	Leu	Glu	Thr	Ser	Val	Ala	Asp	Leu	Gly	Val	Gly	Asp	
			20					25					30			

cgc gta ttt ttg cca cgt ttt agc acc ttt gat aag aaa ctc ggt cgc 144
Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg
35 40 45

tac	cgc	atc	cac	act	gtt	ctc	gga	ttc	gct	gag	aac	gat	ccg	ttt	aac	192
Tyr	Arg	Ile	His	Thr	Val	Leu	Gly	Phe	Ala	Glu	Asn	Asp	Pro	Phe	Asn	
	50					55					60					

cct atg acc agc agc gag cga ttt aaa ggt aag ccc tat gtc gat atg 240
Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met
65 70 75 80

ttc gac aat caa gac aac gcc ttt aac cca aat tcc tat atc act aca 288
Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr
85 90 95

gat acc gtg cgc atc gtt gtc gat cct gta ccg gaa act aat ccc gac 336
Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp
100 105 110

gat gag aaa gca gga cgc tagccatgtc tcgcagctac ccc 377
Asp Glu Lys Ala Gly Arg
115

<210> 802

<211> 118

<212> PRT

<213> Corynebacterium glutamicum

<400> 802

Thr Glu Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser
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Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp
20 25 30

Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg
35 40 45

Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn
50 55 60

Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met
65 70 75 80

Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr
85 90 95

Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp
 100 105 110

Asp Glu Lys Ala Gly Arg
 115

<210> 803
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXN01796

<400> 803
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 Leu Leu Leu Gly Gly
 1 5
 aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc 163
 Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
 10 15 20
 gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc 211
 Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
 25 30 35
 ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca 259
 Gly Ala Asp Ala Asn Ala Ser Asp Cys Arg Leu Tyr Tyr Thr Ser
 40 45 50
 ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt 307
 Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
 55 60 65
 atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa 355
 Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
 70 75 80 85
 acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg 403
 Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
 90 95 100
 tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt 451
 Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
 105 110 115
 cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg 499
 Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala
 120 125 130
 cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg 547
 His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
 135 140 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag 595
 Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu
 150 155 160 165
 ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa 643
 Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
 170 175 180
 ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc 691
 Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
 185 190 195
 gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga 739
 Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
 200 205 210
 tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag 787
 Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
 215 220 225
 cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc 835
 Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
 230 235 240 245
 gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg 884
 Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
 250 255
 cttttcgacg tct 897

<210> 804

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 804

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 20 25 30
 Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
 35 40 45
 Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
 50 55 60
 Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65 70 75 80
 Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
 85 90 95
 Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
 100 105 110
 Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
 115 120 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
130 135 140

Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
145 150 155 160

Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
165 170 175

Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
180 185 190

Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
195 200 205

Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
210 215 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
225 230 235 240

Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn
245 250 255

Asp Ala

<210> 805

<211> 506

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(483)

<223> FRXA01796

<400> 805

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gat cag atg cgt cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg 96
Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met
20 25 30

tac atc gtg gcg cac gag tac ggc cac cac gtc caa aac ctc gag ggc 144
Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly
35 40 45

aca ctc gga ctg tcc aat tac aac gat ccg ggc gct gat tcc aac gcc 192
Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala
50 55 60

gtc aag atc gag ttg cag gcc gat tgc tac gca ggc att tgg gct aat 240
Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn
65 70 75 80

cac tcc agc gaa ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct 288
His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser

	85	90	95	
gag cta gat tcc gct ctc ctt gct gca agc gcc gtg ggc gac gac aat				336
Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn				
	100	105	110	
atc cag caa cga tcc ggt ggc gat gtc aat cct gaa agc tgg act cac				384
Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His				
	115	120	125	
ggc tca tcg cag cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc				432
Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr				
	130	135	140	
ggc cag atg agc gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac				480
Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp				
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<210> 806

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

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Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly
35 40 45

Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala
50 55 60

Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn
65 70 75 80

His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser
85 90 95

Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn
100 105 110

Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His
115 120 125

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<222> (101)..(1060)
<223> RXN01803
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Met Arg Lys Lys Lys																	115
1 5																	115
gac ggt caa aat ctc cca gac ttc cgg aaa aat ccg cca aag ctg gat																	163
Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn Pro Pro Lys Leu Asp																	163
10 15 20																	163
aaa aag gct tat gaa aaa gaa cta aaa aga ctt caa gcc gaa ctc gtc																	211
Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu Gln Ala Glu Leu Val																	211
25 30 35																	211
gat ttg caa caa tgg gtt gtg gaa acc ggt gcg cgc gtg gtc atc gtc																	259
Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala Arg Val Val Ile Val																	259
40 45 50																	259
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Met Glu Gly Arg Asp Ala Ala Glu Gly Lys Gly Ser Ala Ile Lys Arg Ile																	307
55 60 65																	307
acg cag tac ctc aac ccc cgg tcc gca agg atc gaa gcg ctg ccc acc																	355
Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile Glu Ala Leu Pro Thr																	355
70 75 80 85																	355
cca aac tct cgg gaa aaa ggg cag tgg tat ttc cag cgc tac atc gaa																	403
Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe Gln Arg Tyr Ile Glu																	403
90 95 100																	403
aaa ttg ccg act gct ggt gag atc gtt atc ttt gac cgc tcc tgg tac																	451
Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe Asp Arg Ser Trp Tyr																	451
105 110 115																	451
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Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe Cys Thr Ser Gln Glu																	499
120 125 130																	499
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Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe Glu Arg Leu Leu Val																	547
135 140 145																	547
gaa gat ggc att cac ctg cgt aaa tac tgg ttc tct gta tct gat gaa																	595
Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe Ser Val Ser Asp Glu																	595
150 155 160 165																	595
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Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser Asp Pro Leu Arg Arg																	643

170	175	180	
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Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile Thr Arg Trp Glu Asp			
185	190	195	
tac tca cgc gca aaa gat gag atg ttc atc cac acg gac atc ccg tca			739
Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His Thr Asp Ile Pro Ser			
200	205	210	
gca ccg tgg tac acg gtg gaa tct gag gac aag aag cgt tcc cgc atc			787
Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys Lys Arg Ser Arg Ile			
215	220	225	
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Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro Tyr Glu Lys Ile Asp			
230	235	240	245
cgt cca ttg ccg gaa atc cct cat cgc cca gat tct gaa tct gat tat			883
Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp Ser Glu Ser Asp Tyr			
250	255	260	
gta cgt ccc cct cgc gat gag ttc cgt tat gtt cca gat gtg gca gca			931
Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val Pro Asp Val Ala Ala			
265	270	275	
cac ttg gaa gaa gag cgc atc aag aaa gaa gaa aaa gcc aag aag gca			979
His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu Lys Ala Lys Lys Ala			
280	285	290	
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Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser Asp Lys Gln Lys Ser			
295	300	305	
tcc gga gga aaa ggc aag aag aag tcc aag aaa tagaacgcct tttaaggggt			1080
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<211> 320

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<213> Corynebacterium glutamicum

<400> 808

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Gln	Ala	Glu	Leu	Val	Asp	Leu	Gln	Gln	Trp	Val	Val	Glu	Thr	Gly	Ala
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Arg	Val	Val	Ile	Val	Met	Glu	Gly	Arg	Asp	Ala	Ala	Gly	Lys	Gly	Ser
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Ala	Ile	Lys	Arg	Ile	Thr	Gln	Tyr	Leu	Asn	Pro	Arg	Ser	Ala	Arg	Ile
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Glu Ala Leu Pro Thr Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe
85 90 95

Gln Arg Tyr Ile Glu Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe
100 105 110

Asp Arg Ser Trp Tyr Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe
115 120 125

Cys Thr Ser Gln Glu Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe
130 135 140

Glu Arg Leu Leu Val Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe
145 150 155 160

Ser Val Ser Asp Glu Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser
165 170 175

Asp Pro Leu Arg Arg Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile
180 185 190

Thr Arg Trp Glu Asp Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His
195 200 205

Thr Asp Ile Pro Ser Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys
210 215 220

Lys Arg Ser Arg Ile Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro
225 230 235 240

Tyr Glu Lys Ile Asp Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp
245 250 255

Ser Glu Ser Asp Tyr Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val
260 265 270

Pro Asp Val Ala Ala His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu
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Asp Lys Gln Lys Ser Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1060)

<223> FRXA01803

<400> 809

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Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn Pro Pro Lys Leu Asp						
aaa aag gct tat gaa aaa gaa cta aaa aga ctt caa gcc gaa ctc gtc						211
Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu Gln Ala Glu Leu Val						
gat ttg caa caa tgg gtt gtg gaa acc ggt gcg cgc gtg gtc atc gtc						259
Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala Arg Val Val Ile Val						
atg gaa ggc cgc gac gcc gct ggt aaa ggt tct gcg atc aag cgc att						307
Met Glu Gly Arg Asp Ala Ala Glu Lys Gly Ser Ala Ile Lys Arg Ile						
acg cag tac ctc aac ccc cgg tcc gca agg atc gaa gcg ctg ccc acc						355
Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile Glu Ala Leu Pro Thr						
cca aac tct cgg gaa aaa ggg cag tgg tat ttc cag cgc tac atc gaa						403
Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe Gln Arg Tyr Ile Glu						
aaa ttg ccg act gct ggt gag atc gtt atc ttt gac cgc tcc tgg tac						451
Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe Asp Arg Ser Trp Tyr						
aac cgt gca gga gtc gag cgc gtc atg gga ttt tgc acc tcc cag gag						499
Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe Cys Thr Ser Gln Glu						
tac cgc cga ttc ctt cac cag gca cca atc ttt gaa cgc ctg ttg gtg						547
Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe Glu Arg Leu Leu Val						
gaa gat ggc att cac ctg cgt aaa tac tgg ttc tct gta tct gat gaa						595
Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe Ser Val Ser Asp Glu						
gag cag att gag cgt ttc gaa gac cgc ctg agc gat ccg ctg cgc cgg						643
Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser Asp Pro Leu Arg Arg						
tgg aag ttg tcg cca atg gat tta caa tcg atc acc cgc tgg gaa gat						691
Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile Thr Arg Trp Glu Asp						
tac tca cgc gca aaa gat gag atg ttc atc cac acg gac atc ccg tca						739
Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His Thr Asp Ile Pro Ser						
gca ccg tgg tac acg gtg gaa tct gag gac aag aag cgt tcc cgc atc						787
Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys Lys Arg Ser Arg Ile						
aac gtc att tcg cat ctg ctc tcg acg att cct tat gag aag atc gat						835
Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro Tyr Glu Lys Ile Asp						

230	235	240	245	
cgt cca ttg ccg gaa atc cct cat cgc cca gat tct gaa tct gat tat				883
Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp Ser Glu Ser Asp Tyr				
250		255	260	
gta cgt ccc cct cgc gat gag ttc cgt tat gtt cca gat gtg gca gca				931
Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val Pro Asp Val Ala Ala				
265		270	275	
cac ttg gaa gaa gag cgc atc aag aaa gaa gaa aaa gcc aag aag gca				979
His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu Lys Ala Lys Lys Ala				
280		285	290	
aag aag cca gct aag gct gca gga aag aac tcg gat aag cag aag tct				1027
Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser Asp Lys Gln Lys Ser				
295		300	305	
tcc gga gga aaa ggc aag aag aag tcc aag aaa tagaacgcct tttaaggggt				1080
Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys				
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tga				1083
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Gln Ala Glu Leu Val Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala				
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Arg Val Val Ile Val Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser				
	50		55	60
Ala Ile Lys Arg Ile Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile				
	65		70	75
Glu Ala Leu Pro Thr Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe				
	85		90	95
Gln Arg Tyr Ile Glu Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe				
	100		105	110
Asp Arg Ser Trp Tyr Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe				
	115		120	125
Cys Thr Ser Gln Glu Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe				
	130		135	140
Glu Arg Leu Leu Val Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe				
	145		150	155
				160

Ser Val Ser Asp Glu Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser
165 170 175

Asp Pro Leu Arg Arg Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile
180 185 190

Thr Arg Trp Glu Asp Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His
195 200 205

Thr Asp Ile Pro Ser Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys
210 215 220

Lys Arg Ser Arg Ile Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro
225 230 235 240

Tyr Glu Lys Ile Asp Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp
245 250 255

Ser Glu Ser Asp Tyr Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val
260 265 270

Pro Asp Val Ala Ala His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu
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<211> 1299
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<223> RXN01809

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Met Asn Glu Gln Glu
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cga gaa gcc tta gag gat gct gcc ctt gag gaa gct gcc tta gcc gat 163
Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu Ala Ala Leu Ala Asp
10 15 20

gaa tta gct gca tta gag gct gaa gct ggc gta caa ggg tca gtc gag 211
Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val Gln Gly Ser Val Glu
25 30 35

cct tat gac tat gca gca gac ctt gat gat gag gac gag ttt gat gag 259
Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu Asp Glu Phe Asp Glu
40 45 50

gac cct ttt gct cag gat gaa ccc cgt gac gct ggt ccg cta ggt gag 307

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Leu	Ser	Ser	Asp	Asn	His	Val	Ser	Glu	Ala	Val	Ala	Glu	Asp	Thr	Gly	85	
70					75					80							
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Thr	Ser	Thr	Glu	Glu	Ser	Ala	Gln	Glu	Gly	Ser	His	Glu	Glu	Ser	Val	100	
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Asp	Asn	Pro	Arg	Asp	Phe	Thr	Gly	Thr	Ala	Thr	Ala	Val	Arg	Ser	Phe	115	
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Arg	Thr	Gln	Pro	Ala	Val	Asn	Thr	Asp	Ile	Asp	Asp	Gly	Gly	Gln	Glu	145	
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Asn	Thr	Ala	Gly	Ala	Thr	Ala	Ala	Asp	Val	Gly	Ala	Gly	Val	Phe	Phe	165	
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Gly	Thr	His	Phe	Glu	Leu	Ala	Phe	Gly	Gln	Val	Asp	Val	His	Arg	His	180	
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Ile	Arg	His	Glu	Gln	Ala	Met	Arg	Asp	Gly	His	Gln	Asp	Leu	Ser	Val	195	
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Phe	Val	Gly	Ala	Asp	Gly	Ala	Ile	Met	Leu	Glu	Glu	Leu	Lys	Asn	Arg	210	
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Tyr	Gln	Arg	Pro	Pro	Glu	Asn	Glu	Pro	His	Asp	Asp	Asp	Val	Thr	Glu	225	
			215					220									
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Met	Ile	Lys	Thr	Thr	Glu	Glu	Thr	Glu	Lys	Glu	Asn	Val	Glu	Met	Asp	245	
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Gln	Asp	Ile	Ala	Val	Val	Asp	Asn	Val	Asp	Glu	Gln	Val	Val	Val	Thr	260	
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Ala	Ser	Glu	Pro	Thr	Pro	Glu	Pro	Val	Pro	Lys	Val	Glu	His	Val	Glu	290	
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310	315	320	325
cga cgc ttg ggg ctg atg act cag gtg gca cat aat aag gaa ctt gat			1123
Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu Asp			
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gag gtc tac gct aag gca ctt gcc gag ggt gaa tcc cat gct cag cag			1171
Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln Gln			
	345	350	355
cag cat gaa tta gaa gca gaa aat gaa cgg ctt aaa aaa gaa gtt gat			1219
Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val Asp			
	360	365	370
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<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 812

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20 25 30

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35 40 45

Asp Glu Phe Asp Glu Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala
50 55 60

Gly Pro Leu Gly Glu Leu Ser Ser Asp Asn His Val Ser Glu Ala Val
65 70 75 80

Ala Glu Asp Thr Gly Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser
85 90 95

His Glu Glu Ser Val Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr
100 105 110

Ala Val Arg Ser Phe Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg
115 120 125

Pro Gly Pro Pro Ile Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Asp
130 135 140

Asp Gly Gly Gln Glu Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly

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Ala Gly Val Phe	Phe Gly Thr His Phe	Glu Leu Ala Phe	Gly Gln Val			
	165	170	175			
Asp Val His Arg	His Ile Arg His	Glu Gln Ala Met	Arg Asp Gly His			
	180	185	190			
Gln Asp Leu Ser	Val Phe Val Gly	Ala Asp Gly Ala	Ile Met Leu Glu			
	195	200	205			
Glu Leu Lys Asn	Arg Tyr Gln Arg	Pro Pro Glu Asn	Glu Pro His Asp			
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Asp Asp Val Thr	Glu Met Ile Lys	Thr Thr Glu Glu	Thr Glu Lys Glu			
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Asn Val Glu Met	Asp Gln Asp Ile	Ala Val Val Asp	Asn Val Asp Glu			
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Gln Val Val Val	Thr Pro Ala His	Asp Ala Asp Ser	Val Ala Val Val			
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Ala Glu Gln Val	Val Ala Ser Glu	Pro Thr Pro Glu	Pro Val Pro Lys			
	275	280	285			
Val Glu His Val	Glu Met Ser Val	Asp Leu Ala Gly	Glu Thr Ile Thr			
	290	295	300			
Pro Ile Asp Gln	Ala Ile Arg Ser	Phe Met Gln Leu	Asn Gly Ile Glu			
	305	310	315			320
His Ser Val Val	Leu Arg Arg Leu	Gly Leu Met Thr	Gln Val Ala His			
	325	330	335			
Asn Lys Glu Leu	Asp Glu Val Tyr	Ala Lys Ala Leu	Ala Glu Gly Glu			
	340	345	350			
Ser His Ala Gln	Gln Gln His Glu	Leu Glu Ala Glu	Asn Glu Arg Leu			
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Lys Lys Glu Val	Asp Ala Leu Ala	Ala Glu Leu Ser	Ala Ala Leu Met			
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<211> 586

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(586)

<223> FRXA01062

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 Gly Pro Leu Gly Glu Leu Ser Ser Asp Asn His Val Ser Glu Ala Val
 65 70 75 80
 Ala Glu Asp Thr Gly Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser
 85 90 95
 His Glu Glu Ser Val Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr
 100 105 110
 Ala Val Arg Ser Phe Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg
 115 120 125
 Pro Gly Pro Pro Ile Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Tyr
 130 135 140
 Asp Gly Gly Gln Glu Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly
 145 150 155 160
 Ala Gly

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(636)
 <223> FRXA01809

<400> 815
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 His Ile Arg His Glu Gln Ala Met Arg Asp Gly His Gln Asp Leu Ser
 1 5 10 15
 gtc ttt gtc ggt gct gat ggg gcg atc atg ctg gaa gaa ctt aaa aat 96
 Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Glu Leu Lys Asn
 20 25 30
 cgt tac cag cgc cca ccg gag aac gag ccc cat gat gat gat gtc acc 144
 Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr
 35 40 45
 gaa atg ata aag acc acc gag gaa aca gag aag gag aac gta gag atg 192
 Glu Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met
 50 55 60
 gat cag gat ata gct gta gta gac aac gtt gat gaa cag gtt gtg gtg 240
 Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val
 65 70 75 80
 aca cct gct cat gac gct gac agc gta gcg gtt gtt gct gaa cag gtc 288
 Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val
 85 90 95
 gtt gcg tca gaa cca acg cca gag ccg gta ccc aag gtt gag cac gta 336
 Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val

100	105	110	
gag atg agt gtc gat cta gcg ggt	gag act att aca ccg att gat cag		384
Glu Met Ser Val Asp Leu Ala Gly	Glu Thr Ile Thr Pro Ile Asp Gln		
115	120	125	
gca att cgg tct ttt atg cag ctc aac ggt	att gag cac agc gtg gtg		432
Ala Ile Arg Ser Phe Met Gln Leu Asn Gly	Ile Glu His Ser Val Val		
130	135	140	
ttg cga cgc ttg ggg ctg atg act cag gtg gca cat aat aag gaa ctt			480
Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu			
145	150	155	160
gat gag gtc tac gct aag gca ctt gcc gag ggt gaa tcc cat gct cag			528
Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln			
165	170	175	
cag cag cat gaa tta gaa gca gaa aat gaa cgg ctt aaa aaa gaa gtt			576
Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val			
180	185	190	
gat gcg ctc gct gca gag ctt agt gct gcg ttg atg ggc gag ggt ggt			624
Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly			
195	200	205	
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Gly Asp His Asp			
210			

<210> 816

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 816

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20 25 30	
Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr	
35 40 45	
Glu Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met	
50 55 60	
Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val	
65 70 75 80	
Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val	
85 90 95	
Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val	
100 105 110	
Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln	
115 120 125	

Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val
 130 135 140

Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu
 145 150 155 160

Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln
 165 170 175

Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val
 180 185 190

Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly
 195 200 205

Gly Asp His Asp
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<210> 817
 <211> 804
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXN01811

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 Val Phe Glu Phe Asp
 1 5

gat acc ttg gca aaa gat ata caa gta gac cgt acg tcc atg caa gta 163
 Asp Thr Leu Ala Lys Asp Ile Gln Val Asp Arg Thr Ser Met Gln Val
 10 15 20

ttc gaa gct tca gaa acc gtc aaa gaa gcg ata aaa gct tcg att gaa 211
 Phe Glu Ala Ser Glu Thr Val Lys Glu Ala Ile Lys Ala Ser Ile Glu
 25 30 35

caa gga cat act cgc tat ccg gtt atc tta gaa tca aaa gac aat gtt 259
 Gln Gly His Thr Arg Tyr Pro Val Ile Leu Glu Ser Lys Asp Asn Val
 40 45 50

tta ggt tat gtc acc ttg cca gat ttg atc aag caa tct tat aaa gat 307
 Leu Gly Tyr Val Thr Leu Pro Asp Leu Ile Lys Gln Ser Tyr Lys Asp
 55 60 65

gac cag ctg aca gta gaa cag ttg att gaa gag ccg atc gta aca act 355
 Asp Gln Leu Thr Val Glu Gln Leu Ile Glu Glu Pro Ile Val Thr Thr
 70 75 80 85

gaa acg atc cct ata aaa aaa tta ttg acg atc atg cga aaa aag gga 403
 Glu Thr Ile Pro Ile Lys Lys Leu Leu Thr Ile Met Arg Lys Lys Gly
 90 95 100

aag cat att gct atc tta aaa gat gaa tac gga ggg aca agc ggc tta 451

Lys His Ile Ala Ile Leu Lys Asp Glu Tyr Gly Gly Thr Ser Gly Leu
 105 110 115
 gtg acg att gaa gat att tta gaa gaa atc gtc ggg gaa atc cga gat 499
 Val Thr Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Arg Asp
 120 125 130
 gag aca gat ttg gac gaa gca ttg ata gcg gaa cag tca gat ggc tct 547
 Glu Thr Asp Leu Asp Glu Ala Leu Ile Ala Glu Gln Ser Asp Gly Ser
 135 140 145
 tat atc atc tcc ggc aaa cta aca tta gat gat ttc cag cgt tat ttt 595
 Tyr Ile Ile Ser Gly Lys Leu Thr Leu Asp Asp Phe Gln Arg Tyr Phe
 150 155 160 165
 cat gta gag att cca gag ttt gaa gaa acg aat ttt act aca ctt gcg 643
 His Val Glu Ile Pro Glu Phe Glu Glu Thr Asn Phe Thr Thr Leu Ala
 170 175 180
 ggc ttt gct tct agc cga tat aaa gaa ata aaa gca gga aca atc att 691
 Gly Phe Ala Ser Ser Arg Tyr Lys Glu Ile Lys Ala Gly Thr Ile Ile
 185 190 195
 gag att gca tca ttc cgt ttc acg gta tta gaa tac cag cat gca cat 739
 Glu Ile Ala Ser Phe Arg Phe Thr Val Leu Glu Tyr Gln His Ala His
 200 205 210
 atc gat tat ttc aaa gta gag tcc acg gaa aga aaa aca gaa 781
 Ile Asp Tyr Phe Lys Val Glu Ser Thr Glu Arg Lys Thr Glu
 215 220 225
 taaaagaaaa aaggctgtga cat 804

<210> 818
 <211> 227
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 818
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 Lys Ala Ser Ile Glu Gln Gly His Thr Arg Tyr Pro Val Ile Leu Glu
 35 40 45
 Ser Lys Asp Asn Val Leu Gly Tyr Val Thr Leu Pro Asp Leu Ile Lys
 50 55 60
 Gln Ser Tyr Lys Asp Asp Gln Leu Thr Val Glu Gln Leu Ile Glu Glu
 65 70 75 80
 Pro Ile Val Thr Thr Glu Thr Ile Pro Ile Lys Lys Leu Leu Thr Ile
 85 90 95
 Met Arg Lys Lys Gly Lys His Ile Ala Ile Leu Lys Asp Glu Tyr Gly
 100 105 110

Gly Thr Ser Gly Leu Val Thr Ile Glu Asp Ile Leu Glu Glu Ile Val
 115 120 125
 Gly Glu Ile Arg Asp Glu Thr Asp Leu Asp Glu Ala Leu Ile Ala Glu
 130 135 140
 Gln Ser Asp Gly Ser Tyr Ile Ile Ser Gly Lys Leu Thr Leu Asp Asp
 145 150 155 160
 Phe Gln Arg Tyr Phe His Val Glu Ile Pro Glu Phe Glu Glu Thr Asn
 165 170 175
 Phe Thr Thr Leu Ala Gly Phe Ala Ser Ser Arg Tyr Lys Glu Ile Lys
 180 185 190
 Ala Gly Thr Ile Ile Glu Ile Ala Ser Phe Arg Phe Thr Val Leu Glu
 195 200 205
 Tyr Gln His Ala His Ile Asp Tyr Phe Lys Val Glu Ser Thr Glu Arg
 210 215 220
 Lys Thr Glu
 225

<210> 819
 <211> 789
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(766)
 <223> RXN01813

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 Met Val Ala Ile Val
 1 5
 gtc gtt gca atc gtc gtc gtc ggc ttc atc gtc atc caa ggc cag ggc 163
 Val Val Ala Ile Val Val Val Gly Phe Ile Val Ile Gln Gly Gln Gly
 10 15 20
 tca aaa gca gcc aag ctt ggt gac cgc gac tac gaa gac acc tct ttg 211
 Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr Glu Asp Thr Ser Leu
 25 30 35
 gca atg gaa gta ggc tcc gac tcc atc acg ctg acc tcc gca aac acc 259
 Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu Thr Ser Ala Asn Thr
 40 45 50
 tcc gcc gac gca aag tcc gtg cag ctt ttt gaa gac ttc tcc tgc tct 307
 Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu Asp Phe Ser Cys Ser
 55 60 65
 cac tgc tcc gag ctc tcc ctc gcc acc gac gct gac atg aag act cag 355
 His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala Asp Met Lys Thr Gln
 70 75 80 85

atc gaa gac ggc aac ctg gtc gtc gaa atc aag cca ctg aac ttc ctt 403
 Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys Pro Leu Asn Phe Leu
 90 95 100

gac cgc gaa aac atc gac ggc cac tcc acc cac gca ttg gca gca gcc 451
 Asp Arg Glu Asn Ile Asp Gly His Ser Thr His Ala Leu Ala Ala
 105 110 115

ctt gca gtg gca gac tcc aac gac gca acc ctc tac tgg aac ttc cgc 499
 Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu Tyr Trp Asn Phe Arg
 120 125 130

gca ttc ctc atg gaa gat cag tcc gag atc tac aac cag tgg tcc gat 547
 Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr Asn Gln Trp Ser Asp
 135 140 145

gat gac ttc gca gac ggc gtt gaa gcc ctt ggc gca gac tcc tcc gta 595
 Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly Ala Asp Ser Ser Val
 150 155 160 165

gta gac gca atc cga aac ggc gac aac atc cag cgc gca tac gac ctg 643
 Val Asp Ala Ile Arg Asn Gly Asp Asn Ile Gln Arg Ala Tyr Asp Leu
 170 175 180

gca acc gca aac ggt gaa gaa ctc act gaa gaa acc ggc agc ctg tcc 691
 Ala Thr Ala Asn Gly Glu Glu Leu Thr Glu Glu Thr Gly Ser Leu Ser
 185 190 195

tca cca cgc gtc ctc cag gac ggc aag gat gtt gaa ggc aac atc tcc 739
 Ser Pro Arg Val Leu Gln Asp Gly Lys Asp Val Glu Gly Asn Ile Ser
 200 205 210

gac tgg atc acc act gtt cta gct tct taaagaactg atctagaagg 786
 Asp Trp Ile Thr Thr Val Leu Ala Ser
 215 220

aaa 789

<210> 820
 <211> 222
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 820
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Ile Gln Gly Gln Gly Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr
 20 25 30

Glu Asp Thr Ser Leu Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu
 35 40 45

Thr Ser Ala Asn Thr Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu
 50 55 60

Asp Phe Ser Cys Ser His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala
 65 70 75 80

cac tgc tcc gag ctc tcc ctc gcc acc gac gct gac atg aag act cag 355
 His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala Asp Met Lys Thr Gln
 70 75 80 85
 atc gaa gac ggc aac ctg gtc gtc gaa atc aag cca ctg aac ttc ctt 403
 Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys Pro Leu Asn Phe Leu
 90 95 100
 gac cgc gaa aac atc gac ggc cac tcc acc cac gca ttg gca gca gcc 451
 Asp Arg Glu Asn Ile Asp Gly His Ser Thr His Ala Leu Ala Ala Ala
 105 110 115
 ctt gca gtg gca gac tcc aac gac gca acc ctc tac tgg aac ttc cgc 499
 Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu Tyr Trp Asn Phe Arg
 120 125 130
 gca ttc ctc atg gaa gat cag tcc gag atc tac aac cag tgg tcc gat 547
 Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr Asn Gln Trp Ser Asp
 135 140 145
 gat gac ttc gca gac ggc gtt gaa gcc ctt ggc gca gac tcc tcc gta 595
 Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly Ala Asp Ser Ser Val
 150 155 160 165
 gta gac gca atc cga acg gcg aca aca tcc agc gcg cat acg acc tgg 643
 Val Asp Ala Ile Arg Thr Ala Thr Thr Ser Ser Ala His Thr Thr Trp
 170 175 180
 caa ccg caa acg gtg aag aac tca ctg aag aaa ccg gca gcc tgt tct 691
 Gln Pro Gln Thr Val Lys Asn Ser Leu Lys Lys Pro Ala Ala Cys Ser
 185 190 195
 tac cac gcg ttc ttc aag acg gca agg atg ttg aag gca 730
 Tyr His Ala Phe Phe Lys Thr Ala Arg Met Leu Lys Ala
 200 205 210

<210> 822

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 822

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 Ile Gln Gly Gln Gly Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr
 20 25 30
 Glu Asp Thr Ser Leu Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu
 35 40 45
 Thr Ser Ala Asn Thr Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu
 50 55 60
 Asp Phe Ser Cys Ser His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala
 65 70 75 80
 Asp Met Lys Thr Gln Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys
 85 90 95

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<211> 915
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(892)  
<223> RXN01815
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Met Asn Arg Ser Thr																5
1																
att tcc cca gtt gaa gcc cgc cag caa ttc cgc gca ggc ctt atc caa																163
Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg Ala Gly Leu Ile Gln																20
10 15																
ccc acc tcc ggc tgg tcc gcg ggt ttt gcc caa gcc aac ctc att tcc																211
Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln Ala Asn Leu Ile Ser																35
25 30																
atg ccc cag gat ctg gct tat gat ttc ctg ctt ttt gct caa cgc aac																259
Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu Phe Ala Gln Arg Asn																50
40 45																
ccc aag ccc tgc ccc.atc ttg gaa gta tta aat gct ggc gaa acc ttc																307
Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn Ala Gly Glu Thr Phe																65
55 60																
ggc gga att ttc ggc tca aac gcc acc gaa gca gac atc cgc acc gac																355
Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala Asp Ile Arg Thr Asp																85
70 75 80																

gcg ccc caa tac cgc att tac gca cac ggc gaa ctt atc gat tcc ccc 403
 Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu Leu Ile Asp Ser Pro
 90 95 100

gcc agc gcc gtc gat tat tgg cgc gac gac ctc gtc agt ttc atc atc 451
 Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu Val Ser Phe Ile Ile
 105 110 115

ggc tgc tcc ttt act ttt gaa cat ccc atg gtc caa gca ggc gtt ccc 499
 Gly Cys Ser Phe Thr Phe Glu His Pro Met Val Gln Ala Gly Val Pro
 120 125 130

gtc cgc cac ctc gag gcc ggc cgc aac gtc ccc atg tat gaa acc tca 547
 Val Arg His Leu Glu Ala Gly Arg Asn Val Pro Met Tyr Glu Thr Ser
 135 140 145

ctt gcc tgc cga cca gcc ggt tcc cta tca gga aac ctc gtg gtg tca 595
 Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly Asn Leu Val Val Ser
 150 155 160 165

ctg cgc atg atc ccc gca tcc caa gtc gcg gat gcc gtc cgc att acc 643
 Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp Ala Val Arg Ile Thr
 170 175 180

tcc cgc tac ccc gcg gtt cac gga gca cca gtc cac atc ggc gat cct 691
 Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val His Ile Gly Asp Pro
 185 190 195

tca ctg atc gga atc gat gac atc aac aac cct gat ttc ggc gat gcc 739
 Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro Asp Phe Gly Asp Ala
 200 205 210

ccg ctg tcc gaa cca agc gac gtc ccc gtg ttt tgg gcc tgc gga gtt 787
 Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe Trp Ala Cys Gly Val
 215 220 225

acc cct caa gca atg gtc atg tcc tcc aag cca ccg ctg gcg atc act 835
 Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro Pro Leu Ala Ile Thr
 230 235 240 245

cac gca ccc gga cac atg ctg atc acc gac gcc cca gat ctg gga ttc 883
 His Ala Pro Gly His Met Leu Ile Thr Asp Ala Pro Asp Leu Gly Phe
 250 255 260

cag gtt cct taaacctgga tccaccgatg tga 915
 Gln Val Pro

<210> 824

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 824

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 20 25 30

Ala Asn Leu Ile Ser Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu
 35 40 45
 Phe Ala Gln Arg Asn Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn
 50 55 60
 Ala Gly Glu Thr Phe Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala
 65 70 75 80
 Asp Ile Arg Thr Asp Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu
 85 90 95
 Leu Ile Asp Ser Pro Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu
 100 105 110
 Val Ser Phe Ile Ile Gly Cys Ser Phe Thr Phe Glu His Pro Met Val
 115 120 125
 Gln Ala Gly Val Pro Val Arg His Leu Glu Ala Gly Arg Asn Val Pro
 130 135 140
 Met Tyr Glu Thr Ser Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly
 145 150 155 160
 Asn Leu Val Val Ser Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp
 165 170 175
 Ala Val Arg Ile Thr Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val
 180 185 190
 His Ile Gly Asp Pro Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro
 195 200 205
 Asp Phe Gly Asp Ala Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe
 210 215 220
 Trp Ala Cys Gly Val Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro
 225 230 235 240
 Pro Leu Ala Ile Thr His Ala Pro Gly His Met Leu Ile Thr Asp Ala
 245 250 255
 Pro Asp Leu Gly Phe Gln Val Pro
 260

<210> 825

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> FRXA01815

<400> 825

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	Met	Asn	Arg	Ser	Thr	
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att tcc cca gtt gaa gcc cgc cag caa ttc cgc gca ggc ctt atc caa						163
Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg Ala Gly Leu Ile Gln						
	10				20	
ccc acc tcc ggc tgg tcc gcg ggt ttt gcc caa gcc aac ctc att tcc						211
Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln Ala Asn Leu Ile Ser						
	25				35	
atg ccc cag gat ctg gct tat gat ttc ctg ctt ttt gct caa cgc aac						259
Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu Phe Ala Gln Arg Asn						
	40				50	
ccc aag ccc tgc ccc atc ttg gaa gta tta aat gct ggc gaa acc ttc						307
Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn Ala Gly Glu Thr Phe						
	55				65	
ggc gga att ttc ggc tca aac gcc acc gaa gca gac atc cgc acc gac						355
Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala Asp Ile Arg Thr Asp						
	70				80	85
gcg ccc caa tac cgc att tac gca cac ggc gaa ctt atc gat tcc ccc						403
Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu Leu Ile Asp Ser Pro						
	90				95	100
gcc agc gcc gtc gat tat tgg cgc gac gac ctc gtc agt ttc atc atc						451
Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu Val Ser Phe Ile Ile						
	105				110	115
ggc tgc tcc ttt act ttt gaa cat ccc atg gtc caa gca ggc gtt ccc						499
Gly Cys Ser Phe Thr Phe Glu His Pro Met Val Gln Ala Gly Val Pro						
	120				125	130
gtc cgc cac ctc gag gcc ggc cgc aac gtc ccc atg tat gaa acc tca						547
Val Arg His Leu Glu Ala Gly Arg Asn Val Pro Met Tyr Glu Thr Ser						
	135				140	145
ctt gcc tgc cga cca gcc ggt tcc cta tca gga aac ctc gtg gtg tca						595
Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly Asn Leu Val Val Ser						
	150				155	160
ctg cgc atg atc ccc gca tcc caa gtc gcg gat gcc gtc cgc att acc						643
Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp Ala Val Arg Ile Thr						
	170				175	180
tcc cgc tac ccc gcg gtt cac gga gca cca gtc cac atc ggc gat cct						691
Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val His Ile Gly Asp Pro						
	185				190	195
tca ctg atc gga atc gat gac atc aac aac cct gat ttc ggc gat gcc						739
Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro Asp Phe Gly Asp Ala						
	200				205	210
ccg ctg tcc gaa cca agc gac gtc ccc gtg ttt tgg gcc tgc gga gtt						787
Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe Trp Ala Cys Gly Val						
	215				220	225
acc cct caa gca atg gtc atg tcc tcc aag cca ccg ctg gcg atc act						835
Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro Pro Leu Ala Ile Thr						


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Asn  Pro  Ser  Ala  Asn  Arg  Thr  Pro  Val  Lys  Ile  Asn  Ser  Ala  Gly  Thr
          20          25          30
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Pro Met Trp Tyr Lys Val Ile Met Phe Ala Phe Met Ile Val Gly Leu
 35 40 45

Ala Trp Leu Ile Ile Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met
 50 55 60

Ala Asp Leu Gly Ala Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile
 65 70 75 80

Ile Gly Leu Leu Met Thr Met Gly Trp Arg
 85 90

<210> 829
 <211> 393
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(370)
 <223> FRXA01825

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tgggggttttt ccaagacaat aaattatgaa ggtgtgaaca atg cca aag gca aga 115
 Met Pro Lys Ala Arg
 1 5

gta act aaa aac gag acc gca ccg gtt tca agc aac cca agc gca aac 163
 Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser Asn Pro Ser Ala Asn
 10 15 20

cgc acc ccg gtt aag atc aat tcc gcc gga acc cca atg tgg tac aag 211
 Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr Pro Met Trp Tyr Lys
 25 30 35

gtc atc atg ttt gcc ttc atg atc gtc gcc cta gcc tgg ttg atc att 259
 Val Ile Met Phe Ala Phe Met Ile Val Gly Leu Ala Trp Leu Ile Ile
 40 45 50

aac tac ctc gtg ggc cca cag atc cca ttc atg gct gat ctt ggt gca 307
 Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met Ala Asp Leu Gly Ala
 55 60 65

tgg aac tat ggc atc ggc ttc ggt ctg atg atc atc ggc cta ctc atg 355
 Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile Ile Gly Leu Leu Met
 70 75 80 85

acc atg ggt tgg cgt taatccttca aaaaagtgac tgc 393
 Thr Met Gly Trp Arg
 90

<210> 830
 <211> 90
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 830

Met Pro Lys Ala Arg Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser
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Asn Pro Ser Ala Asn Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr
 20 25 30

Pro Met Trp Tyr Lys Val Ile Met Phe Ala Phe Met Ile Val Gly Leu
 35 40 45

Ala Trp Leu Ile Ile Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met
 50 55 60

Ala Asp Leu Gly Ala Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile
 65 70 75 80

Ile Gly Leu Leu Met Thr Met Gly Trp Arg
 85 90

<210> 831

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> RXN01831

<400> 831

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gaagttcgta ttgttagtcc ctagaggag aggttgatca atg gat tct ctg gtc 115
 Met Asp Ser Leu Val
 1 5

ctt ctt ggg ctt cgc atc gct ttg ctt gtg gtg ttg tgg ttt ttc gtc 163
 Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val Leu Trp Phe Phe Val
 10 15 20

ttg atg gcg ctg cgc gct atg agg gca gat ttg aaa gtg acg ggt caa 211
 Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu Lys Val Thr Gly Gln
 25 30 35

gcg tcg aca agc agc tcc tcc gtc gcg gca ccg cag ggc ctt gcc cgg 259
 Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro Gln Gly Leu Ala Arg
 40 45 50

gct ttt aat cgc tcc agc ccg cct cgt ctt ttg acg gtg gtc gag ggc 307
 Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu Thr Val Val Glu Gly
 55 60 65

ccg ttg gcg ggc tcc tcg att gag gtg tcg gag gat atg acg atg ggc 355
 Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu Asp Met Thr Met Gly
 70 75 80 85

cgt agc cct gag tgc acg ttt gtg gtg ggc gat gat tac gcc tcc ggc 403
 Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp Asp Tyr Ala Ser Gly
 90 95 100

atg cat gcg cgg gtg ttt aag cgt ggt tcg gag tgg ttt gtg gag gat 451
Met His Ala Arg Val Phe Lys Arg Gly Ser Glu Trp Phe Val Glu Asp
105 110 115

ctg gat tcg cgc aac ggc act ttt gtc ggt ggt acg cgc att gat cag 499
Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly Thr Arg Ile Asp Gln
120 125 130

cct gag cag att gcg gtg ggc acg gat atc cgt att ggt cgt aca gca 547
Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg Ile Gly Arg Thr Ala
135 140 145

gtg agg ctt gtt ccc tgatgttgaa acttaaatat gcg 585
Val Arg Leu Val Pro
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<210> 832

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 832

Met Asp Ser Leu Val Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val
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Leu Trp Phe Phe Val Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu
20 25 30

Lys Val Thr Gly Gln Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro
35 40 45

Gln Gly Leu Ala Arg Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu
50 55 60

Thr Val Val Glu Gly Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu
65 70 75 80

Asp Met Thr Met Gly Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp
85 90 95

Asp Tyr Ala Ser Gly Met His Ala Arg Val Phe Lys Arg Gly Ser Glu
100 105 110

Trp Phe Val Glu Asp Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly
115 120 125

Thr Arg Ile Asp Gln Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg
130 135 140

Ile Gly Arg Thr Ala Val Arg Leu Val Pro
145 150

<210> 833

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> FRXA01831

<400> 833

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gaagttcgta ttgttagtcc ctagagggag aggttgatca atg gat tct ctg gtc 115
                                         Met Asp Ser Leu Val
                                         1 5

ctt ctt ggg ctt cgc atc gct ttg ctt gtg gtg ttg tgg ttt ttc gtc 163
Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val Leu Trp Phe Phe Val
                        10 15 20

ttg atg gcg ctg cgc gct atg agg gca gat ttg aaa gtg acg ggt caa 211
Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu Lys Val Thr Gly Gln
                        25 30 35

gcg tcg aca agc agc tcc tcc gtc gcg gca ccg cag ggc ctt gcc cgg 259
Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro Gln Gly Leu Ala Arg
                        40 45 50

gct ttt aat cgc tcc agc ccg cct cgt ctt ttg acg gtg gtc gag ggc 307
Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu Thr Val Val Glu Gly
                        55 60 65

ccg ttg gcg ggc tcc tcg att gag gtg tcg gag gat atg acg atg ggc 355
Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu Asp Met Thr Met Gly
                        70 75 80 85

cgt agc cct gag tgc acg ttt gtg gtg ggc gat gat tac gcc tcc ggc 403
Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp Asp Tyr Ala Ser Gly
                        90 95 100

atg cat gcg cgg gtg ttt aag cgt ggt tcg gag tgg ttt gtg gag gat 451
Met His Ala Arg Val Phe Lys Arg Gly Ser Glu Trp Phe Val Glu Asp
                        105 110 115

ctg gat tcg cgc aac ggc act ttt gtc ggt ggt acg cgc att gat cag 499
Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly Thr Arg Ile Asp Gln
                        120 125 130

cct gag cag att gcg gtg ggc acg gat atc cgt att ggt cgt aca gca 547
Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg Ile Gly Arg Thr Ala
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gtg agg ctt gtt ccc tgatgttgaa acttaaatat gcg 585
Val Arg Leu Val Pro
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<210> 834

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 834

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Met Asp Ser Leu Val Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val
 1 5 10 15

Leu Trp Phe Phe Val Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu

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20										25					30														
Lys	Val	Thr	Gly	Gln	Ala	Ser	Thr	Ser	Ser	Ser	Ser	Val	Ala	Ala	Pro														
			35					40					45																
Gln	Gly	Leu	Ala	Arg	Ala	Phe	Asn	Arg	Ser	Ser	Pro	Pro	Arg	Leu	Leu														
	50					55					60																		
Thr	Val	Val	Glu	Gly	Pro	Leu	Ala	Gly	Ser	Ser	Ile	Glu	Val	Ser	Glu														
	65				70					75					80														
Asp	Met	Thr	Met	Gly	Arg	Ser	Pro	Glu	Cys	Thr	Phe	Val	Val	Gly	Asp														
				85					90					95															
Asp	Tyr	Ala	Ser	Gly	Met	His	Ala	Arg	Val	Phe	Lys	Arg	Gly	Ser	Glu														
		100						105					110																
Trp	Phe	Val	Glu	Asp	Leu	Asp	Ser	Arg	Asn	Gly	Thr	Phe	Val	Gly	Gly														
	115						120						125																
Thr	Arg	Ile	Asp	Gln	Pro	Glu	Gln	Ile	Ala	Val	Gly	Thr	Asp	Ile	Arg														
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Ile	Gly	Arg	Thr	Ala	Val	Arg	Leu	Val	Pro																				
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<210> 835

<211> 825

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(802)

<223> RXN01834

<400> 835

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				Met	Leu	Gly	Gly	Gly	
				1				5	

ggt	gcc	atc	ctt	gcc	att	ccg	ctg	ctt	att	tat	gga	ttt	tct	ttt	agc	163
Gly	Ala	Ile	Leu	Ala	Ile	Pro	Leu	Leu	Ile	Tyr	Gly	Phe	Ser	Phe	Ser	
			10						15					20		

gcc	acg	caa	gct	act	gca	gct	tca	tta	atc	atc	atc	gga	ctt	ggc	gcc	211
Ala	Thr	Gln	Ala	Thr	Ala	Ala	Ser	Leu	Ile	Ile	Ile	Gly	Leu	Gly	Ala	
			25					30					35			

ctc	att	gga	ctg	atc	agc	caa	tac	gct	gcc	ggg	cac	gtc	cgc	ctt	aaa	259
Leu	Ile	Gly	Leu	Ile	Ser	Gln	Tyr	Ala	Ala	Gly	His	Val	Arg	Leu	Lys	
		40					45					50				

gag	ggt	cta	agc	ttt	ggc	ctt	tta	ggg	ttg	gtc	ggc	tca	ttt	gtg	ggc	307
Glu	Gly	Leu	Ser	Phe	Gly	Leu	Leu	Gly	Leu	Val	Gly	Ser	Phe	Val	Gly	
	55					60					65					

agt	cac	ctt	gct	agc	aat	atc	ccc	gat	tcc	cta	ctc	ctg	agc	ggc	ttt	355
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Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu Leu Leu Ser Gly Phe
 70 75 80 85
 gcc atc ctc acg ctc gtg gtg gcg ttg acc atg att tct aaa tta aga 403
 Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met Ile Ser Lys Leu Arg
 90 95 100
 agc acc cga gaa tac ata acc aga agg cca agc atc ctt gcc att gct 451
 Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser Ile Leu Ala Ile Ala
 105 110 115
 ctt agt gcc acc ggc gtg gga ttt ttg acg gga ttt ttt ggt gtg ggt 499
 Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly Phe Phe Gly Val Gly
 120 125 130
 ggc ggt ttt gcc att gtg cca gcc ttg att ttt gcg ctc ggt ttt tcc 547
 Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe Ala Leu Gly Phe Ser
 135 140 145
 atg cgg cag gct agc gcc act tcc cta gtg gtg atc gcc gtt aac agc 595
 Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val Ile Ala Val Asn Ser
 150 155 160 165
 gct att gcc atg gga ttt aga tat tcc gat ttg gca agt att gac tgg 643
 Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu Ala Ser Ile Asp Trp
 170 175 180
 tca gtg atc tcg cca att atc atc acc acc gta ttg ggc gct ttt agt 691
 Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val Leu Gly Ala Phe Ser
 185 190 195
 ggc gta aaa cta gcc aaa aag gtc aaa gca tca tca ctg caa cta ggt 739
 Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser Ser Leu Gln Leu Gly
 200 205 210
 ttt gct ggc ttc ttg atc ttc att tcg atc tat atg gga ttt cag aat 787
 Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr Met Gly Phe Gln Asn
 215 220 225
 ttc ccg gac ctt ttt taaaacttca aaatataccc ccc 825
 Phe Pro Asp Leu Phe
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<210> 836

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 836

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 Gly Phe Ser Phe Ser Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile
 20 25 30
 Ile Gly Leu Gly Ala Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly
 35 40 45
 His Val Arg Leu Lys Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val
 50 55 60

Gly Ser Phe Val Gly Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu
 65 70 75 80
 Leu Leu Ser Gly Phe Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met
 85 90 95
 Ile Ser Lys Leu Arg Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser
 100 105 110
 Ile Leu Ala Ile Ala Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly
 115 120 125
 Phe Phe Gly Val Gly Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe
 130 135 140
 Ala Leu Gly Phe Ser Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val
 145 150 155 160
 Ile Ala Val Asn Ser Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu
 165 170 175
 Ala Ser Ile Asp Trp Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val
 180 185 190
 Leu Gly Ala Phe Ser Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser
 195 200 205
 Ser Leu Gln Leu Gly Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr
 210 215 220
 Met Gly Phe Gln Asn Phe Pro Asp Leu Phe
 225 230

<210> 837

<211> 825

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(802)

<223> FRXA01834

<400> 837

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agcccttctt ggcggcctaa taataggcct acttcttggc atg ctc ggt ggt ggc 115
 Met Leu Gly Gly Gly
 1 5

ggt gcc atc ctt gcc att ccg ctg ctt att tat gga ttt tct ttt agc 163
 Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr Gly Phe Ser Phe Ser
 10 15 20

gcc acg caa gct act gca gct tca tta atc atc atc gga ctt ggc gcc 211
 Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile Ile Gly Leu Gly Ala
 25 30 35

ctc att gga ctg atc agc caa tac gct gcc ggg cac gtc cgc ctt aaa 259

Leu	Ile	Gly	Leu	Ile	Ser	Gln	Tyr	Ala	Ala	Gly	His	Val	Arg	Leu	Lys		
40						45						50					
gag	ggt	cta	agc	ttt	ggc	ctt	tta	ggg	ttg	gtc	ggc	tca	ttt	gtg	ggc	307	
Glu	Gly	Leu	Ser	Phe	Gly	Leu	Leu	Gly	Leu	Val	Gly	Ser	Phe	Val	Gly		
55						60						65					
agt	cac	ctt	gct	agc	aat	atc	ccc	gat	tcc	cta	ctc	ctg	agc	ggc	ttt	355	
Ser	His	Leu	Ala	Ser	Asn	Ile	Pro	Asp	Ser	Leu	Leu	Leu	Ser	Gly	Phe		
70						75						80			85		
gcc	atc	ctc	acg	ctc	gtg	gtg	gcg	ttg	acc	atg	att	tct	aaa	tta	aga	403	
Ala	Ile	Leu	Thr	Leu	Val	Val	Ala	Leu	Thr	Met	Ile	Ser	Lys	Leu	Arg		
			90						95						100		
agc	acc	cga	gaa	tac	ata	acc	aga	agg	cca	agc	atc	ctt	gcc	att	gct	451	
Ser	Thr	Arg	Glu	Tyr	Ile	Thr	Arg	Arg	Pro	Ser	Ile	Leu	Ala	Ile	Ala		
			105						110						115		
ctt	agt	gcc	acc	ggc	gtg	gga	ttt	ttg	acg	gga	ttt	ttt	ggc	gtg	ggc	499	
Leu	Ser	Ala	Thr	Gly	Val	Gly	Phe	Leu	Thr	Gly	Phe	Phe	Gly	Val	Gly		
120						125						130					
ggc	ggt	ttt	gcc	att	gtg	cca	gcc	ttg	att	ttt	gcg	ctc	ggc	ttt	tcc	547	
Gly	Gly	Phe	Ala	Ile	Val	Pro	Ala	Leu	Ile	Phe	Ala	Leu	Gly	Phe	Ser		
135						140						145					
atg	cgg	cag	gct	agc	gcc	act	tcc	cta	gtg	gtg	atc	gcc	ggt	aac	agc	595	
Met	Arg	Gln	Ala	Ser	Ala	Thr	Ser	Leu	Val	Val	Ile	Ala	Val	Asn	Ser		
150						155						160			165		
gct	att	gcc	atg	gga	ttt	aga	tat	tcc	gat	ttg	gca	agt	att	gac	tgg	643	
Ala	Ile	Ala	Met	Gly	Phe	Arg	Tyr	Ser	Asp	Leu	Ala	Ser	Ile	Asp	Trp		
			170						175						180		
tca	gtg	atc	tcg	cca	att	atc	atc	acc	acc	gta	ttg	ggc	gct	ttt	agt	691	
Ser	Val	Ile	Ser	Pro	Ile	Ile	Ile	Thr	Thr	Val	Leu	Gly	Ala	Phe	Ser		
			185						190						195		
ggc	gta	aaa	cta	gcc	aaa	aag	gtc	aaa	gca	tca	tca	ctg	caa	cta	ggc	739	
Gly	Val	Lys	Leu	Ala	Lys	Lys	Val	Lys	Ala	Ser	Ser	Leu	Gln	Leu	Gly		
200						205						210					
ttt	gct	ggc	ttc	ttg	atc	ttc	att	tcg	atc	tat	atg	gga	ttt	cag	aat	787	
Phe	Ala	Gly	Phe	Leu	Ile	Phe	Ile	Ser	Ile	Tyr	Met	Gly	Phe	Gln	Asn		
215						220						225					
ttc	ccg	gac	ctt	ttt	taaaa	cttca	aaatata	cccc	ccc							825	
Phe	Pro	Asp	Leu	Phe													
230																	

<210> 838

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 838

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Gly	Phe	Ser	Phe 20	Ser	Ala	Thr	Gln	Ala 25	Thr	Ala	Ala	Ser	Leu 30	Ile	Ile
Ile	Gly	Leu 35	Gly	Ala	Leu	Ile	Gly 40	Leu	Ile	Ser	Gln	Tyr 45	Ala	Ala	Gly
His	Val 50	Arg	Leu	Lys	Glu	Gly 55	Leu	Ser	Phe	Gly	Leu 60	Leu	Gly	Leu	Val
Gly 65	Ser	Phe	Val	Gly	Ser 70	His	Leu	Ala	Ser	Asn 75	Ile	Pro	Asp	Ser	Leu 80
Leu	Leu	Ser	Gly	Phe 85	Ala	Ile	Leu	Thr	Leu 90	Val	Val	Ala	Leu	Thr 95	Met
Ile	Ser	Lys 100	Leu	Arg	Ser	Thr	Arg 105	Glu	Tyr	Ile	Thr	Arg 110	Arg	Pro	Ser
Ile	Leu	Ala 115	Ile	Ala	Leu	Ser	Ala 120	Thr	Gly	Val	Gly	Phe 125	Leu	Thr	Gly
Phe 130	Phe	Gly	Val	Gly	Gly	Gly 135	Phe	Ala	Ile	Val	Pro 140	Ala	Leu	Ile	Phe
Ala 145	Leu	Gly	Phe	Ser	Met 150	Arg	Gln	Ala	Ser	Ala 155	Thr	Ser	Leu	Val	Val 160
Ile	Ala	Val	Asn 165	Ser	Ala	Ile	Ala	Met	Gly 170	Phe	Arg	Tyr	Ser	Asp 175	Leu
Ala	Ser	Ile 180	Asp	Trp	Ser	Val	Ile 185	Ser	Pro	Ile	Ile	Ile 190	Thr	Thr	Val
Leu	Gly	Ala 195	Phe	Ser	Gly	Val	Lys 200	Leu	Ala	Lys	Lys 205	Val	Lys	Ala	Ser
Ser 210	Leu	Gln	Leu	Gly	Phe	Ala 215	Gly	Phe	Leu	Ile	Phe 220	Ile	Ser	Ile	Tyr
Met 225	Gly	Phe	Gln	Asn 230	Phe	Pro	Asp	Leu	Phe						

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<210> 839
<211> 382
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(382)  
<223> RXN01846
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<400> 839
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gtttattact tatgggaata gtgtggaaaag tagggtgaat atg tca att cct gga 115
                                         Met Ser Ile Pro Gly
                                         1                               5

aat gtt agt tat gtt gca cag ggt ggc acc ggt tgg gat ggt gct gat 163

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Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly Trp Asp Gly Ala Asp
      10                      15                      20
cag tac acc acg ggt gag agt tgg gat cta cag tcg ttc ctt gaa aac 211
Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln Ser Phe Leu Glu Asn
      25                      30                      35
tcg act gac tac ctc atg att att ggt ggt tcg ctg ctg gca ctt gtt 259
Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser Leu Leu Ala Leu Val
      40                      45                      50
ggt ggt gct gct gtg att tgg ggc ttt gtc aac gtg atg cgc aag ctc 307
Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn Val Met Arg Lys Leu
      55                      60                      65
ttc ggt ggt cag agt ggt cag cag att cag tgg ttc acc act att ttg 355
Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp Phe Thr Thr Ile Leu
      70                      75                      80
ctc atc att gtc ggt ggt gcg ttg cct 382
Leu Ile Ile Val Gly Gly Ala Leu Pro
      90

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<210> 840

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

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Met Ser Ile Pro Gly Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly
  1                      5                      10                      15
Trp Asp Gly Ala Asp Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln
      20                      25                      30
Ser Phe Leu Glu Asn Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser
      35                      40                      45
Leu Leu Ala Leu Val Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn
      50                      55                      60
Val Met Arg Lys Leu Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp
      65                      70                      75                      80
Phe Thr Thr Ile Leu Leu Ile Ile Val Gly Gly Ala Leu Pro
      85                      90

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<210> 841

<211> 358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(358)

<223> FRXA01846

<400> 841

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gtttattact tatgggaata gtgtggaaag taggggtgaat atg tca att cct gga 115
                                         Met Ser Ile Pro Gly
                                         1                               5

aat gtt agt tat gtt gca cag ggt ggc acc ggt tgg gat ggt gct gat 163
Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly Trp Asp Gly Ala Asp
              10                               15                               20

cag tac acc acg ggt gag agt tgg gat cta cag tcg ttc ctt gaa aac 211
Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln Ser Phe Leu Glu Asn
              25                               30                               35

tcg act gac tac ctc atg att att ggt ggt tcg ctg ctg gca ctt gtt 259
Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser Leu Leu Ala Leu Val
              40                               45                               50

ggg ggt gct gct gtg att tgg ggc ttt gtc aac gtg atg cgc aag ctc 307
Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn Val Met Arg Lys Leu
              55                               60                               65

ttc ggt ggt cag agt ggt cag cag att cag tgg ttc acc act att ttg 355
Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp Phe Thr Thr Ile Leu
              70                               75                               80

ctc 358
Leu

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<210> 842
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 842
Met Ser Ile Pro Gly Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly
  1                               5                               10                               15

Trp Asp Gly Ala Asp Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln
              20                               25                               30

Ser Phe Leu Glu Asn Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser
              35                               40                               45

Leu Leu Ala Leu Val Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn
              50                               55                               60

Val Met Arg Lys Leu Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp
              65                               70                               75                               80

Phe Thr Thr Ile Leu Leu
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(835)
 <223> RXN01847

<400> 843

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                                   Met Leu Ile Val Leu
                                   1 5

cct ccc tca gaa act aag acc cac ggc ggt tca gga aaa cct ctg gat 163
Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser Gly Lys Pro Leu Asp
              10 15 20

ttt cac cat ttg agt ttc ccg tcg ctc acc aag gca cgc caa aca ata 211
Phe His His Leu Ser Phe Pro Ser Leu Thr Lys Ala Arg Gln Thr Ile
              25 30 35

ctc gct gac ctg caa gct ttg gag gta gat gag gcg ctg aaa gtt ttg 259
Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu Ala Leu Lys Val Leu
              40 45 50

ggc att tct gaa aag ctc cgc cct gag gcc gaa tcc aat cgc gcg ctg 307
Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu Ser Asn Arg Ala Leu
              55 60 65

gag acc agc cct acg atg cct gcg att ttt cgg tat tcc gga gtg ctt 355
Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg Tyr Ser Gly Val Leu
              70 75 80 85

tat gat gcg ctc gac gct gca acg ctg ccg gag aaa gca ctg gaa cgc 403
Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu Lys Ala Leu Glu Arg
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ctc gcc atc ggc tcg gca ctt ttc ggc gtc atc cac gcc acc gat ccg 451
Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile His Ala Thr Asp Pro
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atc ccg cat tac cgc ctg tcc ggc ggc aca aaa ctg ccc acc aaa agc 499
Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys Leu Pro Thr Lys Ser
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ggc gag ctg ccc acc atg aag gcg cgt tgg ggc aca agc atc agc gaa 547
Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly Thr Ser Ile Ser Glu
              135 140 145

gcg ctt atc gac gtc aac cag ctg gtg att gat ctt cgc agc ggg acc 595
Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp Leu Arg Ser Gly Thr
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tac caa cag ttg ggt cgc gta aaa gac gcc gtc acg gta cgc gtg gaa 643
Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val Thr Val Arg Val Glu
              170 175 180

tca gtc atg gag gat ggc tcc cgc aaa gta gtc agc cac ttt aac aaa 691
Ser Val Met Glu Asp Gly Ser Arg Lys Val Val Ser His Phe Asn Lys
              185 190 195

cac tac aaa ggt gaa ctc gcc cgc gtg ctc gcg ctc tct gaa aaa gaa 739
His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala Leu Ser Glu Lys Glu

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200	205	210	
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215	220	225	
gtg gtg gag gaa aac ccc aac cac aag gaa acc ctc act ctg gtt gtc			835
Val Val Glu Glu Asn Pro Asn His Lys Glu Thr Leu Thr Leu Val Val			
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 <213> Corynebacterium glutamicum

<400> 844
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 20 25 30
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 35 40 45
 Ala Leu Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu
 50 55 60
 Ser Asn Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg
 65 70 75 80
 Tyr Ser Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu
 85 90 95
 Lys Ala Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile
 100 105 110
 His Ala Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys
 115 120 125
 Leu Pro Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly
 130 135 140
 Thr Ser Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp
 145 150 155 160
 Leu Arg Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val
 165 170 175
 Thr Val Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val
 180 185 190
 Ser His Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala
 195 200 205
 Leu Ser Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala
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Gln Ala Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr
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Leu Thr Leu Val Val
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<222> (52)..(786)

<223> FRXA01847

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 Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser Gly Lys
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cct ctg gat ttt cac cat ttg agt ttc ccg tcg ctc acc aag gca cgc 153
 Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys Ala Arg
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caa aca ata ctc gct gac ctg caa gct ttg gag gta gat gag gcg ctg 201
 Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu Ala Leu
 35 40 45 50

aaa gtt ttg ggc att tct gaa aag ctc cgc cct gag gcc gaa tcc aat 249
 Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu Ser Asn
 55 60 65

cgc gcg ctg gag acc agc cct acg atg cct gcg att ttt cgg tat tcc 297
 Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg Tyr Ser
 70 75 80

gga gtg ctt tat gat gcg ctc gac gct gca acg ctg ccg gag aaa gca 345
 Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu Lys Ala
 85 90 95

ctg gaa cgc ctc gcc atc ggc tcg gca ctt ttc ggc gtc atc cac gcc 393
 Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile His Ala
 100 105 110

acc gat ccg atc ccg cat tac cgc ctg tcc ggc ggc aca aaa ctg ccc 441
 Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys Leu Pro
 115 120 125 130

acc aaa agc ggc gag ctg ccc acc atg aag gcg cgt tgg ggc aca agc 489
 Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly Thr Ser
 135 140 145

atc agc gaa gcg ctt atc gac gtc aac cag ctg gtg att gat ctt cgc 537
 Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp Leu Arg
 150 155 160

agc ggg acc tac caa cag ttg ggt cgc gta aaa gac gcc gtc acg gta 585
 Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val Thr Val
 165 170 175
 cgc gtg gaa tca gtc atg gag gat ggc tcc cgc aaa gta gtc agc cac 633
 Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val Ser His
 180 185 190
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 Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala Leu Ser
 195 200 205 210
 gaa aaa gaa gca cac acc gca gag gac gta atg agc att gcg cag gct 729
 Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala Gln Ala
 215 220 225
 gcg ggc ctt gtg gtg gag gaa aac ccc aac cac aag gaa acc ctc act 777
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 Leu Val Val
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<210> 846
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 <213> Corynebacterium glutamicum

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 35 40 45
 Ala Leu Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu
 50 55 60
 Ser Asn Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg
 65 70 75 80
 Tyr Ser Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu
 85 90 95
 Lys Ala Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile
 100 105 110
 His Ala Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys
 115 120 125
 Leu Pro Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly
 130 135 140
 Thr Ser Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp
 145 150 155 160

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<210> 848
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Ala Ala Leu Gly Ser Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr
 50 55 60
 Lys Ile Arg His Asn Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val
 65 70 75 80
 Ser Leu Pro Ile Ile Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val
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 Ala Ala Thr Gly Leu Ala Ala Tyr Val Ala Ala Trp Leu Leu Ala Met
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<210> 849
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(448)
 <223> FRXA01874

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 Val Ile Ala Tyr Val
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 gcc agc gcg tgc tgc ctg ccg ttt ggc gca ttt gcc gga gcg ttg ttg 163
 Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe Ala Gly Ala Leu Leu
 10 15 20
 tcc aag gag ctg tcg gga cat ctc cag gaa cga gtc ctt ctc acc cac 211
 Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg Val Leu Leu Thr His
 25 30 35

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Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe Ala Ala Leu Gly Ser
40 45 50

ctg tcg gtg ctg ttc gcc gcg att tgg cgc acc aaa att cgc cac aat 307
Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr Lys Ile Arg His Asn
55 60 65

ttc acc ccg tgg tct gtg ggg atc atg gcg gtg agc ctg ccg atc atc 355
Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val Ser Leu Pro Ile Ile
70 75 80 85

gtc acg ggc atc ctg ctc aac aac ggc tat gtc gcc gca cag gcc tgg 403
Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val Ala Ala Gln Ala Trp
90 95 100

ccg cgt acg tgg cag cat ggt tgc tgg cca tgg tgg ggt ggg gga 448
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105 110 115

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20 25 30

Val Leu Leu Thr His Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe
35 40 45

Ala Ala Leu Gly Ser Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr
50 55 60

Lys Ile Arg His Asn Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val
65 70 75 80

Ser Leu Pro Ile Ile Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val
85 90 95

Ala Ala Gln Ala Trp Pro Arg Thr Trp Gln His Gly Cys Trp Pro Trp
100 105 110

Trp Gly Gly Gly
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<210> 851
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 Met Arg Ile Ala Val
 1 5

act gga gca acg gga tct ttg ggt gga cat gtt gtg gat agt ctt cta 163
 Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val Val Asp Ser Leu Leu
 10 15 20

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa 211
 Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asp Glu
 25 30 35

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct 259
 Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
 40 45 50

act ttt gaa gac gaa gcg gca ctg act gca gct ctt gaa ggt gtg gat 307
 Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
 55 60 65

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg cag 355
 Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln
 70 75 80 85

cac acc aat gtc atc aat gcc gct aaa gca gct ggc gtg aca ttc att 403
 His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala Gly Val Thr Phe Ile
 90 95 100

gca tac acc agc ttg ctc aac ctt ggt acc tca aag ctt gca ctt gct 451
 Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser Lys Leu Ala Leu Ala
 105 110 115

cca gag cac att gca acg gaa aag ctc ctg gca gaa agc ggc att gac 499
 Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala Glu Ser Gly Ile Asp
 120 125 130

cac gcg ctg ctg cgc aat ggt tgg tac tgg gag aac tac gaa tct tca 547
 His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu Asn Tyr Glu Ser Ser
 135 140 145

att ggc gca gcg aag gcc acc ggg aag gta ttc ggc gca gct gaa ggc 595
 Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe Gly Ala Ala Glu Gly
 150 155 160 165

gca cgc gtt tcc gca gcc gca cgt aag gac tac gca gag gca gct gct 643
 Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr Ala Glu Ala Ala Ala
 170 175 180

gtt gtc atc acc agc gac aac cag gca ggc aag gtc tat gag ctc gca 691
 Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys Val Tyr Glu Leu Ala
 185 190 195

ggc gca cca gct ttg acc tac cca gag atc gca gct ggc att ggt gag 739
 Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala Ala Gly Ile Gly Glu
 200 205 210

gtc att ggt tct gag gca gaa tac gtc aac ctc tcc gtg gag gag tac 787

Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu Ser Val Glu Glu Tyr
 215 220 225
 caa aat gcg ctg gag cag gct ggc gtt cca gct gaa ttt gca gca ctt 835
 Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala Glu Phe Ala Ala Leu
 230 235 240 245
 ctc gca ggc atg gat ccc atc att gca gag ggc gcg ctg tac tcc gac 883
 Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly Ala Leu Tyr Ser Asp
 250 255 260
 agc acc gac cta cag gat ctc atc gga cgc ccg agc acc tca atc gtt 931
 Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro Ser Thr Ser Ile Val
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<210> 852
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 852
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 20 25 30
 Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
 35 40 45
 Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala
 50 55 60
 Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
 65 70 75 80
 Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala
 85 90 95
 Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser
 100 105 110
 Lys Leu Ala Leu Ala Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala
 115 120 125
 Glu Ser Gly Ile Asp His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu
 130 135 140
 Asn Tyr Glu Ser Ser Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe
 145 150 155 160
 Gly Ala Ala Glu Gly Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr
 165 170 175
 Ala Glu Ala Ala Ala Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys
 180 185 190

Val Tyr Glu Leu Ala Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala
 195 200 205

Ala Gly Ile Gly Glu Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu
 210 215 220

Ser Val Glu Glu Tyr Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala
 225 230 235 240

Glu Phe Ala Ala Leu Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly
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 Val Asp Ser Leu Leu
 1 5

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa 163
 Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
 10 15 20

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct 211
 Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
 25 30 35

act ttt gaa gac gaa gcg gca ctg act gca gct ctt gaa ggt gtg gat 259
 Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
 40 45 50

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg cag 307
 Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln
 55 60 65

cac acc aat gtc atc aat gcc gct aaa gca gct ggc gtg aca ttc att 355
 His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala Gly Val Thr Phe Ile
 70 75 80 85

gca tac acc agc ttg ctc aac ctt ggt acc tca aag ctt gca ctt gct 403
 Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser Lys Leu Ala Leu Ala
 90 95 100

cca gag cac att gca acg gaa aag ctc ctg gca gaa agc ggc att gac 451
 Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala Glu Ser Gly Ile Asp
 105 110 115

cac gcg ctg ctg cgc aat ggt tgg tac tgg gag aac tac gaa tct tca 499
 His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu Asn Tyr Glu Ser Ser
 120 125 130

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 Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe Gly Ala Ala Glu Gly
 135 140 145

gca cgc gtt tcc gca gcc gca cgt aag gac tac gca gag gca gct gct 595
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 150 155 160 165

gtt gtc atc acc agc gac aac cag gca ggc aag gtc tat gag ctc gca 643
 Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys Val Tyr Glu Leu Ala
 170 175 180

ggc gca cca gct ttg acc tac cca gag atc gca gct ggc att ggt gag 691
 Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala Ala Gly Ile Gly Glu
 185 190 195

gtc att ggt tct gag gca gaa tac gtc aac ctc tcc gtg gag gag tac 739
 Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu Ser Val Glu Glu Tyr
 200 205 210

caa aat gcg ctg gag cag gct ggc gtt cca gct gaa ttt gca gca ctt 787
 Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala Glu Phe Ala Ala Leu
 215 220 225

ctc gca ggc atg gat ccc atc att gca gag ggc gcg ctg tac tcc gac 835
 Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly Ala Leu Tyr Ser Asp
 230 235 240 245

agc acc gac cta cag gat ctc atc gga cgc ccg agc acc tca atc gtt 883
 Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro Ser Thr Ser Ile Val
 250 255 260

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 Glu Ala Leu Ser Ser
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<210> 854

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 854

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Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
 20 25 30

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala
 35 40 45

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly

	10	15	20	
aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa				211
Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu				
	25	30	35	
gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct				259
Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala				
	40	45	50	
act ttt gaa gac gaa acg gca ctg act gca gct ctt gaa ggt gtg gat				307
Thr Phe Glu Asp Glu Thr Ala Leu Thr Ala Ala Leu Glu Gly Val Asp				
	55	60	65	
cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg caa				355
Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln				
	70	75	80	85
cac acc aat gtc atc aat gcc gct aaa gca act ggc gtg aca ttc att				403
His Thr Asn Val Ile Asn Ala Ala Lys Ala Thr Gly Val Thr Phe Ile				
	90	95	100	
gca tac acc agc ttg ctc aac ctt ggt cct caa agc ttg cac ttg ctc				451
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Pro Gln Ser Leu His Leu Leu				
	105	110	115	
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Gln Ser Thr Leu Gln Pro Glu Lys Leu Leu Ala				
	120	125		

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<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 856

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Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile				
35	40	45		
Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Thr Ala Leu Thr Ala Ala				
50	55	60		
Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly				
65	70	75	80	
Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Thr				
85	90	95		
Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Pro Gln				
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Ser Leu His Leu Leu Gln Ser Thr Leu Gln Pro Glu Lys Leu Leu Ala				
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<223> RXN01877
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Val Pro Leu Arg Leu															1
gct acc ggt ggc gtg ctc gcc acc ttg ctt atc ggc gga gtc acc gct															163
Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly Val Thr Ala															10 15 20
gca gct acc aaa aag gac atc att gtt gat gtc aac ggc gag cag atg															211
Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly Glu Gln Met															25 30 35
tcc cta gtg act atg tcc ggc act gtt gaa ggt gtg ctg gcg caa gct															259
Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly Val Leu Ala Gln Ala															40 45 50
ggg gtg gaa ctt ggt gac cag gac att gtt tcc cct tca ctg gat tca															307
Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser Leu Asp Ser															55 60 65
tcc atc agt gat gaa gac act gtg act gtt cgt act gcc aag cag gtg															355
Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala Lys Gln Val															70 75 80 85
gcg ctc gtg gtg gaa ggt caa atc caa aac gtg acc acc act gcg gtt															403
Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr Thr Ala Val															90 95 100
tcc gtg gag gac ctc ctg cag gaa gtc ggt ggc att acc ggt gct gat															451
Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr Gly Ala Asp															105 110 115
gcg gtg gac gct gat ctt tca gag acc atc cca gaa tct ggt ttg aag															499
Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser Gly Leu Lys															120 125 130
gtg agt gtt acc aag ccg aag att att tcc atc aat gat ggt ggc aag															547
Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp Gly Gly Lys															135 140 145
gtc act tac gtt tct ttg gca gct cag aac gta cag gaa gcc cta gag															595
Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu Ala Leu Glu															150 155 160 165
ctg cgg gat att gag ctg ggt gct cag gac cgc att aat gtg cct ctg															643
Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg Ile Asn Val Pro Leu															170 175 180

gat cag cag ctg aag aac aac gct gcg atc cag atc gac cgc gtt gac 691
Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln Ile Asp Arg Val Asp
185 190 195

aac acc gaa atc act gaa act gtg tct ttc gat gct gag cca acc tac 739
Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu Pro Thr Tyr
200 205 210

gtg gat gat cca gaa gct cca gct ggc gat gaa act gtg gtc gaa gaa 787
Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val Val Glu Glu
215 220 225

ggc gct cct gga acc aag gaa gtt act cgc acc gta aca acc gtt aat 835
Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr Thr Val Asn
230 235 240 245

ggc cag gaa gaa tct tcc acg gtg atc aat gaa gtt gaa atc acc gca 883
Gly Gln Glu Glu Ser Thr Thr Val Ile Asn Glu Val Glu Ile Thr Ala
250 255 260

gca aag cca gca acc att agc cgt ggc acc aaa act gtc gct gca aac 931
Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val Ala Ala Asn
265 270 275

tcc gtg tgg gat cag ctg gca cag tgt gaa tcc ggc gga aac tgg gca 979
Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp Ala
280 285 290

atc aac aca ggt aat ggc ttc tcc ggc ggc cta cag ttc cac cca cag 1027
Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu Gln Phe His Pro Gln
295 300 305

acc tgg ctc gca tac ggt ggt gga gct ttc tcc ggt gac gct tcc ggt 1075
Thr Trp Leu Ala Tyr Gly Gly Gly Ala Phe Ser Gly Asp Ala Ser Gly
310 315 320 325

gca agc cgt gaa cag caa atc tcc atc gca gaa aag gtt cag gct gca 1123
Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val Gln Ala Ala
330 335 340

caa ggt tgg gga gca tgg cct gct tgc acc gca agc ttg ggc atc cga 1171
Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu Gly Ile Arg
345 350 355

tagtagaaat ctggcatcca ata 1194

<210> 858

<211> 357

<212> PRT

<213> Corynebacterium glutamicum

<400> 858

Val Pro Leu Arg Leu Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile
1 5 10 15

Gly Gly Val Thr Ala Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val
20 25 30

Asn Gly Glu Gln Met Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly

35	40	45
Val Leu Ala Gln Ala Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser 50 55 60		
Pro Ser Leu Asp Ser Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg 65 70 75 80		
Thr Ala Lys Gln Val Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val 85 90 95		
Thr Thr Thr Ala Val Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly 100 105 110		
Ile Thr Gly Ala Asp Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro 115 120 125		
Glu Ser Gly Leu Lys Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile 130 135 140		
Asn Asp Gly Gly Lys Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val 145 150 155 160		
Gln Glu Ala Leu Glu Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg 165 170 175		
Ile Asn Val Pro Leu Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln 180 185 190		
Ile Asp Arg Val Asp Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp 195 200 205		
Ala Glu Pro Thr Tyr Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu 210 215 220		
Thr Val Val Glu Glu Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr 225 230 235 240		
Val Thr Thr Val Asn Gly Gln Glu Glu Ser Ser Thr Val Ile Asn Glu 245 250 255		
Val Glu Ile Thr Ala Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys 260 265 270		
Thr Val Ala Ala Asn Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser 275 280 285		
Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu 290 295 300		
Gln Phe His Pro Gln Thr Trp Leu Ala Tyr Gly Gly Gly Ala Phe Ser 305 310 315 320		
Gly Asp Ala Ser Gly Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu 325 330 335		
Lys Val Gln Ala Ala Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala 340 345 350		
Ser Leu Gly Ile Arg 355		

170	175	180	
cag ctg aag aac aac gct gcg atc	cag atc gac cgc gtt gac aac acc		691
Gln Leu Lys Asn Asn Ala Ala Ile	Gln Ile Asp Arg Val Asp Asn Thr		
185	190	195	
gaa atc act gaa act gtg tct ttc gat gct gag cca acc tac gtg gat			739
Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu Pro Thr Tyr Val Asp			
200	205	210	
gat cca gaa gct cca gct ggc gat gaa act gtg gtc gaa gaa ggc gct			787
Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val Val Glu Glu Gly Ala			
215	220	225	
cct gga acc aag gaa gtt act cgc acc gta aca acc gtt aat ggt cag			835
Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr Thr Val Asn Gly Gln			
230	235	240	245
gaa gaa tct tcc acg gtg atc aat gaa gtt gaa atc acc gca gca aag			883
Glu Glu Ser Ser Thr Val Ile Asn Glu Val Glu Ile Thr Ala Ala Lys			
250	255	260	
cca gca acc att agc cgt ggc acc aaa act gtc gct gca aac tcc gtg			931
Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val Ala Ala Asn Ser Val			
265	270	275	
tgg gat cag ctg gca cag tgt gaa tcc ggc gga aac tgg gca atc aac			979
Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp Ala Ile Asn			
280	285	290	
aca ggt aat ggc ttc tcc ggc ggc cta cag ttc cac cca cag acc tgg			1027
Thr Gly Asn Gly Phe Ser Gly Gly Leu Gln Phe His Pro Gln Thr Trp			
295	300	305	
ctc gca tac ggt ggt gga gct ttc tcc ggt gac gct tcc ggt gca agc			1075
Leu Ala Tyr Gly Gly Gly Ala Phe Ser Gly Asp Ala Ser Gly Ala Ser			
310	315	320	325
cgt gaa cag caa atc tcc atc gca gaa aag gtt cag gct gca caa ggt			1123
Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val Gln Ala Ala Gln Gly			
330	335	340	
tgg gga gca tgg cct gct tgc acc gca agc ttg ggc atc cga			1165
Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu Gly Ile Arg			
345	350	355	
tagtagaaat ctggcatcca ata			1188

<210> 860

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 860

Leu Arg Leu Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly
1 5 10 15

Val Thr Ala Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly
20 25 30

Gly Ile Arg

<210> 861
<211> 1056
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>  
<221> CDS  
<222> (101)..(1033)  
<223> RXN01879
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Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met
 170 175 180

gcg cat ggc ctg tcc acg cct gag gta ttc aaa aag cat gat gag ctg 691
 Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys Lys His Asp Glu Leu
 185 190 195

aat ccg gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt ctc 739
 Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu Leu
 200 205 210

acc ggc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg acc 787
 Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu Thr
 215 220 225

agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa gaa 835
 Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln Glu
 230 235 240 245

ggc atc cgc tcc ggc gcg cat gca gga att gtc tcc ggc tcc ggc ccg 883
 Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly Pro
 250 255 260

acc acg gta ttc ttg tgc gaa tcg gag cac aaa gcg caa gac gtt aaa 931
 Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val Lys
 265 270 275

gag gcg cta atc gac gcc ggc cag gtg tac gct gct tac acc gcc acc 979
 Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala Thr
 280 285 290

ggc cct gcg gcc tca acc gcc gac cag cgc ggc gca cac att ttg act 1027
 Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu Thr
 295 300 305

gtt tca taataaagac aaacttaagt atc 1056
 Val Ser
 310

<210> 862

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 862

Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
 1 5 10 15

Val Gly Pro Ala His Asp Asp Gly Phe His Glu Leu Met Thr Val Phe
 20 25 30

Gln Thr Ile Asp Leu Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu
 35 40 45

Glu Leu Val Glu Glu Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly
 50 55 60

Ala Arg Gly Val Pro Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val
 65 70 75 80

Asp Ala Leu Val Lys Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val
85 90 95

Ser Leu His Ile Ser Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly
100 105 110

Gly Ser Ala Asp Ala Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile
115 120 125

Gly Pro Phe Gly Glu Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly
130 135 140

Ser Asp Val Pro Phe Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly
145 150 155 160

Arg Gly Glu Gln Leu Val Asp Met Leu Thr Arg Gly Lys Leu His Trp
165 170 175

Val Val Ala Ala Met Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys
180 185 190

Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu
195 200 205

Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu
210 215 220

His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg
225 230 235 240

Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val
245 250 255

Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys
260 265 270

Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala
275 280 285

Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly
290 295 300

Ala His Ile Leu Thr Val Ser
305 310

<210> 863

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(688)

<223> FRXA01879

<400> 863

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atgtgcgcct agctgggggtg ttgcagcaaa aggatgagaa gtg aaa att acc gct 115
Val Lys Ile Thr Ala

1 5
 aag gcg tgg gcg aaa acc aac ctg cat tta ggt gtg gga ccg gct cac 163
 Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly Val Gly Pro Ala His
 10 15 20
 gac gat gga ttt cac gag ctg atg acg gtg ttt caa acc att gat ctg 211
 Asp Asp Gly Phe His Glu Leu Met Thr Val Phe Gln Thr Ile Asp Leu
 25 30 35
 ttt gac acc gtc acc tta acc acc ctg gat gag gag ttg gtg gag gag 259
 Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu Glu Leu Val Glu Glu
 40 45 50
 ggg agc gtc gtc aag caa tta tct gtg acc ggt gcc cgt ggc gtg cct 307
 Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly Ala Arg Gly Val Pro
 55 60 65
 gag gac gcc agc aat ctt gcg tgg cgc gct gtg gat gcg ttg gtt aag 355
 Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val Asp Ala Leu Val Lys
 70 75 80 85
 cgg cgc gcg gaa aag acg ccg ctg tct gca gtt tcg ctg cat att tcc 403
 Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val Ser Leu His Ile Ser
 90 95 100
 aag ggg att ccg gtg gct ggc ggc atg gct ggc ggc tct gcg gat gcg 451
 Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly Gly Ser Ala Asp Ala
 105 110 115
 gct gcg aca ctg cgc gca gtg gat gcc tgg att ggg cct ttc ggc gag 499
 Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile Gly Pro Phe Gly Glu
 120 125 130
 gac aca ttg ctg gag gtt gcc gcg gag ctg ggc tca gat gtg ccg ttt 547
 Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly Ser Asp Val Pro Phe
 135 140 145
 tgc ctg ctt ggt ggc acc atg cgc ggt acc ggt cgc ggc gag cag ctg 595
 Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly Arg Gly Glu Gln Leu
 150 155 160 165
 gta gat atg ttg acg cgc ggc aag cta cat tgg gtg gtg gcc gcg atg 643
 Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met
 170 175 180
 gcg cat ggc ctg tcc acc ctg agg tat tca aaa agc atg atg agc 688
 Ala His Gly Leu Ser Thr Leu Arg Tyr Ser Lys Ser Met Met Ser
 185 190 195
 tgaatccgga atcgcatatg gat 711

<210> 864

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 864

Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
 1 5 10 15

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<400> 865
agctcggctc agatgtgccg ttttgacctg ttgggtggcac catgcgcggt accggtcgcg 60
gcgagcagct ggtagatatg ttgacgcgcg gcaagctaca ttg ggt ggt ggc cgc 115
                                         Leu Gly Gly Gly Arg
                                         1                               5
gat ggc gca tgg cct gtc cac cct gag gta ttc aaa aag cat gat gag 163
Asp Gly Ala Trp Pro Val His Pro Glu Val Phe Lys Lys His Asp Glu
                        10                               15                               20
ctg aat ccg gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt 211
Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu

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25	30	35	
ctc acc ggc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg			259
Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu			
40	45	50	
acc agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa			307
Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln			
55	60	65	
gaa ggc atc cgc tcc ggc gcg cat gca gga att gtc tcc ggc tcc ggc			355
Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly			
70	75	80	85
ccg acc acg gta ttc ttg tgc gaa tcg gag cac aaa gcg caa gac gtt			403
Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val			
90	95	100	
aaa gag gcg cta atc gac gcc ggc cag gtg tac gct gct tac acc gcc			451
Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala			
105	110	115	
acc ggc cct gcg gcc tca acc gcc gac cag cgc ggc gca cac att ttg			499
Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu			
120	125	130	
act gtt tca taataaagac aaacttaagt atc			531
Thr Val Ser			
135			

<210> 866

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 866

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1	5	10	15
Lys Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp			
20	25	30	
Leu Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp			
35	40	45	
Leu His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu			
50	55	60	
Arg Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile			
65	70	75	80
Val Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His			
85	90	95	
Lys Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr			
100	105	110	
Ala Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg			
115	120	125	

Gly Ala His Ile Leu Thr Val Ser
130 135

<210> 867
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXN01896

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ttggatccgc gcgaaccaca tcaaacgcta gagtgattcc atg acg cat gcg atc 115
Met Thr His Ala Ile
1 5
ctc ttt gac ctc gac ggc acc ctc gtt gat cac gct tcc gcc gcc cgc 163
Leu Phe Asp Leu Asp Gly Thr Leu Val Asp His Ala Ser Ala Ala Arg
10 15 20
gcc gcc ctg cac gcc tgg tcg ccg acc gtg ggc gtc gac acg gat gtt 211
Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr Asp Val
25 30 35
gag cgc tgg att gag ctg gat aag tgg ggt ttt gcc cgt ttt gag cgc 259
Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe Glu Arg
40 45 50
ggc gaa acc acg cat tta ggt cag cgg cgc gac cgc atc agg gcg tac 307
Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg Ala Tyr
55 60 65
ctc aac aga gag ctt gac gac gcc acc tgc gat gat att tac tcc gcc 355
Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr Ser Gly
70 75 80 85
tac ctt aaa gca tat gag caa aac tgg act gcc tac ccc gat gcc aag 403
Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp Ala Lys
90 95 100
ggc gtt ctc gat cgc gcg gta gcc acc ggt gcc cct gtg gga atc ctg 451
Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly Ile Leu
105 110 115
acc aat ggc gca gcc ccc atg cag caa gac aag ctt gat cgc acc gcc 499
Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg Thr Gly
120 125 130
ctt ggc ctg cca gaa ctc gtc atg ttg gcg gcg tcc act ctg gat tct 547
Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu Asp Ser
135 140 145
gcg aag cct cgc ccc gaa atg tat gcc cga gcg ctc acc cat ttg ggt 595
Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His Leu Gly
150 155 160 165

gcc cga acc gca aca att atc ggc gat gat tgg acc aac gat gtc gca 643
 Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp Val Ala
 170 175 180

gct ccc cgc gaa ctt ggc tgg aat gct ctc tat tta gat cgt tcc gga 691
 Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg Ser Gly
 185 190 195

acc gat cca cgc gcc gat atc cac tcc ctg gat gaa ctc ttt cac 736
 Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe His
 200 205 210

taggctggcc tttattgttt ccg 759

<210> 868
 <211> 212
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 868
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 1 5 10 15

Ala Ser Ala Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly
 20 25 30

Val Asp Thr Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe
 35 40 45

Ala Arg Phe Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp
 50 55 60

Arg Ile Arg Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp
 65 70 75 80

Asp Ile Tyr Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala
 85 90 95

Tyr Pro Asp Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala
 100 105 110

Pro Val Gly Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys
 115 120 125

Leu Asp Arg Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala
 130 135 140

Ser Thr Leu Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala
 145 150 155 160

Leu Thr His Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp
 165 170 175

Thr Asn Asp Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr
 180 185 190

Leu Asp Arg Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp
 195 200 205

Glu Leu Phe His

210

<210> 869
 <211> 602
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(579)
 <223> FRXA01896

<400> 869
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 Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe
 20 25 30
 gag cgc ggc gaa acc acg cat tta ggt cag cgg cgc gac cgc atc agg 144
 Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg
 35 40 45
 gcg tac ctc aac aga gag ctt gac gac gcc acc tgc gat gat att tac 192
 Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr
 50 55 60
 tcc ggc tac ctt aaa gca tat gag caa aac tgg act gcc tac ccc gat 240
 Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp
 65 70 75 80
 gcc aag ggc gtt ctc gat cgc gcg gta gcc acc ggt gcc cct gtg gga 288
 Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly
 85 90 95
 atc ctg acc aat ggc gca gcc ccc atg cag caa gac aag ctt gat cgc 336
 Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg
 100 105 110
 acc ggc ctt ggc ctg cca gaa ctc gtc atg ttg gcg gcg tcc act ctg 384
 Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu
 115 120 125
 gat tct gcg aag cct cgc ccc gaa atg tat gcc cga gcg ctc acc cat 432
 Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His
 130 135 140
 ttg ggt gcc cga acc gca aca att atc ggc gat gat tgg acc aac gat 480
 Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp
 145 150 155 160
 gtc gca gct ccc cgc gaa ctt ggc tgg aat gct ctc tat tta gat cgt 528
 Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg
 165 170 175
 tcc gga acc gat cca cgc gcc gat atc cac tcc ctg gat gaa ctc ttt 576
 Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe
 180 185 190

cac taggctggcc tttattgttt ccg
His

602

<210> 870
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 870
Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr
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Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe
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Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg
35 40 45
Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr
50 55 60
Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp
65 70 75 80
Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly
85 90 95
Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg
100 105 110
Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu
115 120 125
Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His
130 135 140
Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp
145 150 155 160
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Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe
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<222> (101)..(886)
<223> RXN01899

<400> 871

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Trp Ala Val Ser Asp Leu His Val Thr Phe Ala Gln Asn Gln Asn Thr
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Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val Arg Thr Leu Ser Ala
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Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys Pro Leu Phe Thr Leu
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Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr Ala Lys Gln Ala Leu
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gta gac atc ccc gcc tgg tgc gcc gaa cga gtc acc tac aca gaa gac 595
Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val Thr Tyr Thr Glu Asp
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Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu Val Asn His Trp Pro
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ctc atg gcc att cac ggt cac cta cat att cct gcc gaa acc cgc gtt 787

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Leu Met Ala Ile His Gly His Leu His Ile Pro Ala Glu Thr Arg Val
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 Asp Gly Val Ser His Val Glu Val Ser Leu Gly Tyr Pro Phe Glu Lys
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cac cca cct cac atg aag cgt ccg tgg ccg ttt ccg gtc atg cag att 883
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<400> 872

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Arg Thr Leu Ser Ala Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val
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Pro Gly Asn His Glu Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly
 65 70 75 80

Lys Ala Arg Tyr Arg Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val
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Ile Thr Pro Glu Asp Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys
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Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr
 115 120 125

Ala Lys Gln Ala Leu Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu
 130 135 140

Ala Ile Ala Pro Tyr Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val
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Thr Tyr Thr Glu Asp Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu
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Val Asn His Trp Pro Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln
 180 185 190

Lys Asp Ile Ala Leu Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala
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Val Arg Phe Asn Ala Leu Met Ala Ile His Gly His Leu His Ile Pro
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Ala Glu Thr Arg Val Asp Gly Val Ser His Val Glu Val Ser Leu Gly
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 Met Ser Arg Thr Leu
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 Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val Arg Thr Leu Ser Ala
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 Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val Pro Gly Asn His Glu
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 Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly Lys Ala Arg Tyr Arg
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gca tta gtc gga caa ctc cga gcc atc ggc gtg atc acc ccc gaa gat 403
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 Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys Pro Leu Phe Thr Leu
 105 110 115

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 Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr Ala Lys Gln Ala Leu
 120 125 130

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 Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu Ala Ile Ala Pro Tyr
 135 140 145
 gta gac atc ccc gcc tgg tgc gcc gaa cga gtc acc tac aca gaa gac 595
 Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val Thr Tyr Thr Glu Asp
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 Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu Val Asn His Trp Pro
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 ctg gtc att gag ccc acc cac cgg ctc ttc caa aaa gac atc gcg ctg 691
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 tgg tgt gga acc acc gcc acc agg gat tgg gcc gta cga ttc aac gct 739
 Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala Val Arg Phe Asn Ala
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 Leu Met Ala Ile His Gly His Leu His Ile Pro Ala Glu Thr Arg Val
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 Asp Gly Val Ser His Val Glu Val Ser Leu Gly Tyr Pro Phe Glu Lys
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 Arg Thr Leu Ser Ala Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val
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 Lys Ala Arg Tyr Arg Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val
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 Val Asn His Trp Pro Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln
 180 185 190
 Lys Asp Ile Ala Leu Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala
 195 200 205
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 Ala Glu Thr Arg Val Asp Gly Val Ser His Val Glu Val Ser Leu Gly
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 Pro Val Met Gln Ile Asn
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 Val Gln Lys Lys Ser
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 Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro Pro Ile Glu Asn Pro
 10 15 20
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 Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln Ala Asn His Ser Ser
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Arg	Leu	Ala	Val	Asn	Asn	Gly	Asn	His	Asp	Gln	Tyr	Asn	Tyr	Asp	Ala		
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Tyr	Asn	Ala	Met	Tyr	Pro	Arg	Pro	Asn	Gln	Val	Asp	Glu	Asn	Tyr	Phe		
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Phe	Glu	Tyr	Asn	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Asp	Ser	Asn	Asp	Tyr		
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Leu	Asp	Ile	Asp	Asp	Asp	Ile	Ala	Phe	Leu	Arg	Asp	Thr	Val	Ala	Ala		
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ttc	tcc	cag	gcc	tac	cac	atg	gat	gac	gct	cgc	att	aag	tac	cag	cgc	547	
Phe	Ser	Gln	Ala	Tyr	His	Met	Asp	Asp	Ala	Arg	Ile	Lys	Tyr	Gln	Arg		
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gaa	cgc	ctc	acc	cca	gtg	atc	tct	gaa	ctg	aac	gtt	gac	ttg	gtt	ctc	595	
Glu	Arg	Leu	Thr	Pro	Val	Ile	Ser	Glu	Leu	Asn	Val	Asp	Leu	Val	Leu		
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ggt	gga	cac	gac	cac	atc	tac	acc	cgc	tcc	cac	ctg	atg	aac	ggc	ttc	643	
Gly	Gly	His	Asp	His	Ile	Tyr	Thr	Arg	Ser	His	Leu	Met	Asn	Gly	Phe		
				170					175					180			
acc	cca	gtc	gat	gca	ggc	cgc	gaa	gca	gtt	gtc	ggt	gaa	act	ctg	aac	691	
Thr	Pro	Val	Asp	Ala	Gly	Arg	Glu	Ala	Val	Val	Gly	Glu	Thr	Leu	Asn		
			185					190					195				
cct	aag	gcc	ggc	gaa	gtt	gtt	tac	ctt	gca	acc	aac	tct	tcc	tca	ggc	739	
Pro	Lys	Ala	Gly	Glu	Val	Val	Tyr	Leu	Ala	Thr	Asn	Ser	Ser	Ser	Gly		
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tcc	aag	ttc	tac	gac	ttc	tac	gac	ttc	cag	ctc	ggc	cag	cgt	tac	gac	787	
Ser	Lys	Phe	Tyr	Asp	Phe	Tyr	Asp	Phe	Gln	Leu	Gly	Gln	Arg	Tyr	Asp		
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acc	gga	ctg	gat	ttc	cag	gaa	acc	gtc	gat	cag	aag	aag	atc	cgc	acc	835	
Thr	Gly	Leu	Asp	Phe	Gln	Glu	Thr	Val	Asp	Gln	Lys	Lys	Ile	Arg	Thr		
230					235					240					245		
tac	acc	gca	gtc	tgg	aac	cag	gac	cag	gtt	cag	gac	tac	acc	aac	gtt	883	
Tyr	Thr	Ala	Val	Trp	Asn	Gln	Asp	Gln	Val	Gln	Asp	Tyr	Thr	Asn	Val		
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gaa	ctg	acc	cca	gaa	ggc	ctg	act	gtg	acc	act	aag	gac	gca	gtc	tcc	931	
Glu	Leu	Thr	Pro	Glu	Gly	Leu	Thr	Val	Thr	Thr	Lys	Asp	Ala	Val	Ser		
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ggc	gag	ctg	gtt	gac	cag	ttc	acc	ctg	agc	aag	cag	gac	cgc	gac	gaa	979	
Gly	Glu	Leu	Val	Asp	Gln	Phe	Thr	Leu	Ser	Lys	Gln	Asp	Arg	Asp	Glu		

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Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly Asp Asn Ala Thr			
295	300	305	
ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct cca gtt ctg gcc			1075
Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala Pro Val Leu Ala			
310	315	320	325
atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc ggc tcc ctc gct			1123
Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly Gly Ser Leu Ala			
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gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc taatactgtc			1169
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 Thr Leu Arg Asn Tyr Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln
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 Tyr Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val
 65 70 75 80
 Asp Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu
 85 90 95
 Asp Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg
 100 105 110
 Asp Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr
 115 120 125
 Tyr His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg
 130 135 140
 Ile Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn
 145 150 155 160
 Val Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His
 165 170 175
 Leu Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val

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225					230					235					240															
Lys	Lys	Ile	Arg	Thr	Tyr	Thr	Ala	Val	Trp	Asn	Gln	Asp	Gln	Val	Gln															
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Asp	Tyr	Thr	Asn	Val	Glu	Leu	Thr	Pro	Glu	Gly	Leu	Thr	Val	Thr	Thr															
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gag	aac	tac	ttc	ttc	gag	tac	aac	aat	gca	ctc	ttc	ctg	tcc	ctg	gac	96
Glu	Asn	Tyr	Phe	Phe	Glu	Tyr	Asn	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Asp	
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tcc	aac	gac	tac	ttg	gac	atc	gac	gac	gac	atc	gca	ttc	ctt	cgc	gac	144
Ser	Asn	Asp	Tyr	Leu	Asp	Ile	Asp	Asp	Asp	Ile	Ala	Phe	Leu	Arg	Asp	
			35				40					45				
acc	gtc	gca	gca	cac	ggt	gac	gac	aag	gac	tgg	atc	gtc	ctg	acc	tac	192
Thr	Val	Ala	Ala	His	Gly	Asp	Asp	Lys	Asp	Trp	Ile	Val	Leu	Thr	Tyr	

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cac cat tcc act ttc tcc cag gcc tac cac atg gat gac gct cgc att			240
His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile			
65	70	75	80
aag tac cag cgc gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt			288
Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val			
	85	90	95
gac ttg gtt ctc ggt gga cac gac cac atc tac acc cgc tcc cac ctg			336
Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu			
	100	105	110
atg aac ggc ttc acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt			384
Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly			
	115	120	125
gaa act ctg aac cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac			432
Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn			
	130	135	140
tct tcc tca ggc tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc			480
Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly			
	145	150	155
cag cgt tac gac acc gga ctg gat ttc cag gaa acc gtc gat cag aag			528
Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys			
	165	170	175
aag atc cgc acc tac acc gca gtc tgg aac cag gac cag gtt cag gac			576
Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp			
	180	185	190
tac acc aac gtt gaa ctg acc cca gaa ggc ctg act gtg acc act aag			624
Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys			
	195	200	205
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Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln			
	210	215	220
gac cgc gac gaa gaa tct gaa gtc cca gtt gaa gat gac aag gac gga			720
Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly			
	225	230	235
gac aac gcg acc ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct			768
Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala			
	245	250	255
cca gtt ctg gcc atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc			816
Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly			
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ggc tcc ctc gct gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc			864
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<213> Corynebacterium glutamicum

<400> 878
Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp
1 5 10 15
Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp
20 25 30
Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp
35 40 45
Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr
50 55 60
His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile
65 70 75 80
Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val
85 90 95
Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu
100 105 110
Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly
115 120 125
Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn
130 135 140
Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly
145 150 155 160
Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys
165 170 175
Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp
180 185 190
Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys
195 200 205
Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln
210 215 220
Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly
225 230 235 240
Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala
245 250 255
Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly
260 265 270
Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
275 280 285

<400> 879															60	
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cagtctgtct tccatatttc atatcccagc acataccact											atg	cac	tct	gac	cgc	115
											Met	His	Ser	Asp	Arg	
											1				5	
ttt	gag	cac	cca	gac	aac	ggc	tat	ggc	tac	acc	att	cgt	cag	gac	act	163
Phe	Glu	His	Pro	Asp	Asn	Gly	Tyr	Gly	Tyr	Thr	Ile	Arg	Gln	Asp	Thr	
				10					15					20		
gat	gca	gag	aac	cgc	atg	acc	cat	cac	gat	acg	aaa	gat	gca	gct	ctc	211
Asp	Ala	Glu	Asn	Pro	Met	Thr	His	His	Asp	Thr	Lys	Asp	Ala	Ala	Leu	
				25					30					35		
tgg	ggt	cac	aac	cga	cca	cga	cgc	gga	gat	acc	gtc	gcc	gat	aag	cca	259
Trp	Val	His	Asn	Arg	Pro	Arg	Arg	Gly	Asp	Thr	Val	Ala	Asp	Lys	Pro	
				40					45					50		
gaa	ggc	aat	gag	att	ctc	gac	atc	ttt	gcc	aag	ttc	atc	tgc	ggc	cag	307
Glu	Gly	Asn	Glu	Ile	Leu	Asp	Ile	Phe	Ala	Lys	Phe	Ile	Cys	Gly	Gln	
				55					60					65		
cac	gat	aat	gat	gac	aac	cgc	ttc	gaa	gtc	tgg	tcc	gac	ggg	gac	tcg	355
His	Asp	Asn	Asp	Asp	Asn	Pro	Phe	Glu	Val	Trp	Ser	Asp	Gly	Asp	Ser	
70					75					80					85	
gat	gca	tca	ctc	atc	cgc	acc	aag	gcg	tat	ggt	gcc	gag	cac	cac	ccc	403
Asp	Ala	Ser	Leu	Ile	Arg	Thr	Lys	Ala	Tyr	Val	Ala	Glu	His	His	Pro	
				90					95					100		
gaa	ctt	ata	ttc	gac	atc	tct	gcg	aaa	acc	atc	acg	ggg	tat	tcg	caa	451
Glu	Leu	Ile	Phe	Asp	Ile	Ser	Ala	Lys	Thr	Ile	Thr	Gly	Tyr	Ser	Gln	
				105					110					115		
ggc	gat	tgg	ctc	gat	gtg	gtc	tgt	ggt	act	act	gcc	gcc	act	tgc	gac	499
Gly	Asp	Trp	Leu	Asp	Val	Val	Cys	Val	Thr	Thr	Ala	Ala	Thr	Cys	Asp	
				120					125					130		
gaa	ctt	atc	cct	gct	gac	agt	ctt	att	gac	atc	tac	cgc	cag	tgg	gct	547
Glu	Leu	Ile	Pro	Ala	Asp	Ser	Leu	Ile	Asp	Ile	Tyr	Arg	Gln	Trp	Ala	
				135					140					145		
ttt	ggg	gat	gtg	tgg	aca	gtg	att	cct	gat	tct	cag	cca	ggg	ctc	gca	595
Phe	Gly	Asp	Val	Trp	Thr	Val	Ile	Pro	Asp	Ser	Gln	Pro	Gly	Leu	Ala	
150					155					160					165	
ggg	att	tat	gct	gac	gat	cca	gct	gac	gcc	ctt	gcg	tac	tat	caa	gag	643
Gly	Ile	Tyr	Ala	Asp	Asp	Pro	Ala	Asp	Ala	Leu	Ala	Tyr	Tyr	Gln	Glu	
				170					175					180		

aat ttc gaa gat gaa ccc atc tgg gat ctc tta agc cgc cac gac gct 691
 Asn Phe Glu Asp Glu Pro Ile Trp Asp Leu Leu Ser Arg His Asp Ala
 185 190 195
 gac aaa gac gcc gca gca ctg gca gct gcc tct gct gca gaa aac cac 739
 Asp Lys Asp Ala Ala Ala Leu Ala Ala Ser Ala Ala Glu Asn His
 200 205 210
 gca cta gcg cga ggt act acc cca gtc gtt atc cgt acc caa gac atc 787
 Ala Leu Ala Arg Gly Thr Thr Pro Val Val Ile Arg Thr Gln Asp Ile
 215 220 225
 atc act aac gcg cga tac ctc atg tct gat agt gct gat gac aat cca 835
 Ile Thr Asn Ala Arg Tyr Leu Met Ser Asp Ser Ala Asp Asp Asn Pro
 230 235 240 245
 gaa tac gat cgc gcc ttg gtc gaa ctt agt gct tat ctc tta agt atc 883
 Glu Tyr Asp Arg Ala Leu Val Glu Leu Ser Ala Tyr Leu Leu Ser Ile
 250 255 260
 gac ctc gat gat cgc gtt gct gca gag atg acc att tta ggt cgc cct 931
 Asp Leu Asp Asp Arg Val Ala Ala Glu Met Thr Ile Leu Gly Arg Pro
 265 270 275
 gtg cct aaa gaa gga taaccaccac accagaaaag aag 969
 Val Pro Lys Glu Gly
 280

<210> 880
 <211> 282
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 880
 Met His Ser Asp Arg Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr
 1 5 10 15
 Ile Arg Gln Asp Thr Asp Ala Glu Asn Pro Met Thr His His Asp Thr
 20 25 30
 Lys Asp Ala Ala Leu Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr
 35 40 45
 Val Ala Asp Lys Pro Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys
 50 55 60
 Phe Ile Cys Gly Gln His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp
 65 70 75 80
 Ser Asp Gly Asp Ser Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val
 85 90 95
 Ala Glu His His Pro Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile
 100 105 110
 Thr Gly Tyr Ser Gln Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr
 115 120 125
 Ala Ala Thr Cys Asp Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile
 130 135 140

Tyr Arg Gln Trp Ala Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser
 145 150 155 160
 Gln Pro Gly Leu Ala Gly Ile Tyr Ala Asp Asp Pro Ala Asp Ala Leu
 165 170 175
 Ala Tyr Tyr Gln Glu Asn Phe Glu Asp Glu Pro Ile Trp Asp Leu Leu
 180 185 190
 Ser Arg His Asp Ala Asp Lys Asp Ala Ala Ala Leu Ala Ala Ala Ser
 195 200 205
 Ala Ala Glu Asn His Ala Leu Ala Arg Gly Thr Thr Pro Val Val Ile
 210 215 220
 Arg Thr Gln Asp Ile Ile Thr Asn Ala Arg Tyr Leu Met Ser Asp Ser
 225 230 235 240
 Ala Asp Asp Asn Pro Glu Tyr Asp Arg Ala Leu Val Glu Leu Ser Ala
 245 250 255
 Tyr Leu Leu Ser Ile Asp Leu Asp Asp Arg Val Ala Ala Glu Met Thr
 260 265 270
 Ile Leu Gly Arg Pro Val Pro Lys Glu Gly
 275 280

<210> 881
 <211> 583
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(583)
 <223> FRXA01908

<400> 881
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 cagtctgtct tccatatttc atatcccagc acataccact atg cac tct gac cgc 115
 Met His Ser Asp Arg
 1 5
 ttt gag cac cca gac aac ggc tat ggc tac acc att cgt cag gac act 163
 Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr Ile Arg Gln Asp Thr
 10 15 20
 gat gca gag aac ccg atg acc cat cac gat acg aaa gat gca gct ctc 211
 Asp Ala Glu Asn Pro Met Thr His His Asp Thr Lys Asp Ala Ala Leu
 25 30 35
 tgg gtt cac aac cga cca cga cgc gga gat acc gtc gcc gat aag cca 259
 Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr Val Ala Asp Lys Pro
 40 45 50
 gaa ggc aat gag att ctc gac atc ttt gcc aag ttc atc tgc ggc cag 307
 Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys Phe Ile Cys Gly Gln
 55 60 65

cac gat aat gat gac aac ccg ttc gaa gtc tgg tcc gac ggt gac tcg 355
 His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp Ser Asp Gly Asp Ser
 70 75 80 85

gat gca tca ctc atc cgc acc aag gcg tat gtt gcc gag cac cac ccc 403
 Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val Ala Glu His His Pro
 90 95 100

gaa ctt ata ttc gac atc tct gcg aaa acc atc acg ggt tat tcc caa 451
 Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile Thr Gly Tyr Ser Gln
 105 110 115

ggc gat tgg ctc gat gtg gtc tgt gtt act act gcc gcc act tgc gac 499
 Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr Ala Ala Thr Cys Asp
 120 125 130

gaa ctt atc cct gct gac agt ctt att gac atc tac cgc cag tgg gct 547
 Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile Tyr Arg Gln Trp Ala
 135 140 145

ttt ggt gat gtg tgg aca gtg att cct gat tct cag 583
 Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser Gln
 150 155 160

<210> 882

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 882

Met His Ser Asp Arg Phe Glu His Pro Asp Asn Gly Tyr Gly Tyr Thr
 1 5 10 15

Ile Arg Gln Asp Thr Asp Ala Glu Asn Pro Met Thr His His Asp Thr
 20 25 30

Lys Asp Ala Ala Leu Trp Val His Asn Arg Pro Arg Arg Gly Asp Thr
 35 40 45

Val Ala Asp Lys Pro Glu Gly Asn Glu Ile Leu Asp Ile Phe Ala Lys
 50 55 60

Phe Ile Cys Gly Gln His Asp Asn Asp Asp Asn Pro Phe Glu Val Trp
 65 70 75 80

Ser Asp Gly Asp Ser Asp Ala Ser Leu Ile Arg Thr Lys Ala Tyr Val
 85 90 95

Ala Glu His His Pro Glu Leu Ile Phe Asp Ile Ser Ala Lys Thr Ile
 100 105 110

Thr Gly Tyr Ser Gln Gly Asp Trp Leu Asp Val Val Cys Val Thr Thr
 115 120 125

Ala Ala Thr Cys Asp Glu Leu Ile Pro Ala Asp Ser Leu Ile Asp Ile
 130 135 140

Tyr Arg Gln Trp Ala Phe Gly Asp Val Trp Thr Val Ile Pro Asp Ser
 145 150 155 160

<400> 883																
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tttgtatc atg gct aat ttt cga agc aag gat aaa gat ggc aat gtc atc																110
Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile																
1 5 10																
aat ccg aac gcg tct act aaa ggt gta gat ctt gtt gtc aac gtc tac																158
Asn Pro Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr																
15 20 25 30																
gac agc gcc aag cat gtg acc gaa aag ggt aac act gtc cac ttt gtg																206
Asp Ser Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val																
35 40 45																
gat gtt cag gta gcg caa att ccg att gac gct gac ggc act cgt gcg																254
Asp Val Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala																
50 55 60																
aat gcg aat ctt gca cca cag act atg cct cat ctg cat ctt gac act																302
Asn Ala Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr																
65 70 75																
aag gac ggt cag cgc aac aca ggt gtt gcg tat tct gat gcg cag att																350
Lys Asp Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile																
80 85 90																
caa gcg atg cag acg gtg gca gca cag ggg cgc aac cat atg acc ccg																398
Gln Ala Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro																
95 100 105 110																
ctc ttg agc aaa gac ggt gag aca gtt ggt tac tcc atg ttg gtc aag																446
Leu Leu Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys																
115 120 125																
gct gat gtc atg ttc ccg aag acc aag gac ggc aag tct ctc cct gcg																494
Ala Asp Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala																
130 135 140																
gtc atg aac act aag tct ctg cag cca tct ggg gtt cct att tcg gac																542
Val Met Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp																
145 150 155																
gcg atg aat att cag cag cag cag ttt atg gct gtg gca atg aat cgc																590
Ala Met Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg																
160 165 170																

caa gca gca gaa gcg cag aag gct gca caa gcc caa gcg acc cag gct 638
 Gln Ala Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala
 175 180 185 190
 caa gca cca cag gtg gca ccg cag cca gtt atg cag aat cag caa ttc 686
 Gln Ala Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe
 195 200 205
 cag gca cca gtg cca cag gcc cag cag cca gca tat gca gga gcc cct 734
 Gln Ala Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro
 210 215 220
 gtc tat gca gac gcg gta gct cat gca acc gcg cag cag cag gca gca 782
 Val Tyr Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala
 225 230 235
 gca gct cag gca ccg cag gca cct gct ggg aat ccg ttt aac cag ccg 830
 Ala Ala Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro
 240 245 250
 cca gca gta gca gca gct ctg gca ccg cag acg cag ccg cca gca gta 878
 Pro Ala Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val
 255 260 265 270
 gca gca gct ctg gca ccg cag acg cag cag ccg gca gca caa cct cag 926
 Ala Ala Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln
 275 280 285
 atg gat aac gag cca ccg ttt taaaggcgca atacaccaca ccc 970
 Met Asp Asn Glu Pro Pro Phe
 290

<210> 884

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 884

Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro
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 Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser
 20 25 30
 Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val
 35 40 45
 Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala
 50 55 60
 Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp
 65 70 75 80
 Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala
 85 90 95
 Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu
 100 105 110

Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp
115 120 125

Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met
130 135 140

Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met
145 150 155 160

Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala
165 170 175

Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala
180 185 190

Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala
195 200 205

Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr
210 215 220

Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala
225 230 235 240

Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala
245 250 255

Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala
260 265 270

Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp
275 280 285

Asn Glu Pro Pro Phe
290

<210> 885

<211> 960

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (59)..(937)

<223> FRXA01909

<400> 885

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Met
1

gct aat ttt cga agc aag gat aaa gat ggc aat gtc atc aat ccg aac 109
Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro Asn
5 10 15

gcg tct act aaa ggt gta gat ctt gtt gtc aac gtc tac gac agc gcc 157
Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser Ala
20 25 30

aag cat gtg acc gaa aag ggt aac act gtc cac ttt gtg gat gtt cag 205

Lys	His	Val	Thr	Glu	Lys	Gly	Asn	Thr	Val	His	Phe	Val	Asp	Val	Gln		
35						40					45						
gta	gcg	caa	att	ccg	att	gac	gct	gac	ggc	act	cgt	gcg	aat	gcg	aat	253	
Val	Ala	Gln	Ile	Pro	Ile	Asp	Ala	Asp	Gly	Thr	Arg	Ala	Asn	Ala	Asn	50	65
50					55				60								
ctt	gca	cca	cag	act	atg	cct	cat	ctg	cat	ctt	gac	act	aag	gac	ggc	301	
Leu	Ala	Pro	Gln	Thr	Met	Pro	His	Leu	His	Leu	Asp	Thr	Lys	Asp	Gly	70	80
				70				75									
cag	cgc	aac	aca	ggc	gtt	gag	tat	tct	gat	gag	cag	att	caa	gag	atg	349	
Gln	Arg	Asn	Thr	Gly	Val	Ala	Tyr	Ser	Asp	Ala	Gln	Ile	Gln	Ala	Met	85	95
			85				90										
cag	acg	gtg	gca	gca	cag	ggg	cgc	aac	cat	atg	acc	ccg	ctc	ttg	agc	397	
Gln	Thr	Val	Ala	Ala	Gln	Gly	Arg	Asn	His	Met	Thr	Pro	Leu	Leu	Ser	100	110
		100					105					110					
aaa	gac	ggc	gag	aca	gtt	ggc	tac	tcc	atg	ttg	gtc	aag	gct	gat	gtc	445	
Lys	Asp	Gly	Glu	Thr	Val	Gly	Tyr	Ser	Met	Leu	Val	Lys	Ala	Asp	Val	115	125
	115					120					125						
atg	ttc	ccg	aag	acc	aag	gac	ggc	aag	tct	ctc	cct	gag	gtc	atg	aac	493	
Met	Phe	Pro	Lys	Thr	Lys	Asp	Gly	Lys	Ser	Leu	Pro	Ala	Val	Met	Asn	130	145
					135					140							
act	aag	tct	ctg	cag	cca	tct	ggg	gtt	cct	att	tgc	gac	gag	atg	aat	541	
Thr	Lys	Ser	Leu	Gln	Pro	Ser	Gly	Val	Pro	Ile	Ser	Asp	Ala	Met	Asn	150	160
				150					155								
att	cag	cag	cag	cag	ttt	atg	gct	gtg	gca	atg	aat	cgc	caa	gca	gca	589	
Ile	Gln	Gln	Gln	Gln	Phe	Met	Ala	Val	Ala	Met	Asn	Arg	Gln	Ala	Ala	165	175
				165				170					175				
gaa	gag	cag	aag	gct	gca	caa	gcc	caa	gag	acc	cag	gct	caa	gca	cca	637	
Glu	Ala	Gln	Lys	Ala	Ala	Gln	Ala	Gln	Ala	Thr	Gln	Ala	Gln	Ala	Pro	180	190
		180					185					190					
cag	gtg	gca	ccg	cag	cca	gtt	atg	cag	aat	cag	caa	ttc	cag	gca	cca	685	
Gln	Val	Ala	Pro	Gln	Pro	Val	Met	Gln	Asn	Gln	Gln	Phe	Gln	Ala	Pro	195	205
						200						205					
gtg	cca	cag	ggc	cag	cag	cca	gca	tat	gca	gga	gcc	cct	gtc	tat	gca	733	
Val	Pro	Gln	Gly	Gln	Gln	Pro	Ala	Tyr	Ala	Gly	Ala	Pro	Val	Tyr	Ala	210	225
					215					220							
gac	gag	gta	gct	cat	gca	acc	gag	cag	cag	cag	gca	gca	gca	gct	cag	781	
Asp	Ala	Val	Ala	His	Ala	Thr	Ala	Gln	Gln	Gln	Ala	Ala	Ala	Ala	Gln	230	240
				230					235								
gca	ccg	cag	gca	cct	gct	ggg	aat	ccg	ttt	aac	cag	ccg	cca	gca	gta	829	
Ala	Pro	Gln	Ala	Pro	Ala	Gly	Asn	Pro	Phe	Asn	Gln	Pro	Pro	Ala	Val	245	255
				245				250									
gca	gca	gct	ctg	gca	ccg	cag	acg	cag	ccg	cca	gca	gta	gca	gca	gct	877	
Ala	Ala	Ala	Leu	Ala	Pro	Gln	Thr	Gln	Pro	Pro	Ala	Val	Ala	Ala	Ala	260	270
							265										
ctg	gca	ccg	cag	acg	cag	cag	ccg	gca	gca	caa	cct	cag	atg	gat	aac	925	
Leu	Ala	Pro	Gln	Thr	Gln	Gln	Pro	Ala	Ala	Gln	Pro	Gln	Met	Asp	Asn		

275

280

285

gag cca ccg ttt taaaggcgca atacaccaca ccc
Glu Pro Pro Phe
290

960

<210> 886

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 886

Met Ala Asn Phe Arg Ser Lys Asp Lys Asp Gly Asn Val Ile Asn Pro
1 5 10 15

Asn Ala Ser Thr Lys Gly Val Asp Leu Val Val Asn Val Tyr Asp Ser
20 25 30

Ala Lys His Val Thr Glu Lys Gly Asn Thr Val His Phe Val Asp Val
35 40 45

Gln Val Ala Gln Ile Pro Ile Asp Ala Asp Gly Thr Arg Ala Asn Ala
50 55 60

Asn Leu Ala Pro Gln Thr Met Pro His Leu His Leu Asp Thr Lys Asp
65 70 75 80

Gly Gln Arg Asn Thr Gly Val Ala Tyr Ser Asp Ala Gln Ile Gln Ala
85 90 95

Met Gln Thr Val Ala Ala Gln Gly Arg Asn His Met Thr Pro Leu Leu
100 105 110

Ser Lys Asp Gly Glu Thr Val Gly Tyr Ser Met Leu Val Lys Ala Asp
115 120 125

Val Met Phe Pro Lys Thr Lys Asp Gly Lys Ser Leu Pro Ala Val Met
130 135 140

Asn Thr Lys Ser Leu Gln Pro Ser Gly Val Pro Ile Ser Asp Ala Met
145 150 155 160

Asn Ile Gln Gln Gln Gln Phe Met Ala Val Ala Met Asn Arg Gln Ala
165 170 175

Ala Glu Ala Gln Lys Ala Ala Gln Ala Gln Ala Thr Gln Ala Gln Ala
180 185 190

Pro Gln Val Ala Pro Gln Pro Val Met Gln Asn Gln Gln Phe Gln Ala
195 200 205

Pro Val Pro Gln Gly Gln Gln Pro Ala Tyr Ala Gly Ala Pro Val Tyr
210 215 220

Ala Asp Ala Val Ala His Ala Thr Ala Gln Gln Gln Ala Ala Ala Ala
225 230 235 240

Gln Ala Pro Gln Ala Pro Ala Gly Asn Pro Phe Asn Gln Pro Pro Ala
245 250 255

Val Ala Ala Ala Leu Ala Pro Gln Thr Gln Pro Pro Ala Val Ala Ala
 260 265 270

Ala Leu Ala Pro Gln Thr Gln Gln Pro Ala Ala Gln Pro Gln Met Asp
 275 280 285

Asn Glu Pro Pro Phe
 290

<210> 887

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXN01910

<400> 887

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gtctcagatc atgaacagca caatgtagga gaagattgat atg gca ttt ccg ctt 115
 Met Ala Phe Pro Leu
 1 5

cta gcg gtt gct ggc aca gtt gcc ccc gtt gca gca gga tgg gca aaa 163
 Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala Ala Gly Trp Ala Lys
 10 15 20

gat aag ttt ctc agc aac tct cag aat aat cag cag gcc cag aat cag 211
 Asp Lys Phe Leu Ser Asn Ser Gln Asn Asn Gln Gln Ala Gln Asn Gln
 25 30 35

cag atg agt ttt gga cag gtc aac aac agc gca cag aat tct gga tca 259
 Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala Gln Asn Ser Gly Ser
 40 45 50

gaa aac agc ggt ttc atg ggt caa tac ggc aat ctg ggt gca ggt ttg 307
 Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn Leu Gly Ala Gly Leu
 55 60 65

gca ggt gct gct aca ggc gca ggg ctt gcg tat agc gat ttt gaa gat 355
 Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr Ser Asp Phe Glu Asp
 70 75 80 85

ggt caa agt ttg tcc tcg aag gcc cgc aac atg gtc ggc aaa ggg ctc 403
 Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met Val Gly Lys Gly Leu
 90 95 100

gct ggt gcc gga gct ggt gtg ttc acc aag ctt gcc aat gat gca att 451
 Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu Ala Asn Asp Ala Ile
 105 110 115

cag gcc gag ggt ggc tcg atg aag gct agt gct tat tct gcc att gca 499
 Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala Tyr Ser Ala Ile Ala
 120 125 130

ggc ggc ttg gga tcg tat ctc aaa gac ggc ggt ccg ggt gtg att aaa 547
 Gly Gly Leu Gly Ser Tyr Leu Lys Asp Gly Gly Pro Gly Val Ile Lys

135	140	145	
tcc gcg atg gcc agc ggt gca gcc ggt ttt ggt gcg gat aaa gtg cac			595
Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly Ala Asp Lys Val His			
150	155	160	165
gat aaa tta gct gag tct ggt cat gag ggg ttg gct gat tcc ttg tcg			643
Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu Ala Asp Ser Leu Ser			
	170	175	180
ggc gct att caa gga ggt ggt ctt ggt tac tcc acg ctt ggc ggt gtc			691
Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser Thr Leu Gly Gly Val			
	185	190	195
act ggt gct ggt att ggc ggt gcg acg ggc ggt ctc gca gga cta gca			739
Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly Leu Ala Gly Leu Ala			
	200	205	210
caa aac tac ttt ggt ggt ggc gat gac tac agc aac gct ggg gca tct			787
Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser Asn Ala Gly Ala Ser			
	215	220	225
gca tcg ggg ttt agt gcc aac cag gtt aat agt gag atc agc acc gag			835
Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser Glu Ile Ser Thr Glu			
	230	235	240
att ccg cag ttt gcg aat ctt ggt caa cca cag cga tcc gag ctt gaa			883
Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln Arg Ser Glu Leu Glu			
	250	255	260
caa tta gcg cta cct caa gaa tca cgg tct gta gat aag agc tac gac			931
Gln Leu Ala Leu Pro Gln Glu Ser Arg Ser Val Asp Lys Ser Tyr Asp			
	265	270	275
caa ggc tac gaa gcg taagcgcttt ataacaaccc cgt			969
Gln Gly Tyr Glu Ala			
	280		

<210> 888

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 888

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Ala	Gly	Trp	Ala	Lys	Asp	Lys	Phe	Leu	Ser	Asn	Ser	Gln	Asn	Asn	Gln
		20						25					30		

Gln	Ala	Gln	Asn	Gln	Gln	Met	Ser	Phe	Gly	Gln	Val	Asn	Asn	Ser	Ala
		35				40						45			

Gln	Asn	Ser	Gly	Ser	Glu	Asn	Ser	Gly	Phe	Met	Gly	Gln	Tyr	Gly	Asn
	50					55					60				

Leu	Gly	Ala	Gly	Leu	Ala	Gly	Ala	Ala	Thr	Gly	Ala	Gly	Leu	Ala	Tyr
	65				70					75					80

Ser	Asp	Phe	Glu	Asp	Gly	Gln	Ser	Leu	Ser	Ser	Lys	Ala	Arg	Asn	Met
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85								90				95			
Val	Gly	Lys	Gly	Leu	Ala	Gly	Ala	Gly	Ala	Gly	Val	Phe	Thr	Lys	Leu
			100				105						110		
Ala	Asn	Asp	Ala	Ile	Gln	Ala	Glu	Gly	Gly	Ser	Met	Lys	Ala	Ser	Ala
			115				120						125		
Tyr	Ser	Ala	Ile	Ala	Gly	Gly	Leu	Gly	Ser	Tyr	Leu	Lys	Asp	Gly	Gly
			130				135						140		
Pro	Gly	Val	Ile	Lys	Ser	Ala	Met	Ala	Ser	Gly	Ala	Ala	Gly	Phe	Gly
			145				150						155		
Ala	Asp	Lys	Val	His	Asp	Lys	Leu	Ala	Glu	Ser	Gly	His	Glu	Gly	Leu
			165				170						175		
Ala	Asp	Ser	Leu	Ser	Gly	Ala	Ile	Gln	Gly	Gly	Gly	Leu	Gly	Tyr	Ser
			180				185						190		
Thr	Leu	Gly	Gly	Val	Thr	Gly	Ala	Gly	Ile	Gly	Gly	Ala	Thr	Gly	Gly
			195				200						205		
Leu	Ala	Gly	Leu	Ala	Gln	Asn	Tyr	Phe	Gly	Gly	Gly	Asp	Asp	Tyr	Ser
			210				215						220		
Asn	Ala	Gly	Ala	Ser	Ala	Ser	Gly	Phe	Ser	Ala	Asn	Gln	Val	Asn	Ser
			225				230						235		
Glu	Ile	Ser	Thr	Glu	Ile	Pro	Gln	Phe	Ala	Asn	Leu	Gly	Gln	Pro	Gln
			245				250						255		
Arg	Ser	Glu	Leu	Glu	Gln	Leu	Ala	Leu	Pro	Gln	Glu	Ser	Arg	Ser	Val
			260				265						270		
Asp	Lys	Ser	Tyr	Asp	Gln	Gly	Tyr	Glu	Ala						
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<211> 969
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(946)
<223> FRXA01910
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gtctcagatc atgaacagca caatgtagga gaagattgat  atg gca ttt ccg ctt  115
                                         Met Ala Phe Pro Leu
                                         1                               5

cta gcg gtt gct ggc aca gtt gcc ccc gtt gca gca gga tgg gca aaa 163
Leu Ala Val Ala Gly Thr Val Ala Pro Val Ala Ala Gly Trp Ala Lys
                        10                        15                        20

gat aag ttt ctc agc aac tct cag aat aat cag cag gcc cag aat cag 211

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Asp	Lys	Phe	Leu	Ser	Asn	Ser	Gln	Asn	Asn	Gln	Gln	Ala	Gln	Asn	Gln			
			25					30					35					
cag	atg	agt	ttt	gga	cag	gtc	aac	aac	agc	gca	cag	aat	tct	gga	tca		259	
Gln	Met	Ser	Phe	Gly	Gln	Val	Asn	Asn	Ser	Ala	Gln	Asn	Ser	Gly	Ser			
		40					45					50						
gaa	aac	agc	ggg	ttc	atg	ggg	caa	tac	ggc	aat	ctg	ggg	gca	ggg	ttg		307	
Glu	Asn	Ser	Gly	Phe	Met	Gly	Gln	Tyr	Gly	Asn	Leu	Gly	Ala	Gly	Leu			
	55					60					65							
gca	ggg	gct	gct	aca	ggc	gca	ggg	ctt	gcg	tat	agc	gat	ttt	gaa	gat		355	
Ala	Gly	Ala	Ala	Thr	Gly	Ala	Gly	Leu	Ala	Tyr	Ser	Asp	Phe	Glu	Asp			
	70				75				80						85			
ggg	caa	agt	ttg	tcc	tcg	aag	gcc	cg	aac	atg	gtc	ggc	aaa	ggg	ctc		403	
Gly	Gln	Ser	Leu	Ser	Ser	Lys	Ala	Arg	Asn	Met	Val	Gly	Lys	Gly	Leu			
			90					95						100				
gct	ggg	gcc	gga	gct	ggg	gtg	ttc	acc	aag	ctt	gcc	aat	gat	gca	att		451	
Ala	Gly	Ala	Gly	Ala	Gly	Val	Phe	Thr	Lys	Leu	Ala	Asn	Asp	Ala	Ile			
			105					110					115					
cag	gcc	gag	ggg	ggc	tcg	atg	aag	gct	agt	gct	tat	tct	gcc	att	gca		499	
Gln	Ala	Glu	Gly	Gly	Ser	Met	Lys	Ala	Ser	Ala	Tyr	Ser	Ala	Ile	Ala			
		120					125					130						
agc	ggc	ttg	gga	tcg	tat	ctc	aaa	aac	ggc	ggg	ccg	ggg	gtg	att	aaa		547	
Ser	Gly	Leu	Gly	Ser	Tyr	Leu	Lys	Asn	Gly	Gly	Pro	Gly	Val	Ile	Lys			
	135					140					145							
tcc	gcg	atg	gcc	agc	ggg	gca	gcc	ggg	ttt	ggg	gcg	gat	aaa	gtg	cac		595	
Ser	Ala	Met	Ala	Ser	Gly	Ala	Ala	Gly	Phe	Gly	Ala	Asp	Lys	Val	His			
	150				155					160					165			
gat	aaa	tta	gct	gag	tct	ggg	cat	gag	ggg	ttg	gct	gat	tcc	ttg	tcg		643	
Asp	Lys	Leu	Ala	Glu	Ser	Gly	His	Glu	Gly	Leu	Ala	Asp	Ser	Leu	Ser			
			170					175						180				
ggc	gct	att	caa	gga	ggg	ggg	ctt	ggg	tac	tcc	acg	ctt	ggc	ggg	gtc		691	
Gly	Ala	Ile	Gln	Gly	Gly	Gly	Leu	Gly	Tyr	Ser	Thr	Leu	Gly	Gly	Val			
			185					190					195					
act	ggg	gct	ggg	att	ggc	ggg	gcg	acg	ggc	ggg	ctc	gca	gga	cta	gca		739	
Thr	Gly	Ala	Gly	Ile	Gly	Gly	Ala	Thr	Gly	Gly	Leu	Ala	Gly	Leu	Ala			
		200					205					210						
caa	aac	tac	ttt	ggg	ggg	ggc	gat	gac	tac	agc	aac	gct	ggg	gca	tct		787	
Gln	Asn	Tyr	Phe	Gly	Gly	Gly	Asp	Asp	Tyr	Ser	Asn	Ala	Gly	Ala	Ser			
		215				220					225							
gca	tcg	ggg	ttt	agt	gcc	aac	cag	gtt	aat	agt	gag	atc	agc	acc	gag		835	
Ala	Ser	Gly	Phe	Ser	Ala	Asn	Gln	Val	Asn	Ser	Glu	Ile	Ser	Thr	Glu			
	230				235					240					245			
att	ccg	cag	ttt	gcg	aat	ctt	ggg	caa	cca	cag	cga	tcc	gag	ctt	gaa		883	
Ile	Pro	Gln	Phe	Ala	Asn	Leu	Gly	Gln	Pro	Gln	Arg	Ser	Glu	Leu	Glu			
			250					255						260				
caa	tta	gcg	cta	cct	caa	gaa	tca	cg	tct	gta	gat	aag	agc	tac	gac		931	
Gln	Leu	Ala	Leu	Pro	Gln	Glu	Ser	Arg	Ser	Val	Asp	Lys	Ser	Tyr	Asp			

265

270

275

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 Gln Gly Tyr Glu Ala
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969

<210> 890

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 890

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Gln Ala Gln Asn Gln Gln Met Ser Phe Gly Gln Val Asn Asn Ser Ala
 35 40 45

Gln Asn Ser Gly Ser Glu Asn Ser Gly Phe Met Gly Gln Tyr Gly Asn
 50 55 60

Leu Gly Ala Gly Leu Ala Gly Ala Ala Thr Gly Ala Gly Leu Ala Tyr
 65 70 75 80

Ser Asp Phe Glu Asp Gly Gln Ser Leu Ser Ser Lys Ala Arg Asn Met
 85 90 95

Val Gly Lys Gly Leu Ala Gly Ala Gly Ala Gly Val Phe Thr Lys Leu
 100 105 110

Ala Asn Asp Ala Ile Gln Ala Glu Gly Gly Ser Met Lys Ala Ser Ala
 115 120 125

Tyr Ser Ala Ile Ala Ser Gly Leu Gly Ser Tyr Leu Lys Asn Gly Gly
 130 135 140

Pro Gly Val Ile Lys Ser Ala Met Ala Ser Gly Ala Ala Gly Phe Gly
 145 150 155 160

Ala Asp Lys Val His Asp Lys Leu Ala Glu Ser Gly His Glu Gly Leu
 165 170 175

Ala Asp Ser Leu Ser Gly Ala Ile Gln Gly Gly Gly Leu Gly Tyr Ser
 180 185 190

Thr Leu Gly Gly Val Thr Gly Ala Gly Ile Gly Gly Ala Thr Gly Gly
 195 200 205

Leu Ala Gly Leu Ala Gln Asn Tyr Phe Gly Gly Gly Asp Asp Tyr Ser
 210 215 220

Asn Ala Gly Ala Ser Ala Ser Gly Phe Ser Ala Asn Gln Val Asn Ser
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Glu Ile Ser Thr Glu Ile Pro Gln Phe Ala Asn Leu Gly Gln Pro Gln
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Asp Lys Ser Tyr Asp Gln Gly Tyr Glu Ala
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<222> (101)..(1039)
<223> RXN01911
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Val Phe Ile Ile Gly 5															
gcc ggc ttg cca ctg ttg tac gtg ccg att ttt gtg act gtc atc gtc 163															
Ala Gly Leu Pro Leu Leu Tyr Val Pro Ile Phe Val Thr Val Ile Val 20															
atg gtg gtg tat gcg cta ttg cgc tat gag cag cgc atg tca ggc aca 211															
Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln Arg Met Ser Gly Thr 35															
gtc tac gag gaa gca gat cct gtc gaa atg gat tca gtg atc tgg gag 259															
Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp Ser Val Ile Trp Glu 50															
ggc atc aag tgc gat att gcc tcg gat att gca gcc cga gca gaa gcg 307															
Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala Ala Arg Ala Glu Ala 65															
aaa aaa gcg aaa aag cca gtt gcg tca gat gct gtt gct gtt ggt aac 355															
Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala Val Ala Val Gly Asn 85															
tat atc gcg tcc ttg cgt cag cat atg ttg gta gaa acc cag cga cgt 403															
Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val Glu Thr Gln Arg Arg 100															
tat cac cac aag ctt ggt cgt gag ctg cat aat gat cca gcg caa cta 451															
Tyr His His Lys Leu Gly Arg Glu Leu His Asn Asp Pro Ala Gln Leu 115															
gag gat tat ggc tct ggt ctg cgt gac tgt gag tgt cgg gca tgt gtg 499															
Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu Cys Arg Ala Cys Val 130															
gtg gct cag aaa ttg ggt gtc acg gtg cac gct cat ggt gtg gtg cag 547															
Val Ala Gln Lys Leu Gly Val Thr Val His Ala His Gly Val Val Gln 145															
gcg aqc qca cgt aaa aaa gat cgc gtc att att ggg cga gcc gat ggt 595															

Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile Gly Arg Ala Asp Gly
 150 155 160 165

att gat gtg gcc ggc tgg tgg aac cac cgc caa gaa gct cga cgt aaa 643
 Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln Glu Ala Arg Arg Lys
 170 175 180

acg agc gcg gct aag cag ttg gag cgc gat gca caa cgc aag cga acc 691
 Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala Gln Arg Lys Arg Thr
 185 190 195

caa gct gag cgc gat aaa gag att gag cgt aag cgt aag gct caa gaa 739
 Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys Arg Lys Ala Gln Glu
 200 205 210

ttt gta gcg gag cag tca ggg aaa gct gct gca gca caa cgg cgg gcc 787
 Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala Gln Arg Arg Ala
 215 220 225

gag aaa aag gct gcg aag caa gcg cgt gta gat gaa ctg gtg gcg cag 835
 Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp Glu Leu Val Ala Gln
 230 235 240 245

aaa cag gct gct cag gag cag aaa act cac tgt aag cgg gac aag cag 883
 Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys Lys Arg Asp Lys Gln
 250 255 260

cgt gcg aag aaa gca caa ggg cgc aaa gtt ggt gcc gtt gat aat tcc 931
 Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly Ala Val Asp Asn Ser
 265 270 275

gct gtg gac gat gtg ttg gcg tat gcg gag aaa acc cgc agt ata gct 979
 Ala Val Asp Asp Val Leu Ala Tyr Ala Glu Lys Thr Arg Ser Ile Ala
 280 285 290

ggc tgt aga gat gac gac agc gtt gtg cac gtt gat atg gca gcg ggt 1027
 Gly Cys Arg Asp Asp Asp Ser Val Val His Val Asp Met Ala Ala Gly
 295 300 305

gtc cgc gat gtc taaatcgag gatgatcgaa aaa 1062
 Val Arg Asp Val
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<210> 892
 <211> 313
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 892
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Arg Met Ser Gly Thr Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp
 35 40 45

Ser Val Ile Trp Glu Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala
 50 55 60

Ala Arg Ala Glu Ala Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala
65 70 75 80

Val Ala Val Gly Asn Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val
85 90 95

Glu Thr Gln Arg Arg Tyr His His Lys Leu Gly Arg Glu Leu His Asn
100 105 110

Asp Pro Ala Gln Leu Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu
115 120 125

Cys Arg Ala Cys Val Val Ala Gln Lys Leu Gly Val Thr Val His Ala
130 135 140

His Gly Val Val Gln Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile
145 150 155 160

Gly Arg Ala Asp Gly Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln
165 170 175

Glu Ala Arg Arg Lys Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala
180 185 190

Gln Arg Lys Arg Thr Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys
195 200 205

Arg Lys Ala Gln Glu Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala
210 215 220

Ala Gln Arg Arg Ala Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp
225 230 235 240

Glu Leu Val Ala Gln Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys
245 250 255

Lys Arg Asp Lys Gln Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly
260 265 270

Ala Val Asp Asn Ser Ala Val Asp Asp Val Leu Ala Tyr Ala Glu Lys
275 280 285

Thr Arg Ser Ile Ala Gly Cys Arg Asp Asp Asp Ser Val Val His Val
290 295 300

Asp Met Ala Ala Gly Val Arg Asp Val
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<210> 893

<211> 946

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> FRXA01911

<400> 893

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gcc ggc ttg cca ctg ttg tac gtg ccg att ttt gtg act gtc atc gtc															163
<div>Ala Gly Leu Pro. Leu Leu Tyr Val Pro Ile Phe Val Thr Val Ile Val</div> <div>10 15 20</div>															
atg gtg gtg tat gcg cta ttg cgc tat gag cag cgc atg tca ggc aca															211
<div>Met Val Val Tyr Ala Leu Leu Arg Tyr Glu Gln Arg Met Ser Gly Thr</div> <div>25 30 35</div>															
gtc tac gag gaa gca gat cct gtc gaa atg gat tca gtg atc tgg gag															259
<div>Val Tyr Glu Ala Asp Pro Val Glu Met Asp Ser Val Ile Trp Glu</div> <div>40 45 50</div>															
ggc atc aag tgc gat att gcc tcg gat att gca gcc cga gca gaa gcg															307
<div>Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala Ala Arg Ala Glu Ala</div> <div>55 60 65</div>															
aaa aaa gcg aaa aag cca gtt gcg tca gat gct gtt gct gtt ggt aac															355
<div>Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala Val Ala Val Gly Asn</div> <div>70 75 80 85</div>															
tat atc gcg tcc ttg cgt cag cat atg ttg gta gaa acc cag cga cgt															403
<div>Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val Glu Thr Gln Arg Arg</div> <div>90 95 100</div>															
tat cac cac aag ctt ggt cgt gag ctg cat aat gat cca gcg caa cta															451
<div>Tyr His His Lys Leu Gly Arg Glu Leu His Asn Asp Pro Ala Gln Leu</div> <div>105 110 115</div>															
gag gat tat ggc tct ggt ctg cgt gac tgt gag tgt cgg gca tgt gtg															499
<div>Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu Cys Arg Ala Cys Val</div> <div>120 125 130</div>															
gtg gct cag aaa ttg ggt gtc acg gtg cac gct cat ggt gtg gtg cag															547
<div>Val Ala Gln Lys Leu Gly Val Thr Val His Ala His Gly Val Val Gln</div> <div>135 140 145</div>															
gcg agc gca cgt aaa aaa gat cgc gtc att att ggg cga gcc gat ggt															595
<div>Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile Gly Arg Ala Asp Gly</div> <div>150 155 160 165</div>															
att gat gtg gcc ggc tgg tgg aac cac cgc caa gaa gct cga cgt aaa															643
<div>Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln Glu Ala Arg Arg Lys</div> <div>170 175 180</div>															
acg agc gcg gct aag cag ttg gag cgc gat gca caa cgc aag cga acc															691
<div>Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala Gln Arg Lys Arg Thr</div> <div>185 190 195</div>															
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<div>Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys Arg Lys Ala Gln Glu</div> <div>200 205 210</div>															
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<div>Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala Gln Arg Arg Ala</div> <div>215 220 225</div>															

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 Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp Glu Leu Val Ala Gln
 230 235 240 245
 aaa cag gct gct cag gag cag aaa act cac tgt aag cgg gac aag cag 883
 Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys Lys Arg Asp Lys Gln
 250 255 260
 cgt gcg aag aaa gca caa ggg cgc aaa gtt ggt gcc gtt gat aat tcc 931
 Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly Ala Val Asp Asn Ser
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 Ala Val Asp Asp Val
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<210> 894
 <211> 282
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 894
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 Arg Met Ser Gly Thr Val Tyr Glu Glu Ala Asp Pro Val Glu Met Asp
 35 40 45
 Ser Val Ile Trp Glu Gly Ile Lys Cys Asp Ile Ala Ser Asp Ile Ala
 50 55 60
 Ala Arg Ala Glu Ala Lys Lys Ala Lys Lys Pro Val Ala Ser Asp Ala
 65 70 75 80
 Val Ala Val Gly Asn Tyr Ile Ala Ser Leu Arg Gln His Met Leu Val
 85 90 95
 Glu Thr Gln Arg Arg Tyr His His Lys Leu Gly Arg Glu Leu His Asn
 100 105 110
 Asp Pro Ala Gln Leu Glu Asp Tyr Gly Ser Gly Leu Arg Asp Cys Glu
 115 120 125
 Cys Arg Ala Cys Val Val Ala Gln Lys Leu Gly Val Thr Val His Ala
 130 135 140
 His Gly Val Val Gln Ala Ser Ala Arg Lys Lys Asp Arg Val Ile Ile
 145 150 155 160
 Gly Arg Ala Asp Gly Ile Asp Val Ala Gly Trp Trp Asn His Arg Gln
 165 170 175
 Glu Ala Arg Arg Lys Thr Ser Ala Ala Lys Gln Leu Glu Arg Asp Ala
 180 185 190
 Gln Arg Lys Arg Thr Gln Ala Glu Arg Asp Lys Glu Ile Glu Arg Lys

195	200	205
Arg Lys Ala Gln Glu Phe Val Ala Glu Gln Ser Gly Lys Ala Ala Ala 210 215 220		
Ala Gln Arg Arg Ala Glu Lys Lys Ala Ala Lys Gln Ala Arg Val Asp 225 230 235 240		
Glu Leu Val Ala Gln Lys Gln Ala Ala Gln Glu Gln Lys Thr His Cys 245 250 255		
Lys Arg Asp Lys Gln Arg Ala Lys Lys Ala Gln Gly Arg Lys Val Gly 260 265 270		
Ala Val Asp Asn Ser Ala Val Asp Asp Val 275 280		

<210> 895
 <211> 1074
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1051)
 <223> RXN01930

<400> 895
 cgaaagaagc cataatttag agaggacaat tctctactat tgggtcaaggc tcccacccgg 60

tgtcattcga cattattacc gctcactcac aatcgatgaa	gtg att tca aca aat	115
	Val Ile Ser Thr Asn	
	1 5	
gag att gaa aat att cac tca act cgt cgg gat att gaa ata gcg ctt	163	
Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp Ile Glu Ile Ala Leu		
	10 15 20	
gat gaa tct tcc act agt gag cca aag aga ttt tcg gaa att tca cac	211	
Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe Ser Glu Ile Ser His		
	25 30 35	
ctt tac ctg gca ctt gcc gaa ggt aaa ata tcc ttt ccg gaa agc cca	259	
Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser Phe Pro Glu Ser Pro		
	40 45 50	
agt gaa ctt cga gaa ctg tat gac cat tta atg cac ggc gag cta ggt	307	
Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met His Gly Glu Leu Gly		
	55 60 65	
aaa gaa aat gaa tta gat ggt gag att ttc cgc caa gga ccc gtg gaa	355	
Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg Gln Gly Pro Val Glu		
	70 75 80 85	
atc cgc gat agt cgg caa aaa gtg att cat tca ggt ttt tct cca gaa	403	
Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser Gly Phe Ser Pro Glu		
	90 95 100	
tca cag atc atc gaa gga atc aac gca att att aag ctg gcg cac tca	451	
Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile Lys Leu Ala His Ser		

105	110	115	
gaa gag gaa tcc aac ctt gtt ggc atc atg atg tca cac ttc atg ttt			499
Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met Ser His Phe Met Phe			
120	125	130	
gaa tca att cac ccg ttt tat gat gga aac gga aga act ggg cgc tac			547
Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly Arg Thr Gly Arg Tyr			
135	140	145	
ctt ctc ggg ata caa tta agc aaa att ctc tcc cct gct aca gca ctg			595
Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser Pro Ala Thr Ala Leu			
150	155	160	165
aca atg tct tcg gca att aat caa ttt cga aac aag tac tac aaa gcg			643
Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn Lys Tyr Tyr Lys Ala			
170	175	180	
ttt cat gcc gta gaa cac cga tta aat cgc gga gac gga aca ccg ttt			691
Phe His Ala Val Glu His Arg Leu Asn Arg Gly Asp Gly Thr Pro Phe			
185	190	195	
gtt att tcc atg ctt gag ctg tta att gca gcg caa gaa ggt ctc att			739
Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala Gln Glu Gly Leu Ile			
200	205	210	
gag aat ata aaa caa aga atc gac ttt ttg gca agc ctt gag gac gcc			787
Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala Ser Leu Glu Asp Ala			
215	220	225	
att aaa acg ctt cgg ggt acc aat tcc ttt aag aac cat cag atc aat			835
Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys Asn His Gln Ile Asn			
230	235	240	245
ctg ttg tac att ctc ggc cag att cag ctt ttc ggt aag gac gaa aca			883
Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe Gly Lys Asp Glu Thr			
250	255	260	
ctt tca ctt gaa tcg gca gca aag ttt ctt aaa gtt tct aag gca act			931
Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys Val Ser Lys Ala Thr			
265	270	275	
gca acg agg tat ttt aga act ctc cga gaa atg gaa tta gtt cac gag			979
Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met Glu Leu Val His Glu			
280	285	290	
gtc agc aaa cgc cct ttg cgg ttt gcg ctc acg gat aaa ggt cgt gag			1027
Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr Asp Lys Gly Arg Glu			
295	300	305	
ata gta ggt ctt gag gta aaa att tgactccata acgagaactt aat			1074
Ile Val Gly Leu Glu Val Lys Ile			
310	315		

<210> 896

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 896

Val Ile Ser Thr Asn Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp
 1 5 10 15
 Ile Glu Ile Ala Leu Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe
 20 25 30
 Ser Glu Ile Ser His Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser
 35 40 45
 Phe Pro Glu Ser Pro Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met
 50 55 60
 His Gly Glu Leu Gly Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg
 65 70 75 80
 Gln Gly Pro Val Glu Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser
 85 90 95
 Gly Phe Ser Pro Glu Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile
 100 105 110
 Lys Leu Ala His Ser Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met
 115 120 125
 Ser His Phe Met Phe Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly
 130 135 140
 Arg Thr Gly Arg Tyr Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser
 145 150 155 160
 Pro Ala Thr Ala Leu Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn
 165 170 175
 Lys Tyr Tyr Lys Ala Phe His Ala Val Glu His Arg Leu Asn Arg Gly
 180 185 190
 Asp Gly Thr Pro Phe Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala
 195 200 205
 Gln Glu Gly Leu Ile Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala
 210 215 220
 Ser Leu Glu Asp Ala Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys
 225 230 235 240
 Asn His Gln Ile Asn Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe
 245 250 255
 Gly Lys Asp Glu Thr Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys
 260 265 270
 Val Ser Lys Ala Thr Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met
 275 280 285
 Glu Leu Val His Glu Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr
 290 295 300
 Asp Lys Gly Arg Glu Ile Val Gly Leu Glu Val Lys Ile
 305 310 315

<400> 897
cgaaagaagc cataatthag agaggacaat tctctactat tgggtcaagc tcccacccgg 60

aca atg tct tcg gca att aat caa ttt cga aac aag tac tac aaa gcg 643
Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn Lys Tyr Tyr Lys Ala
170 175 180

ttt cat gcc gta gaa cac cga tta aat cgc gga gac gga aca ccg ttt 691
 Phe His Ala Val Glu His Arg Leu Asn Arg Gly Asp Gly Thr Pro Phe
 185 190 195
 gtt att tcc atg ctt gag ctg tta att gca gcg caa gaa ggt ctc att 739
 Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala Gln Glu Gly Leu Ile
 200 205 210
 gag aat ata aaa caa aga atc gac ttt ttg gca agc ctt gag gac gcc 787
 Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala Ser Leu Glu Asp Ala
 215 220 225
 att aaa acg ctt cgg ggt acc aat tcc ttt aag aac cat cag atc aat 835
 Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys Asn His Gln Ile Asn
 230 235 240 245
 ctg ttg tac att ctc ggc cag att cag ctt ttc ggt aag gac gaa aca 883
 Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe Gly Lys Asp Glu Thr
 250 255 260
 ctt tca ctt gaa tcg gca gca aag ttt ctt aaa gtt tct aag gca act 931
 Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys Val Ser Lys Ala Thr
 265 270 275
 gca acg agg tat ttt aga act ctc cga gaa atg gaa tta gtt cac gag 979
 Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met Glu Leu Val His Glu
 280 285 290
 gtc agc aaa cgc cct ttg cgg ttt gcg ctc acg gat aaa ggt cgt gag 1027
 Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr Asp Lys Gly Arg Glu
 295 300 305
 ata gta ggt ctt gag gta aaa att tgactccata acgagaactt aat 1074
 Ile Val Gly Leu Glu Val Lys Ile
 310 315

<210> 898

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 898

Val Ile Ser Thr Asn Glu Ile Glu Asn Ile His Ser Thr Arg Arg Asp
 1 5 10 15

Ile Glu Ile Ala Leu Asp Glu Ser Ser Thr Ser Glu Pro Lys Arg Phe
 20 25 30

Ser Glu Ile Ser His Leu Tyr Leu Ala Leu Ala Glu Gly Lys Ile Ser
 35 40 45

Phe Pro Glu Ser Pro Ser Glu Leu Arg Glu Leu Tyr Asp His Leu Met
 50 55 60

His Gly Glu Leu Gly Lys Glu Asn Glu Leu Asp Gly Glu Ile Phe Arg
 65 70 75 80

Gln Gly Pro Val Glu Ile Arg Asp Ser Arg Gln Lys Val Ile His Ser
 85 90 95

Gly Phe Ser Pro Glu Ser Gln Ile Ile Glu Gly Ile Asn Ala Ile Ile
 100 105 110
 Lys Leu Ala His Ser Glu Glu Glu Ser Asn Leu Val Gly Ile Met Met
 115 120 125
 Ser His Phe Met Phe Glu Ser Ile His Pro Phe Tyr Asp Gly Asn Gly
 130 135 140
 Arg Thr Gly Arg Tyr Leu Leu Gly Ile Gln Leu Ser Lys Ile Leu Ser
 145 150 155 160
 Pro Ala Thr Ala Leu Thr Met Ser Ser Ala Ile Asn Gln Phe Arg Asn
 165 170 175
 Lys Tyr Tyr Lys Ala Phe His Ala Val Glu His Arg Leu Asn Arg Gly
 180 185 190
 Asp Gly Thr Pro Phe Val Ile Ser Met Leu Glu Leu Leu Ile Ala Ala
 195 200 205
 Gln Glu Gly Leu Ile Glu Asn Ile Lys Gln Arg Ile Asp Phe Leu Ala
 210 215 220
 Ser Leu Glu Asp Ala Ile Lys Thr Leu Arg Gly Thr Asn Ser Phe Lys
 225 230 235 240
 Asn His Gln Ile Asn Leu Leu Tyr Ile Leu Gly Gln Ile Gln Leu Phe
 245 250 255
 Gly Lys Asp Glu Thr Leu Ser Leu Glu Ser Ala Ala Lys Phe Leu Lys
 260 265 270
 Val Ser Lys Ala Thr Ala Thr Arg Tyr Phe Arg Thr Leu Arg Glu Met
 275 280 285
 Glu Leu Val His Glu Val Ser Lys Arg Pro Leu Arg Phe Ala Leu Thr
 290 295 300
 Asp Lys Gly Arg Glu Ile Val Gly Leu Glu Val Lys Ile
 305 310 315

<210> 899

<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1072)

<223> RXN01944

<400> 899

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ccgtttacct tcgccttcaa atatcaccga tgatgtccag gtg cgc acg gca aca 115
 Val Arg Thr Ala Thr
 1 5

ctg cat gtt act tcc agt gct ggc gaa gcc gcg aca acc atc aac ctc 163

Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala Thr Thr Ile Asn Leu	
10 15 20	
acc gag gat gac ggc tct ttc aat tgg gct ctg cct gca gcg gat ctc	211
Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu Pro Ala Ala Asp Leu	
25 30 35	
acc gga aaa tcc tgg ttc gaa tac acc gta acc gcc acc gac gga ttc	259
Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr Ala Thr Asp Gly Phe	
40 45 50	
aac agc gtt acc acc gag ccg gta cgc gtc acc gtc gac ggc gcc aac	307
Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr Val Asp Gly Ala Asn	
55 60 65	
acc gac ccg ctg cgc ctc aac ctg gaa gaa aac caa tgg gtc agt ggc	355
Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn Gln Trp Val Ser Gly	
70 75 80 85	
acc acc gat gtt atc ggt gct tca gat gtc ttc ggc gac aag ctt gaa	403
Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe Gly Asp Lys Leu Glu	
90 95 100	
ttg ctt atc gac gac gcg cct gca gtc acc aac tcc agc ctg tct gcg	451
Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn Ser Ser Leu Ser Ala	
105 110 115	
gcc ccg acg ttt gcg atg gaa gta acc caa act gat gtg ttc ttc cgc	499
Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr Asp Val Phe Phe Arg	
120 125 130	
aac ggc atc ctt gcc ggt ggg gaa gaa ctc cgc att ttc gat caa gga	547
Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg Ile Phe Asp Gln Gly	
135 140 145	
act tac gcc aac acc gaa acc atc tcc aca cca gtc ccg ctg tat cac	595
Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro Val Pro Leu Tyr His	
150 155 160 165	
atc aat gag gac ggt acc ctc aca gtc agt gtg tat gcg gga act aaa	643
Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val Tyr Ala Gly Thr Lys	
170 175 180	
gca gca cca gaa att gac ctc aac gag aac aat gac gat ttc cag atc	691
Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn Asn Asp Asp Phe Gln Ile	
185 190 195	
aga aac ctt cga cta att ctg cct gat ggc cgg acc ctc acc cct gcc	739
Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg Thr Leu Thr Pro Ala	
200 205 210	
gga att tcc gat tct aat gcg tgg ctc aac atg gga gac agc gct gga	787
Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala Gly	
215 220 225	
aaa ctc gat ttc ttc gat gcc acc ttc gcc ctc cct gag gat gct ttc	835
Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala Phe	
230 235 240 245	
acc ggt gtg gca cac gca tgg gat acc acc caa agc aca gat gga gaa	883
Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly Glu	

250	255	260	
cac cac atc acc att tcc cgc gaa gac ggc ggg gaa atc agc cgc acc			931
His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg Thr			
265	270	275	
atc cgg gtt gat aat act gcc cca gaa ctc acc gtt tct gga gtt gaa			979
Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val Glu			
280	285	290	
gaa gga caa gaa ctg cgc ggc acc gta gaa att gat gcc cag gca acc			1027
Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala Thr			
295	300	305	
gat gcg ggt gcg ggc gtg aag agc gtc gag acg ctt ctc gac ggc			1072
Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly			
310	315	320	
taacgcgtgc aacttccact aac			1095

<210> 900
 <211> 324
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 900
 Val Arg Thr Ala Thr Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala
 1 5 10 15
 Thr Thr Ile Asn Leu Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu
 20 25 30
 Pro Ala Ala Asp Leu Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr
 35 40 45
 Ala Thr Asp Gly Phe Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr
 50 55 60
 Val Asp Gly Ala Asn Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn
 65 70 75 80
 Gln Trp Val Ser Gly Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe
 85 90 95
 Gly Asp Lys Leu Glu Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn
 100 105 110
 Ser Ser Leu Ser Ala Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr
 115 120 125
 Asp Val Phe Phe Arg Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg
 130 135 140
 Ile Phe Asp Gln Gly Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro
 145 150 155 160
 Val Pro Leu Tyr His Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val
 165 170 175
 Tyr Ala Gly Thr Lys Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn Asn

180										185					190				
Asp	Asp	Phe	Gln	Ile	Arg	Asn	Leu	Arg	Leu	Ile	Leu	Pro	Asp	Gly	Arg				
		195					200					205							
Thr	Leu	Thr	Pro	Ala	Gly	Ile	Ser	Asp	Ser	Asn	Ala	Trp	Leu	Asn	Met				
	210					215					220								
Gly	Asp	Ser	Ala	Gly	Lys	Leu	Asp	Phe	Phe	Asp	Ala	Thr	Phe	Ala	Leu				
225					230					235					240				
Pro	Glu	Asp	Ala	Phe	Thr	Gly	Val	Ala	His	Ala	Trp	Asp	Thr	Thr	Gln				
				245					250					255					
Ser	Thr	Asp	Gly	Glu	His	His	Ile	Thr	Ile	Ser	Arg	Glu	Asp	Gly	Gly				
			260					265					270						
Glu	Ile	Ser	Arg	Thr	Ile	Arg	Val	Asp	Asn	Thr	Ala	Pro	Glu	Leu	Thr				
		275					280					285							
Val	Ser	Gly	Val	Glu	Glu	Gly	Gln	Glu	Leu	Arg	Gly	Thr	Val	Glu	Ile				
	290					295					300								
Asp	Ala	Gln	Ala	Thr	Asp	Ala	Gly	Ala	Gly	Val	Lys	Ser	Val	Glu	Thr				
305					310					315					320				
Leu	Leu	Asp	Gly																

<210> 901
 <211> 407
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(384)
 <223> FRXA01944

<400> 901	
atc aga aac ctt cga cta att ctg cct gat ggc cgg acc ctc acc cct	48
Ile Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg Thr Leu Thr Pro	
1 5 10 15	
gcc gga att tcc gat tct aat gcg tgg ctc aac atg gga gac agc gct	96
Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala	
20 25 30	
gga aaa ctc gat ttc ttc gat gcc acc ttc gcc ctc cct gag gat gct	144
Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala	
35 40 45	
ttc acc ggt gtg gca cac gca tgg gat acc acc caa agc aca gat gga	192
Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly	
50 55 60	
gaa cac cac atc acc att tcc cgc gaa gac ggc ggg gaa atc agc cgc	240
Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg	
65 70 75 80	

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acc atc cgg gtt gat aat act gcc cca gaa ctc acc gtt tct gga gtt 288
Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val
      85                      90                      95

gaa gaa gga caa gaa ctg cgc ggc acc gta gaa att gat gcc cag gca 336
Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala
      100                      105                      110

acc gat gcg ggt gcg ggc gtg aag agc gtc gag acg ctt ctc gac ggc 384
Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
      115                      120                      125

taacgcgtgc aacttccact aac 407

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<210> 902
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

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<400> 902
Ile Arg Asn Leu Arg Leu Ile Leu Pro Asp Gly Arg Thr Leu Thr Pro
  1              5              10              15

Ala Gly Ile Ser Asp Ser Asn Ala Trp Leu Asn Met Gly Asp Ser Ala
      20              25              30

Gly Lys Leu Asp Phe Phe Asp Ala Thr Phe Ala Leu Pro Glu Asp Ala
      35              40              45

Phe Thr Gly Val Ala His Ala Trp Asp Thr Thr Gln Ser Thr Asp Gly
      50              55              60

Glu His His Ile Thr Ile Ser Arg Glu Asp Gly Gly Glu Ile Ser Arg
      65              70              75              80

Thr Ile Arg Val Asp Asn Thr Ala Pro Glu Leu Thr Val Ser Gly Val
      85              90              95

Glu Glu Gly Gln Glu Leu Arg Gly Thr Val Glu Ile Asp Ala Gln Ala
      100              105              110

Thr Asp Ala Gly Ala Gly Val Lys Ser Val Glu Thr Leu Leu Asp Gly
      115              120              125

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<210> 903
<211> 673
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(673)
<223> FRXA01636

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<400> 903
gctgattctt ctgtaccact catcacagat aataccgcaa ccagtatcaa ccctgcggag 60

ccgtttacct tcgcottcaa atatcaccga tgatgtccag gtg cgc acg gca aca 115
                        Val Arg Thr Ala Thr

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1

5

ctg cat gtt act tcc agt gct ggc gaa gcc gcg aca acc atc aac ctc 163
 Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala Thr Thr Ile Asn Leu
 10 15 20

acc gag gat gac ggc tct ttc aat tgg gct ctg cct gca gcg gat ctc 211
 Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu Pro Ala Ala Asp Leu
 25 30 35

acc gga aaa tcc tgg ttc gaa tac acc gta acc gcc acc gac gga ttc 259
 Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr Ala Thr Asp Gly Phe
 40 45 50

aac agc gtt acc acc gag ccg gta cgc gtc acc gtc gac ggc gcc aac 307
 Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr Val Asp Gly Ala Asn
 55 60 65

acc gac ccg ctg cgc ctc aac ctg gaa gaa aac caa tgg gtc agt ggc 355
 Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn Gln Trp Val Ser Gly
 70 75 80 85

acc acc gat gtt atc ggt gct tca gat gtc ttc ggc gac aag ctt gaa 403
 Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe Gly Asp Lys Leu Glu
 90 95 100

ttg ctt atc gac gac gcg cct gca gtc acc aac tcc agc ctg tct gcg 451
 Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn Ser Ser Leu Ser Ala
 105 110 115

gcc ccg acg ttt gcg atg gaa gta acc caa act gat gtg ttc ttc cgc 499
 Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr Asp Val Phe Phe Arg
 120 125 130

aac ggc atc ctt gcc ggt ggg gaa gaa ctc cgc att ttc gat caa gga 547
 Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg Ile Phe Asp Gln Gly
 135 140 145

act tac gcc aac acc gaa acc atc tcc aca cca gtc ccg ctg tat cac 595
 Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro Val Pro Leu Tyr His
 150 155 160 165

atc aat gag gac ggt acc ctc aca gtc agt gtg tat gcg gga act aaa 643
 Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val Tyr Ala Gly Thr Lys
 170 175 180

gca gca cca gaa att gac ctc aac gag aac 673
 Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn
 185 190

<210> 904

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 904

Val Arg Thr Ala Thr Leu His Val Thr Ser Ser Ala Gly Glu Ala Ala
 1 5 10 15

Thr Thr Ile Asn Leu Thr Glu Asp Asp Gly Ser Phe Asn Trp Ala Leu

20	25	30
Pro Ala Ala Asp Leu Thr Gly Lys Ser Trp Phe Glu Tyr Thr Val Thr 35 40 45		
Ala Thr Asp Gly Phe Asn Ser Val Thr Thr Glu Pro Val Arg Val Thr 50 55 60		
Val Asp Gly Ala Asn Thr Asp Pro Leu Arg Leu Asn Leu Glu Glu Asn 65 70 75 80		
Gln Trp Val Ser Gly Thr Thr Asp Val Ile Gly Ala Ser Asp Val Phe 85 90 95		
Gly Asp Lys Leu Glu Leu Leu Ile Asp Asp Ala Pro Ala Val Thr Asn 100 105 110		
Ser Ser Leu Ser Ala Ala Pro Thr Phe Ala Met Glu Val Thr Gln Thr 115 120 125		
Asp Val Phe Phe Arg Asn Gly Ile Leu Ala Gly Gly Glu Glu Leu Arg 130 135 140		
Ile Phe Asp Gln Gly Thr Tyr Ala Asn Thr Glu Thr Ile Ser Thr Pro 145 150 155 160		
Val Pro Leu Tyr His Ile Asn Glu Asp Gly Thr Leu Thr Val Ser Val 165 170 175		
Tyr Ala Gly Thr Lys Ala Ala Pro Glu Ile Asp Leu Asn Glu Asn 180 185 190		

<210> 905

<211> 2115

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2092)

<223> RXN01945

<400> 905

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gggcgtgaag agcgtcgaga cgcttctcga cggctaacgc gtg caa ctt cca cta	115
Val Gln Leu Pro Leu	
1 5	

acc acc ggt tcc atc gct ttg gat aaa ggt gaa cac acc ttg gtt atc	163
Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu His Thr Leu Val Ile	
10 15 20	

cgt gca gaa gat gaa gta gga aac cgc acc gag aaa acc atc acg ttt	211
Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu Lys Thr Ile Thr Phe	
25 30 35	

agc act ccg gat gaa aac ccc atc agt ggt gac tac gct cca agc aat	259
Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp Tyr Ala Pro Ser Asn	
40 45 50	

ggg gcc acc gtg ggc gtc ggt gac gtt aag tta tct gca cga gca agt	307
Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu Ser Ala Arg Ala Ser	
55 60 65	
gat cca agt ggc gat act gtc aag atg acg ttc ctg gaa gcc gat tca	355
Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe Leu Glu Ala Asp Ser	
70 75 80 85	
cca aaa tta gat agt ggt cgc gtc cga atg tca tca gga acg gta gaa	403
Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser Ser Gly Thr Val Glu	
90 95 100	
gat gcc gga agt gtc tcg cgc gcc gag gcg aaa atg ttg gag agg gga	451
Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys Met Leu Glu Arg Gly	
105 110 115	
gac gtc gag aag cta tcc agc ctg gat ggg ctg ggc atg gaa gtt acc	499
Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu Gly Met Glu Val Thr	
120 125 130	
tcc gac gcc gca ctg ccg tac cag ctt ttt gaa gtc gat gcg gcg gat	547
Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu Val Asp Ala Ala Asp	
135 140 145	
gca ctc gcg gcc gac act gaa gtg cgc ctg aat tgg gcg gga tcc gcc	595
Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn Trp Ala Gly Ser Ala	
150 155 160 165	
gat ggt cgc gcg cag gtg atc atg tat gtt ttc gat ggc gag gcg tgg	643
Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe Asp Gly Glu Ala Trp	
170 175 180	
gtt gag gtg gat cgt cac ttg acc ggc gat gag ctg gaa gag ttt acg	691
Val Glu Val Asp Arg His Leu Thr Gly Asp Glu Leu Glu Glu Phe Thr	
185 190 195	
ctg cag ggc gtc gtc aat gcg gaa aaa ttt gca atc ggc ggc act gtc	739
Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala Ile Gly Gly Thr Val	
200 205 210	
acc gta ttg att cag cac tcc gaa ggc ttc gcc ggt gcg gat cat tca	787
Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala Gly Ala Asp His Ser	
215 220 225	
act aga aat tcc gac gtg acc gca gcg cac ccg gat gat gtg gct cgc	835
Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro Asp Asp Val Ala Arg	
230 235 240 245	
tct gag tac gat ttc acc ctc gcg tgg gaa tct gac acc cag tac tac	883
Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser Asp Thr Gln Tyr Tyr	
250 255 260	
aac gag gaa ttc cac gag cac caa acc aac atc cat gac tac gtg ctc	931
Asn Glu Glu Phe His Glu His Gln Thr Asn Ile His Asp Tyr Val Leu	
265 270 275	
gcc gaa cgg gag aac aag aat att cag ttc atg ttc cac act ggc gat	979
Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met Phe His Thr Gly Asp	
280 285 290	

gtt gtc gac gac tgg gat cag ccc gcg cag tgg gcc aca gcc aac ccc	1027
Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp Ala Thr Ala Asn Pro	
295 300 305	
gaa tac cag cgc ctc gac gac gcc ggc ctg cca tat tct gtc ctt gcc	1075
Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro Tyr Ser Val Leu Ala	
310 315 320 325	
gga aac cac gat gtt ggc cac acc agc aat gac tac acc gaa ttc agc	1123
Gly Asn His Asp Val Gly His Thr Ser Asn Asp Tyr Thr Glu Phe Ser	
330 335 340	
cga cac ttc ggc gaa cag cgc tac gta gac aac ccg tgg tac ggc gaa	1171
Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn Pro Trp Tyr Gly Glu	
345 350 355	
tcc tac caa gac aac cga ggg cac tac gat cta ttt tct gcc ggc gga	1219
Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu Phe Ser Ala Gly Gly	
360 365 370	
att gac ttc att aac gta gcg atg ggc tgg ggt cca gac gac gaa gaa	1267
Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly Pro Asp Asp Glu Glu	
375 380 385	
atc gcg tgg atg aac gag gtc ctg gcc aag cat ccc gag cgt gtg gcg	1315
Ile Ala Trp Met Asn Glu Val Leu Ala Lys His Pro Glu Arg Val Ala	
390 395 400 405	
atc ctc aac ctc cac gaa ttc atg ctc acc acc ggc gga ctt ggc ccg	1363
Ile Leu Asn Leu His Glu Phe Met Leu Thr Thr Gly Gly Leu Gly Pro	
410 415 420	
atc ccg cag cgc att ctc gac gag gtc gca gcc acc aac cca aat gtc	1411
Ile Pro Gln Arg Ile Leu Asp Glu Val Ala Ala Thr Asn Pro Asn Val	
425 430 435	
agc atg atc atg tcc ggc cac tac cac gac gca ttc caa cgc acc gac	1459
Ser Met Ile Met Ser Gly His Tyr His Asp Ala Phe Gln Arg Thr Asp	
440 445 450	
tcc ttt gac gac gat ggt gat gga gta gat gac cgc acc gtc acc tct	1507
Ser Phe Asp Asp Asp Gly Asp Gly Val Asp Asp Arg Thr Val Thr Ser	
455 460 465	
atg ctt ttc gat tac caa ggc cta ccg gag ggc gga cag ggg tac ctc	1555
Met Leu Phe Asp Tyr Gln Gly Leu Pro Glu Gly Gly Gln Gly Tyr Leu	
470 475 480 485	
cga ctt ctc cac ttt gat aac caa ggc caa aag atg atg gtg cgc acc	1603
Arg Leu Leu His Phe Asp Asn Gln Gly Gln Lys Met Met Val Arg Thr	
490 495 500	
tat tca cca tcc ctg aag gat tac aac tct gat gaa ccc tca ctg ttg	1651
Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser Leu Leu	
505 510 515	
ggg cct gca gaa gac ccc aac atg tat caa gaa ttc gaa gtg tcc tac	1699
Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val Ser Tyr	
520 525 530	
gag cag ctc ggc atc aaa cca gag ggc cgc acc ctg atc ggc gat tcc	1747

Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly Asp Ser
 535 540 545
 ttc agc gcc gat ttc ttg acc tcc aat gaa att gga ata gtt gat gag 1795
 Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val Asp Glu
 550 555 560 565
 gtt cct tct gga acg atc gct ttc acg aac tgg aag gac gta acc gaa 1843
 Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val Thr Glu
 570 575 580
 ggt cgc cac agt tgg tat gtt cgc tcc gag gat cct ttc ggc ggc gtc 1891
 Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly Gly Val
 585 590 595
 gag att tca ccc gtg cag tcc ttc att gcc ggg gaa gag gct ggc ggg 1939
 Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala Gly Gly
 600 605 610
 aac gcg ccc ggc act gga agc tcc aat ggc ggt tca tcc cac gga tta 1987
 Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His Gly Leu
 615 620 625
 tgg ggt gcg ctt gcg gaa ttc ttt gcc gga gcg gca gcc ctg gct gga 2035
 Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu Ala Gly
 630 635 640 645
 gct gcg atc gca ttt gtc ccc gga att tgg gac tat gtg acc aac gca 2083
 Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr Asn Ala
 650 655 660
 ttc aag cga taattatgga taggtaaacg ctc 2115
 Phe Lys Arg

<210> 906
 <211> 664
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 906
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 His Thr Leu Val Ile Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu
 20 25 30
 Lys Thr Ile Thr Phe Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp
 35 40 45
 Tyr Ala Pro Ser Asn Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu
 50 55 60
 Ser Ala Arg Ala Ser Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe
 65 70 75 80
 Leu Glu Ala Asp Ser Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser
 85 90 95
 Ser Gly Thr Val Glu Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys

100					105					110					
Met	Leu	Glu	Arg	Gly	Asp	Val	Glu	Lys	Leu	Ser	Ser	Leu	Asp	Gly	Leu
	115						120					125			
Gly	Met	Glu	Val	Thr	Ser	Asp	Ala	Ala	Leu	Pro	Tyr	Gln	Leu	Phe	Glu
	130					135					140				
Val	Asp	Ala	Ala	Asp	Ala	Leu	Ala	Ala	Asp	Thr	Glu	Val	Arg	Leu	Asn
145					150					155					160
Trp	Ala	Gly	Ser	Ala	Asp	Gly	Arg	Ala	Gln	Val	Ile	Met	Tyr	Val	Phe
				165					170					175	
Asp	Gly	Glu	Ala	Trp	Val	Glu	Val	Asp	Arg	His	Leu	Thr	Gly	Asp	Glu
			180					185					190		
Leu	Glu	Glu	Phe	Thr	Leu	Gln	Gly	Val	Val	Asn	Ala	Glu	Lys	Phe	Ala
	195						200					205			
Ile	Gly	Gly	Thr	Val	Thr	Val	Leu	Ile	Gln	His	Ser	Glu	Gly	Phe	Ala
	210					215					220				
Gly	Ala	Asp	His	Ser	Thr	Arg	Asn	Ser	Asp	Val	Thr	Ala	Ala	His	Pro
225					230					235					240
Asp	Asp	Val	Ala	Arg	Ser	Glu	Tyr	Asp	Phe	Thr	Leu	Ala	Trp	Glu	Ser
				245					250					255	
Asp	Thr	Gln	Tyr	Tyr	Asn	Glu	Glu	Phe	His	Glu	His	Gln	Thr	Asn	Ile
			260					265					270		
His	Asp	Tyr	Val	Leu	Ala	Glu	Arg	Glu	Asn	Lys	Asn	Ile	Gln	Phe	Met
		275					280					285			
Phe	His	Thr	Gly	Asp	Val	Val	Asp	Asp	Trp	Asp	Gln	Pro	Ala	Gln	Trp
	290					295					300				
Ala	Thr	Ala	Asn	Pro	Glu	Tyr	Gln	Arg	Leu	Asp	Asp	Ala	Gly	Leu	Pro
305					310					315					320
Tyr	Ser	Val	Leu	Ala	Gly	Asn	His	Asp	Val	Gly	His	Thr	Ser	Asn	Asp
				325					330					335	
Tyr	Thr	Glu	Phe	Ser	Arg	His	Phe	Gly	Glu	Gln	Arg	Tyr	Val	Asp	Asn
			340					345					350		
Pro	Trp	Tyr	Gly	Glu	Ser	Tyr	Gln	Asp	Asn	Arg	Gly	His	Tyr	Asp	Leu
		355					360					365			
Phe	Ser	Ala	Gly	Gly	Ile	Asp	Phe	Ile	Asn	Val	Ala	Met	Gly	Trp	Gly
	370					375					380				
Pro	Asp	Asp	Glu	Glu	Ile	Ala	Trp	Met	Asn	Glu	Val	Leu	Ala	Lys	His
385					390					395					400
Pro	Glu	Arg	Val	Ala	Ile	Leu	Asn	Leu	His	Glu	Phe	Met	Leu	Thr	Thr
				405					410					415	
Gly	Gly	Leu	Gly	Pro	Ile	Pro	Gln	Arg	Ile	Leu	Asp	Glu	Val	Ala	Ala
			420					425					430		

Thr Asn Pro Asn Val Ser Met Ile Met Ser Gly His Tyr His Asp Ala
 435 440 445
 Phe Gln Arg Thr Asp Ser Phe Asp Asp Asp Gly Asp Gly Val Asp Asp
 450 455 460
 Arg Thr Val Thr Ser Met Leu Phe Asp Tyr Gln Gly Leu Pro Glu Gly
 465 470 475 480
 Gly Gln Gly Tyr Leu Arg Leu Leu His Phe Asp Asn Gln Gly Gln Lys
 485 490 495
 Met Met Val Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp
 500 505 510
 Glu Pro Ser Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu
 515 520 525
 Phe Glu Val Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr
 530 535 540
 Leu Ile Gly Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile
 545 550 555 560
 Gly Ile Val Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp
 565 570 575
 Lys Asp Val Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp
 580 585 590
 Pro Phe Gly Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly
 595 600 605
 Glu Glu Ala Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly
 610 615 620
 Ser Ser His Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala
 625 630 635 640
 Ala Ala Leu Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp
 645 650 655
 Tyr Val Thr Asn Ala Phe Lys Arg
 660

<210> 907
 <211> 1342
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1342)
 <223> FRXA01945

<400> 907
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 gggcgtgaag agcgtcgaga cgcttctcga cggctaacgc gtg caa ctt cca cta 115

	Val	Gln	Leu	Pro	Leu	
	1				5	
acc acc ggt tcc atc gct ttg gat aaa ggt gaa cag acc ttg gtt atc						163
Thr Thr Gly Ser Ile Ala Leu Asp Lys Gly Glu His Thr Leu Val Ile						
	10				20	
cgt gca gaa gat gaa gta gga aac cgc acc gag aaa acc atc acg ttt						211
Arg Ala Glu Asp Glu Val Gly Asn Arg Thr Glu Lys Thr Ile Thr Phe						
	25				35	
agc act ccg gat gaa aac ccc atc agt ggt gac tac gct cca agc aat						259
Ser Thr Pro Asp Glu Asn Pro Ile Ser Gly Asp Tyr Ala Pro Ser Asn						
	40				50	
ggg gcc acc gtg ggc gtc ggt gac gtt aag tta tct gca cga gca agt						307
Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu Ser Ala Arg Ala Ser						
	55				65	
gat cca agt ggc gat act gtc aag atg acg ttc ctg gaa gcc gat tca						355
Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe Leu Glu Ala Asp Ser						
	70				80	85
cca aaa tta gat agt ggt cgc gtc cga atg tca tca gga acg gta gaa						403
Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser Ser Gly Thr Val Glu						
	90				95	100
gat gcc gga agt gtc tcg cgc gcc gag gcg aaa atg ttg gag agg gga						451
Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys Met Leu Glu Arg Gly						
	105				110	115
gac gtc gag aag cta tcc agc ctg gat ggg ctg ggc atg gaa gtt acc						499
Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu Gly Met Glu Val Thr						
	120				125	130
tcc gac gcc gca ctg ccg tac cag ctt ttt gaa gtc gat gcg gcg gat						547
Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu Val Asp Ala Ala Asp						
	135				140	145
gca ctc gcg gcc gac act gaa gtg cgc ctg aat tgg gcg gga tcc gcc						595
Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn Trp Ala Gly Ser Ala						
	150				155	160
gat ggt cgc gcg cag gtg atc atg tat gtt ttc gat ggc gag gcg tgg						643
Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe Asp Gly Glu Ala Trp						
	170				175	180
gtt gag gtg gat cgt cac ttg acc ggc gat gag ctg gaa gag ttt acg						691
Val Glu Val Asp Arg His Leu Thr Gly Asp Glu Leu Glu Glu Phe Thr						
	185				190	195
ctg cag ggc gtc gtc aat gcg gaa aaa ttt gca atc ggc ggc act gtc						739
Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala Ile Gly Gly Thr Val						
	200				205	210
acc gta ttg att cag cac tcc gaa ggc ttc gcc ggt gcg gat cat tca						787
Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala Gly Ala Asp His Ser						
	215				220	225
act aga aat tcc gac gtg acc gca gcg cac ccg gat gat gtg gct cgc						835
Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro Asp Asp Val Ala Arg						

230	235	240	245	
tct gag tac gat ttc acc ctc gcg tgg gaa tct gac acc cag tac tac				883
Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser Asp Thr Gln Tyr Tyr				
	250	255	260	
aac gag gaa ttc cac gag cac caa acc aac atc cat gac tac gtg ctc				931
Asn Glu Glu Phe His Glu His Gln Thr Asn Ile His Asp Tyr Val Leu				
	265	270	275	
gcc gaa cgg gag aac aag aat att cag ttc atg ttc cac act ggc gat				979
Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met Phe His Thr Gly Asp				
	280	285	290	
gtt gtc gac gac tgg gat cag ccc gcg cag tgg gcc aca gcc aac ccc				1027
Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp Ala Thr Ala Asn Pro				
	295	300	305	
gaa tac cag cgc ctc gac gac gcc ggc ctg cca tat tct gtc ctt gcc				1075
Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro Tyr Ser Val Leu Ala				
	310	315	320	325
gga aac cac gat gtt ggc cac acc agc aat gac tac acc gaa ttc agc				1123
Gly Asn His Asp Val Gly His Thr Ser Asn Asp Tyr Thr Glu Phe Ser				
	330	335	340	
cga cac ttc ggc gaa cag cgc tac gta gac aac ccg tgg tac ggc gaa				1171
Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn Pro Trp Tyr Gly Glu				
	345	350	355	
tcc tac caa gac aac cga ggg cac tac gat cta ttt tct gcc ggc gga				1219
Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu Phe Ser Ala Gly Gly				
	360	365	370	
att gac ttc att aac gta gcg atg ggc tgg ggt cca gac gac gaa gaa				1267
Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly Pro Asp Asp Glu Glu				
	375	380	385	
atc gcg tgg atg aac gag gtc ctg gcc aag cat ccc gag cgt gtg gcg				1315
Ile Ala Trp Met Asn Glu Val Leu Ala Lys His Pro Glu Arg Val Ala				
	390	395	400	405
atc ctc aac ctc cac gaa ttc atg ctc				1342
Ile Leu Asn Leu His Glu Phe Met Leu				
	410			

<210> 908

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 908

Val	Gln	Leu	Pro	Leu	Thr	Thr	Gly	Ser	Ile	Ala	Leu	Asp	Lys	Gly	Glu
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His	Thr	Leu	Val	Ile	Arg	Ala	Glu	Asp	Glu	Val	Gly	Asn	Arg	Thr	Glu
		20						25					30		

Lys	Thr	Ile	Thr	Phe	Ser	Thr	Pro	Asp	Glu	Asn	Pro	Ile	Ser	Gly	Asp
		35					40					45			

Tyr Ala Pro Ser Asn Gly Ala Thr Val Gly Val Gly Asp Val Lys Leu
 50 55 60
 Ser Ala Arg Ala Ser Asp Pro Ser Gly Asp Thr Val Lys Met Thr Phe
 65 70 75 80
 Leu Glu Ala Asp Ser Pro Lys Leu Asp Ser Gly Arg Val Arg Met Ser
 85 90 95
 Ser Gly Thr Val Glu Asp Ala Gly Ser Val Ser Arg Ala Glu Ala Lys
 100 105 110
 Met Leu Glu Arg Gly Asp Val Glu Lys Leu Ser Ser Leu Asp Gly Leu
 115 120 125
 Gly Met Glu Val Thr Ser Asp Ala Ala Leu Pro Tyr Gln Leu Phe Glu
 130 135 140
 Val Asp Ala Ala Asp Ala Leu Ala Ala Asp Thr Glu Val Arg Leu Asn
 145 150 155 160
 Trp Ala Gly Ser Ala Asp Gly Arg Ala Gln Val Ile Met Tyr Val Phe
 165 170 175
 Asp Gly Glu Ala Trp Val Glu Val Asp Arg His Leu Thr Gly Asp Glu
 180 185 190
 Leu Glu Glu Phe Thr Leu Gln Gly Val Val Asn Ala Glu Lys Phe Ala
 195 200 205
 Ile Gly Gly Thr Val Thr Val Leu Ile Gln His Ser Glu Gly Phe Ala
 210 215 220
 Gly Ala Asp His Ser Thr Arg Asn Ser Asp Val Thr Ala Ala His Pro
 225 230 235 240
 Asp Asp Val Ala Arg Ser Glu Tyr Asp Phe Thr Leu Ala Trp Glu Ser
 245 250 255
 Asp Thr Gln Tyr Tyr Asn Glu Glu Phe His Glu His Gln Thr Asn Ile
 260 265 270
 His Asp Tyr Val Leu Ala Glu Arg Glu Asn Lys Asn Ile Gln Phe Met
 275 280 285
 Phe His Thr Gly Asp Val Val Asp Asp Trp Asp Gln Pro Ala Gln Trp
 290 295 300
 Ala Thr Ala Asn Pro Glu Tyr Gln Arg Leu Asp Asp Ala Gly Leu Pro
 305 310 315 320
 Tyr Ser Val Leu Ala Gly Asn His Asp Val Gly His Thr Ser Asn Asp
 325 330 335
 Tyr Thr Glu Phe Ser Arg His Phe Gly Glu Gln Arg Tyr Val Asp Asn
 340 345 350
 Pro Trp Tyr Gly Glu Ser Tyr Gln Asp Asn Arg Gly His Tyr Asp Leu
 355 360 365

Phe Ser Ala Gly Gly Ile Asp Phe Ile Asn Val Ala Met Gly Trp Gly
 370 375 380

Pro Asp Asp Glu Glu Ile Ala Trp Met Asn Glu Val Leu Ala Lys His
 385 390 395 400

Pro Glu Arg Val Ala Ile Leu Asn Leu His Glu Phe Met Leu
 405 410

<210> 909

<211> 518

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(495)

<223> FRXA01627

<400> 909

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 Arg Thr Tyr Ser Pro Ser Leu Lys Asp Tyr Asn Ser Asp Glu Pro Ser
 1 5 10 15

ctg ttg ggg cct gca gaa gac ccc aac atg tat caa gaa ttc gaa gtg 96
 Leu Leu Gly Pro Ala Glu Asp Pro Asn Met Tyr Gln Glu Phe Glu Val
 20 25 30

tcc tac gag cag ctc ggc atc aaa cca gag ggc cgc acc ctg atc ggc 144
 Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly
 35 40 45

gat tcc ttc agc gcc gat ttc ttg acc tcc aat gaa att gga ata gtt 192
 Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val
 50 55 60

gat gag gtt cct tct gga acg atc gct ttc acg aac tgg aag gac gta 240
 Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val
 65 70 75 80

acc gaa ggt cgc cac agt tgg tat gtt cgc tcc gag gat cct ttc ggc 288
 Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly
 85 90 95

ggc gtc gag att tca ccc gtg cag tcc ttc att gcc ggg gaa gag gct 336
 Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala
 100 105 110

ggc ggg aac gcg ccc ggc act gga agc tcc aat ggc ggt tca tcc cac 384
 Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His
 115 120 125

gga tta tgg ggt gcg ctt gcg gaa ttc ttt gcc gga gcg gca gcc ctg 432
 Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu
 130 135 140

gct gga gct gcg atc gca ttt gtc ccc gga att tgg gac tat gtg acc 480
 Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr
 145 150 155 160

aac gca ttc aag cga taattatgga taggtaaacg ctc
 Asn Ala Phe Lys Arg
 165

518

<210> 910
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 910
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 20 25 30
 Ser Tyr Glu Gln Leu Gly Ile Lys Pro Glu Gly Arg Thr Leu Ile Gly
 35 40 45
 Asp Ser Phe Ser Ala Asp Phe Leu Thr Ser Asn Glu Ile Gly Ile Val
 50 55 60
 Asp Glu Val Pro Ser Gly Thr Ile Ala Phe Thr Asn Trp Lys Asp Val
 65 70 75 80
 Thr Glu Gly Arg His Ser Trp Tyr Val Arg Ser Glu Asp Pro Phe Gly
 85 90 95
 Gly Val Glu Ile Ser Pro Val Gln Ser Phe Ile Ala Gly Glu Glu Ala
 100 105 110
 Gly Gly Asn Ala Pro Gly Thr Gly Ser Ser Asn Gly Gly Ser Ser His
 115 120 125
 Gly Leu Trp Gly Ala Leu Ala Glu Phe Phe Ala Gly Ala Ala Ala Leu
 130 135 140
 Ala Gly Ala Ala Ile Ala Phe Val Pro Gly Ile Trp Asp Tyr Val Thr
 145 150 155 160
 Asn Ala Phe Lys Arg
 165

<210> 911
 <211> 441
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(418)
 <223> RXN01960

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 Met Pro Gln His Phe
 1 5

tct caa gaa aac tac aga aag gcc ccc gtc att atg tct gca ccg ctc 163
 Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile Met Ser Ala Pro Leu
 10 15 20

acc att cat gat ctg ctg tcc acc aat tcg aag ctt aac ctc aag tgg 211
 Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys Leu Asn Leu Lys Trp
 25 30 35

ctg acc tgc act gtc ttg aac agc cca aat ctc acc gaa ccc tgc atc 259
 Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu Thr Glu Pro Cys Ile
 40 45 50

acg gtt tct gtg aac cac acc gaa ggc atg tcc ctg gtc tct ttc gaa 307
 Thr Val Ser Val Asn His Thr Glu Gly Met Ser Leu Val Ser Phe Glu
 55 60 65

ggt ggt cac ggg ctc acc gag att gcc aac acc cag cta gtg cct gtg 355
 Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr Gln Leu Val Pro Val
 70 75 80 85

ctt gag cta cca aag ttc aat cct ttt gag gca ctt gct atc cac ctt 403
 Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala Leu Ala Ile His Leu
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 Glu Ala Ala Asn Asn
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 <212> PRT
 <213> Corynebacterium glutamicum

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Met Ser Ala Pro Leu Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys
 20 25 30

Leu Asn Leu Lys Trp Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu
 35 40 45

Thr Glu Pro Cys Ile Thr Val Ser Val Asn His Thr Glu Gly Met Ser
 50 55 60

Leu Val Ser Phe Glu Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr
 65 70 75 80

Gln Leu Val Pro Val Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala
 85 90 95

Leu Ala Ile His Leu Glu Ala Ala Asn Asn
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<222> (101)..(418)

<223> FRXA01960

<400> 913

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                                         Met Pro Gln His Phe
                                         1           5

tct caa gaa aac tac aga aag gcc ccc gtc att atg tct gca ccg ctc 163
Ser Gln Glu Asn Tyr Arg Lys Ala Pro Val Ile Met Ser Ala Pro Leu
              10              15              20

acc att cat gat ctg ctg tcc acc aat tcg aag ctt aac ctc aag tgg 211
Thr Ile His Asp Leu Leu Ser Thr Asn Ser Lys Leu Asn Leu Lys Trp
              25              30              35

ctg acc tgc act gtc ttg aac agc cca aat ctc ccc gaa ccc tgc atc 259
Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu Pro Glu Pro Cys Ile
              40              45              50

acg gtt tct gtg aac cac acc gaa ggc atg tcc ctg gtc tct ttc gaa 307
Thr Val Ser Val Asn His Thr Glu Gly Met Ser Leu Val Ser Phe Glu
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ggt ggt cac ggg ctc acc gag att gcc aac acc cag cta gtg cct gtg 355
Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr Gln Leu Val Pro Val
              70              75              80              85

ctt gag cta cca aag ttc aat cct ttt gag gca ctt gct atc cac ctt 403
Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala Leu Ala Ile His Leu
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<400> 914

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Leu Asn Leu Lys Trp Leu Thr Cys Thr Val Leu Asn Ser Pro Asn Leu
 35           40           45

Pro Glu Pro Cys Ile Thr Val Ser Val Asn His Thr Glu Gly Met Ser
 50           55           60

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Leu Val Ser Phe Glu Gly Gly His Gly Leu Thr Glu Ile Ala Asn Thr
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Gln Leu Val Pro Val Leu Glu Leu Pro Lys Phe Asn Pro Phe Glu Ala
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gttattccgt tgttggtcga gaaagagaga gaaacttttc atg cgt acg tct cgc 115
Met Arg Thr Ser Arg
1 5

gtt cta gcc ggc att ctt gcc gca acc ctg acg gtg tcc ctg gcg gcc 163
Val Leu Ala Gly Ile Leu Ala Ala Thr Leu Thr Val Ser Leu Ala Ala
10 15 20

tgc tcc cag gat tct tca gaa acg tcc tcc aat tcg tct tca gca gca 211
Cys Ser Gln Asp Ser Ser Glu Thr Ser Ser Asn Ser Ser Ser Ala Ala
25 30 35

tcc caa agc tct gac gtt tcc aac gag gcg ttc cct gtc acc att gag 259
Ser Gln Ser Ser Asp Val Ser Asn Glu Ala Phe Pro Val Thr Ile Glu
40 45 50

cac gct ttc ggc gag acc acc att gag tcc aag cca gaa cgc atc gca 307
His Ala Phe Gly Glu Thr Thr Ile Glu Ser Lys Pro Glu Arg Ile Ala
55 60 65

act gtt ggc tgg tcc aac cat gaa gtc cct ctg gca ttg ggt gtg act 355
Thr Val Gly Trp Ser Asn His Glu Val Pro Leu Ala Leu Gly Val Thr
70 75 80 85

cct gtc ggc ttt gag aag gtc acg tgg ggc gac gat gac aac aac ggc 403
Pro Val Gly Phe Glu Lys Val Thr Trp Gly Asp Asp Asp Asn Asn Gly
90 95 100

atc ttg cca tgg gtg gaa gaa acc ttg agc aag ctg ggc tcc gat gag 451
Ile Leu Pro Trp Val Glu Glu Thr Leu Ser Lys Leu Gly Ser Asp Glu
105 110 115

cct gtg ctt ttc gat gcc acc gat tcc att cct ttt gag gag atc gcc 499
Pro Val Leu Phe Asp Ala Thr Asp Ser Ile Pro Phe Glu Glu Ile Ala
120 125 130

aac act gct ccg gat gtc att ttg gcg tcc tac tct ggc atc acc cag 547
Asn Thr Ala Pro Asp Val Ile Leu Ala Ser Tyr Ser Gly Ile Thr Gln

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Glu Asp Tyr Asp Gln Leu Ser Gln Ile Ala Pro Val Val Ala Tyr Pro			
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gaa atc gca tgg ggc acc tcc ctg gat gaa atg att gag atg aac tct			643
Glu Ile Ala Trp Gly Thr Ser Leu Asp Glu Met Ile Glu Met Asn Ser			
	170	175	180
aag gcg att ggc ttg gag caa gaa ggc aag gat ctc atc gca gat ctg			691
Lys Ala Ile Gly Leu Glu Gln Glu Gly Lys Asp Leu Ile Ala Asp Leu			
	185	190	195
gat gca gag gtt gct tcc gcc atc gat gcc aac cca gag ttg aag gat			739
Asp Ala Glu Val Ala Ser Ala Ile Asp Ala Asn Pro Glu Leu Lys Asp			
	200	205	210
gcg aag cct gta ttc gcg ttc ttc gat gag agc gat ttc tcg cag att			787
Ala Lys Pro Val Phe Ala Phe Phe Asp Glu Ser Asp Phe Ser Gln Ile			
	215	220	225
ggt gtg tac acc agc att gat cct cgc atg agc ttc ttg ctt gat gcg			835
Gly Val Tyr Thr Ser Ile Asp Pro Arg Met Ser Phe Leu Leu Asp Ala			
	230	235	240
ggt gtc cag gaa gct tca gtc ctc aag gag cac tcc agc cca gat agc			883
Gly Val Gln Glu Ala Ser Val Leu Lys Glu His Ser Ser Pro Asp Ser			
	250	255	260
ttc tac gag cag gtt tct gca gaa aac cct gaa acc ttc gac gat gtt			931
Phe Tyr Glu Gln Val Ser Ala Glu Asn Pro Glu Thr Phe Asp Asp Val			
	265	270	275
gat gtg atc atc acc tac ggc acc gaa gat gat gct gca aac gct gag			979
Asp Val Ile Ile Thr Tyr Gly Thr Glu Asp Asp Ala Ala Asn Ala Glu			
	280	285	290
ctg ttg tcc aag atg cag gct gat cca ctg ctg tct cga atc cca gct			1027
Leu Leu Ser Lys Met Gln Ala Asp Pro Leu Leu Ser Arg Ile Pro Ala			
	295	300	305
atc gcc gag ggc aag gtt gtg ttc ttg ggt gct aac cca ctg gct gct			1075
Ile Ala Glu Gly Lys Val Phe Leu Gly Ala Asn Pro Leu Ala Ala			
	310	315	320
tca gcg aat gaa tcc cca cta tct att cct tgg ggt atc aac gat tac			1123
Ser Ala Asn Glu Ser Pro Leu Ser Ile Pro Trp Gly Ile Asn Asp Tyr			
	330	335	340
ttt gca aaa ctc gcc gaa cct ctg aag taaaactgct tgatgtcaac			1170
Phe Ala Lys Leu Ala Glu Pro Leu Lys			
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aac			1173

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<212> PRT

<213> Corynebacterium glutamicum

<400> 916

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 Ser Ser Ser Ala Ala Ser Gln Ser Ser Asp Val Ser Asn Glu Ala Phe
 35 40 45
 Pro Val Thr Ile Glu His Ala Phe Gly Glu Thr Thr Ile Glu Ser Lys
 50 55 60
 Pro Glu Arg Ile Ala Thr Val Gly Trp Ser Asn His Glu Val Pro Leu
 65 70 75 80
 Ala Leu Gly Val Thr Pro Val Gly Phe Glu Lys Val Thr Trp Gly Asp
 85 90 95
 Asp Asp Asn Asn Gly Ile Leu Pro Trp Val Glu Glu Thr Leu Ser Lys
 100 105 110
 Leu Gly Ser Asp Glu Pro Val Leu Phe Asp Ala Thr Asp Ser Ile Pro
 115 120 125
 Phe Glu Glu Ile Ala Asn Thr Ala Pro Asp Val Ile Leu Ala Ser Tyr
 130 135 140
 Ser Gly Ile Thr Gln Glu Asp Tyr Asp Gln Leu Ser Gln Ile Ala Pro
 145 150 155 160
 Val Val Ala Tyr Pro Glu Ile Ala Trp Gly Thr Ser Leu Asp Glu Met
 165 170 175
 Ile Glu Met Asn Ser Lys Ala Ile Gly Leu Glu Gln Glu Gly Lys Asp
 180 185 190
 Leu Ile Ala Asp Leu Asp Ala Glu Val Ala Ser Ala Ile Asp Ala Asn
 195 200 205
 Pro Glu Leu Lys Asp Ala Lys Pro Val Phe Ala Phe Phe Asp Glu Ser
 210 215 220
 Asp Phe Ser Gln Ile Gly Val Tyr Thr Ser Ile Asp Pro Arg Met Ser
 225 230 235 240
 Phe Leu Leu Asp Ala Gly Val Gln Glu Ala Ser Val Leu Lys Glu His
 245 250 255
 Ser Ser Pro Asp Ser Phe Tyr Glu Gln Val Ser Ala Glu Asn Pro Glu
 260 265 270
 Thr Phe Asp Asp Val Asp Val Ile Ile Thr Tyr Gly Thr Glu Asp Asp
 275 280 285
 Ala Ala Asn Ala Glu Leu Leu Ser Lys Met Gln Ala Asp Pro Leu Leu
 290 295 300
 Ser Arg Ile Pro Ala Ile Ala Glu Gly Lys Val Val Phe Leu Gly Ala
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Asn Pro Leu Ala Ala Ser Ala Asn Glu Ser Pro Leu Ser Ile Pro Trp
325 330 335

Gly Ile Asn Asp Tyr Phe Ala Lys Leu Ala Glu Pro Leu Lys
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<223> RXN01987

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Met Thr Phe Pro Ala
1 5

caa tct cga cga ctc gcc cga agc acc acc gac aaa tgg atc ggc ggc 163
Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp Lys Trp Ile Gly Gly
10 15 20

gtc gct ggt ggc ctc gca gag acc tac ggt tgg aat ccg gcc tat gtg 211
Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp Asn Pro Ala Tyr Val
25 30 35

cgt ctc gcg ttc gtg gcg tcg gtt ctg ttt cca ctg cca ggt tca cag 259
Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro Leu Pro Gly Ser Gln
40 45 50

atc ctg ttc tac gcc cta gcg tgg ctg atc atc cca tcc cga gaa aat 307
Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile Pro Ser Arg Glu Asn
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Arg Phe
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<212> PRT
<213> Corynebacterium glutamicum

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Asn Pro Ala Tyr Val Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro
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Pro Ser Arg Glu Asn Arg Phe
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 Met Thr Phe Pro Ala
 1 5
 caa tct cga cga ctc gcc cga agc acc acc gac aaa tgg atc ggc ggc 163
 Gln Ser Arg Arg Leu Ala Arg Ser Thr Thr Asp Lys Trp Ile Gly Gly
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 Val Ala Gly Gly Leu Ala Glu Thr Tyr Gly Trp Asn Pro Ala Tyr Val
 25 30 35
 cgt ctc gcg ttc gtg gcg tcg gtt ctg ttt cca ctg cca ggt tca cag 259
 Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro Leu Pro Gly Ser Gln
 40 45 50
 atc ctg ttc tac gcc cta gcg tgg ctg atc atc cca tcc cga gaa aat 307
 Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile Pro Ser Arg Glu Asn
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 Arg Phe
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 Asn Pro Ala Tyr Val Arg Leu Ala Phe Val Ala Ser Val Leu Phe Pro
 35 40 45
 Leu Pro Gly Ser Gln Ile Leu Phe Tyr Ala Leu Ala Trp Leu Ile Ile

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55

60

Pro Ser Arg Glu Asn Arg Phe
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<212> DNA
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gccccctagtt gttgcgaata tttatagatt gttgagaaag atg aac atg aag acg 115
Met Asn Met Lys Thr
1 5

cac ccg gct tcc gcc aag cag acc acc gag ctt cga ctc ctg aca gcc 163
His Pro Ala Ser Ala Lys Gln Thr Thr Glu Leu Arg Leu Leu Thr Ala
10 15 20

acc gtg tac ttc aaa gca ctc aat gaa gtc cac aac gtc atg cag atg 211
Thr Val Tyr Phe Lys Ala Leu Asn Glu Val His Asn Val Met Gln Met
25 30 35

atc gac cca cta act cca gtc gtt ccc atc acc acg ggc acc tca gtt 259
Ile Asp Pro Leu Thr Pro Val Val Pro Ile Thr Thr Gly Thr Ser Val
40 45 50

gcc gag ctt tat gct gac gcc cgc gag cac ctc gac aat ggt gca acc 307
Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala Thr
55 60 65

cag gtg atg atc ccc gtc att tca cct tcc aac ctg acc ttg tca gta 355
Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser Val
70 75 80 85

gtt gcc ctg ggc aat gaa gag gtt gac gca ctg ggc cat tcc gaa gga 403
Val Ala Leu Gly Asn Glu Glu Val Asp Ala Leu Gly His Ser Glu Gly
90 95 100

caa gca gtt cac tcc ctt ctg gaa att cat acc ccg aag cgc agc tgg 451
Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser Trp
105 110 115

cct ctt tcc gag ctt tat att gat gac aat gag ggt ttg gct cag gtg 499
Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln Val
120 125 130

tcg cgc tgc ttc gcc cgc ctt gtt ggc tagtcccacc ccaccaattg 546
Ser Arg Cys Phe Ala Arg Leu Val Gly
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cat 549

<210> 922
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 922
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 35 40 45
 Thr Gly Thr Ser Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu
 50 55 60
 Asp Asn Gly Ala Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn
 65 70 75 80
 Leu Thr Leu Ser Val Val Ala Leu Gly Asn Glu Glu Val Asp Ala Leu
 85 90 95
 Gly His Ser Glu Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr
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 Pro Lys Arg Ser Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu
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 <212> DNA
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 Val Ala Glu Leu Tyr Ala Asp Ala Arg Glu His Leu Asp Asn Gly Ala
 20 25 30
 acc cag gtg atg atc ccc gtc att tca cct tcc aac ctg acc ttg tca 144
 Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser
 35 40 45
 gta gtt gcc ctg ggc aat caa gag gtt gac gca ctg ggc cat tcc gaa 192
 Val Val Ala Leu Gly Asn Gln Glu Val Asp Ala Leu Gly His Ser Glu
 50 55 60

gga caa gca gtt cac tcc ctt ctg gaa att cat acc ccg aag cgc agc 240
 Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser
 65 70 75 80
 tgg cct ctt tcc gag ctt tat att gat gac aat gag ggt ttg gct cag 288
 Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln
 85 90 95
 gtg tgc cgc tgc ttc gcc cgc ctt gtt ggc tagtcccacc ccaccaattg 338
 Val Ser Arg Cys Phe Ala Arg Leu Val Gly
 100 105
 cat 341

<210> 924
 <211> 106
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 924
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 20 25 30
 Thr Gln Val Met Ile Pro Val Ile Ser Pro Ser Asn Leu Thr Leu Ser
 35 40 45
 Val Val Ala Leu Gly Asn Gln Glu Val Asp Ala Leu Gly His Ser Glu
 50 55 60
 Gly Gln Ala Val His Ser Leu Leu Glu Ile His Thr Pro Lys Arg Ser
 65 70 75 80
 Trp Pro Leu Ser Glu Leu Tyr Ile Asp Asp Asn Glu Gly Leu Ala Gln
 85 90 95
 Val Ser Arg Cys Phe Ala Arg Leu Val Gly
 100 105

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 <222> (101)..(973)
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 Met Thr Asn Leu Leu
 1 5

ccg cat ttc ccg agt acc gac gta gct gcg tgg gaa cca acc gtt gtg	163
Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp Glu Pro Thr Val Val	
10 15 20	
tat tca gcg gat aag acc aca gca aca gcg acg ttt aag aat att cct	211
Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr Phe Lys Asn Ile Pro	
25 30 35	
tcg gat att tcc ttt agt tgg act ggt att gaa gca cta gag cca ttt	259
Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu Ala Leu Glu Pro Phe	
40 45 50	
agc cct ggt aaa acc ttc gaa cat aag gtg caa ggt tct gtt ggt gaa	307
Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln Gly Ser Val Gly Glu	
55 60 65	
cca gcg ggg gcg ttc act agg gat aac tat ttc act gag ggt gag ctc	355
Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe Thr Glu Gly Glu Leu	
70 75 80 85	
tac aaa cat cgc cac gca gac gat ctg ctt tcc ggt gat ggc ttg ttt	403
Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser Gly Asp Gly Leu Phe	
90 95 100	
ggc ccc aac atc acc gat ggc gat ggc aac ctc ccc tct gtt gat gac	451
Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu Pro Ser Val Asp Asp	
105 110 115	
ggc aag gac ggt gac gat ggg tct gat ggc tca gac ggc cga gac ggt	499
Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser Asp Gly Arg Asp Gly	
120 125 130	
gtt gtc gcc att gat gtt gtt gac aat gct gac ggc acg gtg act gtc	547
Val Val Ala Ile Asp Val Val Asp Asn Ala Asp Gly Thr Val Thr Val	
135 140 145	
acc ttg tcc gat ggc act acg ttt act ctt gat gct ggt caa gac ggc	595
Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp Ala Gly Gln Asp Gly	
150 155 160 165	
aaa gat ggt ctt gac ggg ctt gat ggt act ggc cta acg ctg gaa tct	643
Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly Leu Thr Leu Glu Ser	
170 175 180	
gct acc cct gat gag gac ggc aac atc acc tat gtt ctt tct gac ggt	691
Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr Val Leu Ser Asp Gly	
185 190 195	
act gag ttc act gtg cgc aac ggt gtt gat ggg tca gac ggt aag gac	739
Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly Ser Asp Gly Lys Asp	
200 205 210	
ggc aaa gat gga gtc aat ggc aca gat ggc gta gac ggg tca gac ggt	787
Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val Asp Gly Ser Asp Gly	
215 220 225	
aaa ggt ctg gta gag gtg tcc cga gtt acc aac gac aac ggc tca gtg	835
Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn Asp Asn Gly Ser Val	
230 235 240 245	
acc att acc tac gag gac ggt tca cag atc acc acg aag cca acg ccg	883

Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr Thr Lys Pro Thr Pro
 250 255 260
 aca aac tgg ctg tcc aag ctg ctt gat ttg ctt ctc ccg ctg ttt aat 931
 Thr Asn Trp Leu Ser Lys Leu Leu Asp Leu Leu Leu Pro Leu Phe Asn
 265 270 275
 ctg ttc ggt ctt ggt ggc ggc tcc gtc att agt tcc agt aag 973
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 280 285 290
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<210> 926

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 926

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 20 25 30
 Phe Lys Asn Ile Pro Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu
 35 40 45
 Ala Leu Glu Pro Phe Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln
 50 55 60
 Gly Ser Val Gly Glu Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe
 65 70 75 80
 Thr Glu Gly Glu Leu Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser
 85 90 95
 Gly Asp Gly Leu Phe Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu
 100 105 110
 Pro Ser Val Asp Asp Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser
 115 120 125
 Asp Gly Arg Asp Gly Val Val Ala Ile Asp Val Val Asp Asn Ala Asp
 130 135 140
 Gly Thr Val Thr Val Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp
 145 150 155 160
 Ala Gly Gln Asp Gly Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly
 165 170 175
 Leu Thr Leu Glu Ser Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr
 180 185 190
 Val Leu Ser Asp Gly Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly
 195 200 205
 Ser Asp Gly Lys Asp Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val
 210 215 220

Asp Gly Ser Asp Gly Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn
 225 230 235 240
 Asp Asn Gly Ser Val Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr
 245 250 255
 Thr Lys Pro Thr Pro Thr Asn Trp Leu Ser Lys Leu Leu Asp Leu Leu
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 Ser Ser Lys
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<210> 927
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 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(895)
 <223> FRXA01991

<400> 927
 tccggagggtg gatttgagga tttcgacggtt ttctcggaag ttccctcggt agaggaaaca 60
 tcgacgagga tcagctattc ttacaaaaat tcatttgaat atg acg aat ttg ttg 115
 Met Thr Asn Leu Leu
 1 5
 ccg cat ttc ccg agt acc gac gta gct gcg tgg gaa cca acc gtt gtg 163
 Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp Glu Pro Thr Val Val
 10 15 20
 tat tca gcg gat aag acc aca gca aca gcg acg ttt aag aat att cct 211
 Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr Phe Lys Asn Ile Pro
 25 30 35
 tcg gat att tcc ttt agt tgg act ggt att gaa gca cta gag cca ttt 259
 Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu Ala Leu Glu Pro Phe
 40 45 50
 agc cct ggt aaa acc ttc gaa cat aag gtg caa ggt tct gtt ggt gaa 307
 Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln Gly Ser Val Gly Glu
 55 60 65
 cca gcg ggg gcg ttc act agg gat aac tat ttc act gag ggt gag ctc 355
 Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe Thr Glu Gly Glu Leu
 70 75 80 85
 tac aaa cat cgc cac gca gac gat ctg ctt tcc ggt gat ggc ttg ttt 403
 Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser Gly Asp Gly Leu Phe
 90 95 100
 ggc ccc aac atc acc gat ggc gat ggc aac ctc ccc tct gtt gat gac 451
 Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu Pro Ser Val Asp Asp
 105 110 115

ggc aag gac ggt gac gat ggg tct gat ggc tca gac ggc cga gac ggt 499
 Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser Asp Gly Arg Asp Gly
 120 125 130
 gtt gtc gcc att gat gtt gtt gac aat gct gac ggc acg gtg act gtc 547
 Val Val Ala Ile Asp Val Val Asp Asn Ala Asp Gly Thr Val Thr Val
 135 140 145
 acc ttg tcc gat ggc act acg ttt act ctt gat gct ggt caa gac ggc 595
 Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp Ala Gly Gln Asp Gly
 150 155 160 165
 aaa gat ggt ctt gac ggg ctt gat ggt act ggc cta acg ctg gaa tct 643
 Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly Leu Thr Leu Glu Ser
 170 175 180
 gct acc cct gat gag gac ggc aac atc acc tat gtt ctt tct gac ggt 691
 Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr Val Leu Ser Asp Gly
 185 190 195
 act gag ttc act gtg cgc aac ggt gtt gat ggg tca gac ggt aag gac 739
 Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly Ser Asp Gly Lys Asp
 200 205 210
 ggc aaa gat gga gtc aat ggc aca gat ggc gta gac ggc tca gac ggt 787
 Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val Asp Gly Ser Asp Gly
 215 220 225
 aaa ggt ctg gta gag gtg tcc cga gtt acc aac gac aac ggc tca gtg 835
 Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn Asp Asn Gly Ser Val
 230 235 240 245
 acc att acc tac gag gac ggt tca cag atc acc acg aag cca acg ccg 883
 Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr Thr Lys Pro Thr Pro
 250 255 260
 aca aac tgg ctg 895
 Thr Asn Trp Leu
 265

<210> 928

<211> 265

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 928

Met Thr Asn Leu Leu Pro His Phe Pro Ser Thr Asp Val Ala Ala Trp
 1 5 10 15

Glu Pro Thr Val Val Tyr Ser Ala Asp Lys Thr Thr Ala Thr Ala Thr
 20 25 30

Phe Lys Asn Ile Pro Ser Asp Ile Ser Phe Ser Trp Thr Gly Ile Glu
 35 40 45

Ala Leu Glu Pro Phe Ser Pro Gly Lys Thr Phe Glu His Lys Val Gln
 50 55 60

Gly Ser Val Gly Glu Pro Ala Gly Ala Phe Thr Arg Asp Asn Tyr Phe

65	70	75	80
Thr Glu Gly Glu Leu Tyr Lys His Arg His Ala Asp Asp Leu Leu Ser	85	90	95
Gly Asp Gly Leu Phe Gly Pro Asn Ile Thr Asp Gly Asp Gly Asn Leu	100	105	110
Pro Ser Val Asp Asp Gly Lys Asp Gly Asp Asp Gly Ser Asp Gly Ser	115	120	125
Asp Gly Arg Asp Gly Val Val Ala Ile Asp Val Val Asp Asn Ala Asp	130	135	140
Gly Thr Val Thr Val Thr Leu Ser Asp Gly Thr Thr Phe Thr Leu Asp	145	150	155
Ala Gly Gln Asp Gly Lys Asp Gly Leu Asp Gly Leu Asp Gly Thr Gly	165	170	175
Leu Thr Leu Glu Ser Ala Thr Pro Asp Glu Asp Gly Asn Ile Thr Tyr	180	185	190
Val Leu Ser Asp Gly Thr Glu Phe Thr Val Arg Asn Gly Val Asp Gly	195	200	205
Ser Asp Gly Lys Asp Gly Lys Asp Gly Val Asn Gly Thr Asp Gly Val	210	215	220
Asp Gly Ser Asp Gly Lys Gly Leu Val Glu Val Ser Arg Val Thr Asn	225	230	235
Asp Asn Gly Ser Val Thr Ile Thr Tyr Glu Asp Gly Ser Gln Ile Thr	245	250	255
Thr Lys Pro Thr Pro Thr Asn Trp Leu	260	265	

<210> 929

<211> 660

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(637)

<223> RXN01996

<400> 929

ctagtataga acggaacacg gcagcgacac aaactgcaca gatgcaagag tgtcggtacc 60

gttaaaaacg aaacacactt tcaccgaaaa ggacttccca atg agc aag ttg act	115
Met Ser Lys Leu Thr	
1 5	

ggc acc tgg acc ctc gac cct gca cac acc gaa atc aag ttc gtg gct	163
Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu Ile Lys Phe Val Ala	
10 15 20	

cgc cac gca atg gtt acc aag gtt cgc ggt gaa ttc acc gag tac acc	211
---	-----

Arg His Ala Met Val Thr Lys Val Arg Gly Glu Phe Thr Glu Tyr Thr
 25 30 35
 gac tcc att gtc gta gat gct gaa aac cca gag aac tcc tct gca aag 259
 Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu Asn Ser Ser Ala Lys
 40 45 50
 gtt gtt atc aag acc gct tcc gtt acc acc ggc aac gca gac cgc gat 307
 Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly Asn Ala Asp Arg Asp
 55 60 65
 gca cac gtt aag ggc gac gac ttc ttc gca gta gac aag ttc cct gaa 355
 Ala His Val Lys Gly Asp Asp Phe Phe Ala Val Asp Lys Phe Pro Glu
 70 75 80 85
 atg act ttc gaa gct act tcc ttt gtt atc aag aac gaa aac gaa ggc 403
 Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys Asn Glu Asn Glu Gly
 90 95 100
 acc gtt acc ggc gac ctc aca att cgt gac acc acc aag tcc gtc acc 451
 Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr Thr Lys Ser Val Thr
 105 110 115
 ctg gac gtt gag gtt ggt ggc gtt gct gag gat cca ttc ggc aac acc 499
 Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp Pro Phe Gly Asn Thr
 120 125 130
 cgc ctt ggc ttc gaa gcc tcc acc gaa atc aac cgc aag gac ttc ggc 547
 Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn Arg Lys Asp Phe Gly
 135 140 145
 gta gat ttc cag gct cca ctc tcc acc ggt ggc gtt ctg gtt tct gag 595
 Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly Val Leu Val Ser Glu
 150 155 160 165
 aag atc aag atc gag atc gac ggc tcc gca atc aag gct gct 637
 Lys Ile Lys Ile Glu Ile Asp Gly Ser Ala Ile Lys Ala Ala
 170 175
 taagcgccca caaacaacaaa gcc 660

<210> 930

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 930

Met Ser Lys Leu Thr Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu
 1 5 10 15
 Ile Lys Phe Val Ala Arg His Ala Met Val Thr Lys Val Arg Gly Glu
 20 25 30
 Phe Thr Glu Tyr Thr Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu
 35 40 45
 Asn Ser Ser Ala Lys Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly
 50 55 60
 Asn Ala Asp Arg Asp Ala His Val Lys Gly Asp Asp Phe Phe Ala Val

65		70		75		80									
Asp	Lys	Phe	Pro	Glu	Met	Thr	Phe	Glu	Ala	Thr	Ser	Phe	Val	Ile	Lys
				85					90					95	
Asn	Glu	Asn	Glu	Gly	Thr	Val	Thr	Gly	Asp	Leu	Thr	Ile	Arg	Asp	Thr
			100					105					110		
Thr	Lys	Ser	Val	Thr	Leu	Asp	Val	Glu	Val	Gly	Gly	Val	Ala	Glu	Asp
		115					120					125			
Pro	Phe	Gly	Asn	Thr	Arg	Leu	Gly	Phe	Glu	Ala	Ser	Thr	Glu	Ile	Asn
	130					135					140				
Arg	Lys	Asp	Phe	Gly	Val	Asp	Phe	Gln	Ala	Pro	Leu	Ser	Thr	Gly	Gly
145					150					155					160
Val	Leu	Val	Ser	Glu	Lys	Ile	Lys	Ile	Glu	Ile	Asp	Gly	Ser	Ala	Ile
				165					170					175	

Lys Ala Ala

<210> 931
 <211> 647
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (88)..(624)
 <223> FRXA01996

<400> 931
 gaacacggca gcgacacaaa ctgcacagat gcaagagtgt cggtaccgtt aaaaacgaaa 60
 cacactttca ccgaaaagga cttccca atg agc aag ttg act ggc acc tgg acc 114
 Met Ser Lys Leu Thr Gly Thr Trp Thr
 1 5
 ctc gac cct gca cac acc gaa atc aag ttc gtg gct cgc cac gca atg 162
 Leu Asp Pro Ala His Thr Glu Ile Lys Phe Val Ala Arg His Ala Met
 10 15 20 25
 gtt acc aag gtt cgc ggt gaa ttc acc gag tac acc gac tcc att gtc 210
 Val Thr Lys Val Arg Gly Glu Phe Thr Glu Tyr Thr Asp Ser Ile Val
 30 35 40
 gta gat gct gaa aac cca gag aac tcc tct gca aag gtt gtt atc aag 258
 Val Asp Ala Glu Asn Pro Glu Asn Ser Ser Ala Lys Val Val Ile Lys
 45 50 55
 acc gct tcc gtt acc acc ggc aac gca gac cgc gat gca cac gtt aag 306
 Thr Ala Ser Val Thr Thr Gly Asn Ala Asp Arg Asp Ala His Val Lys
 60 65 70
 ggc gac gac ttc ttc gca gta gac aag ttc cct gaa atg act ttc gaa 354
 Gly Asp Asp Phe Phe Ala Val Asp Lys Phe Pro Glu Met Thr Phe Glu
 75 80 85

gct act tcc ttt gtt atc aag aac gaa aac gaa ggc acc gtt acc ggc 402
 Ala Thr Ser Phe Val Ile Lys Asn Glu Asn Glu Gly Thr Val Thr Gly
 90 95 100 105
 gac ctc aca att cgt gac acc acc aag tcc gtc acc ctg gac gtt gag 450
 Asp Leu Thr Ile Arg Asp Thr Thr Lys Ser Val Thr Leu Asp Val Glu
 110 115 120
 gtt ggt ggc gtt gct gag gat cca ttc ggc aac acc cgc ctt ggc ttc 498
 Val Gly Gly Val Ala Glu Asp Pro Phe Gly Asn Thr Arg Leu Gly Phe
 125 130 135
 gaa gcc tcc acc gaa atc aac cgc aag gac ttc ggc gta gat ttc cag 546
 Glu Ala Ser Thr Glu Ile Asn Arg Lys Asp Phe Gly Val Asp Phe Gln
 140 145 150
 gct cca ctc tcc acc ggt ggc gtt ctg gtt tct gag aag atc aag atc 594
 Ala Pro Leu Ser Thr Gly Gly Val Leu Val Ser Glu Lys Ile Lys Ile
 155 160 165
 gag atc gac ggc tcc gca atc aag gct gct taagcgccca caaacaaaaa 644
 Glu Ile Asp Gly Ser Ala Ile Lys Ala Ala
 170 175
 gcc 647

<210> 932
 <211> 179
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 932
 Met Ser Lys Leu Thr Gly Thr Trp Thr Leu Asp Pro Ala His Thr Glu
 1 5 10 15
 Ile Lys Phe Val Ala Arg His Ala Met Val Thr Lys Val Arg Gly Glu
 20 25 30
 Phe Thr Glu Tyr Thr Asp Ser Ile Val Val Asp Ala Glu Asn Pro Glu
 35 40 45
 Asn Ser Ser Ala Lys Val Val Ile Lys Thr Ala Ser Val Thr Thr Gly
 50 55 60
 Asn Ala Asp Arg Asp Ala His Val Lys Gly Asp Asp Phe Phe Ala Val
 65 70 75 80
 Asp Lys Phe Pro Glu Met Thr Phe Glu Ala Thr Ser Phe Val Ile Lys
 85 90 95
 Asn Glu Asn Glu Gly Thr Val Thr Gly Asp Leu Thr Ile Arg Asp Thr
 100 105 110
 Thr Lys Ser Val Thr Leu Asp Val Glu Val Gly Gly Val Ala Glu Asp
 115 120 125
 Pro Phe Gly Asn Thr Arg Leu Gly Phe Glu Ala Ser Thr Glu Ile Asn
 130 135 140
 Arg Lys Asp Phe Gly Val Asp Phe Gln Ala Pro Leu Ser Thr Gly Gly

ggc tac tcc gtg atg atg tcc aag gaa gag tac ttg gag cgc caa aag 595
 Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln Lys
 150 155 160 165

gca ctg ggc aag cca gtt cag ttg aac ttc gat gac gac acc gat ggg 643
 Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp Gly
 170 175 180

aat aca aca caa aca gaa agc gtt gaa tcc caa gag acc gga caa gcc 691
 Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln Ala
 185 190 195

gcg tct gaa acc tca cat cgt gat aac cct gcg tca cag cac 733
 Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
 200 205 210

tagagtgtaa taagccgtcc gaa 756

<210> 934

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 934

Met Ser Ser Asp Ala Glu Lys Ala Ser Val Glu Leu Ser Glu Lys Phe
 1 5 10 15

His Pro Glu Arg Thr His Ile Leu Gly Ala Val Val Phe Gly Leu Ile
 20 25 30

Ser Leu Leu Val Ile Gly Ala Ala Pro Gln Tyr Leu Phe Trp Leu Leu
 35 40 45

Ala Leu Pro Val Ile Phe Gly Tyr Trp Val Leu Lys Ser Ser Thr Ile
 50 55 60

Val Asp Glu Gln Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys
 65 70 75 80

Val Val Ala Trp Glu Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg
 85 90 95

Thr Phe Ala Arg Thr Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val
 100 105 110

Thr Phe Asn Ser Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile
 115 120 125

Pro Asp Ala Ile Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val
 130 135 140

Val Val Gln Glu Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr
 145 150 155 160

Leu Glu Arg Gln Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp
 165 170 175

Asp Asp Thr Asp Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln
 180 185 190

Glu Thr Gly Gln Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala
 195 200 205

Ser Gln His
 210

<210> 935
 <211> 452
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(429)
 <223> FRXA02007

<400> 935
 ggc atc acc gca aac tac gcc ttc aag ggc aaa aag gtt gtg gct tgg 48
 Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp
 1 5 10 15
 aaa gac ctc gca gga atc gga ttc aag ggt gcc cgc act ttc gct cgc 96
 Lys Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg
 20 25 30
 ccc acc tcc gat gca gaa gtc acc ctc ccg ggc gtc acc ttc aac tcc 144
 Pro Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser
 35 40 45
 ctt ccc cgc ctt gaa gct gct tcc cac ggc cgc atc ccc gat gcg atc 192
 Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile
 50 55 60
 acc gca agc aag gaa gca gcc gac ggc aag gtt gta gtc gtt caa gaa 240
 Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu
 65 70 75 80
 gac ggc tac tcc gtg atg atg tcc aag gaa gag tac ttg gag cgc caa 288
 Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln
 85 90 95
 aag gca ctg ggc aag cca gtt cag ttg aac ttc gat gac gac acc gat 336
 Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp
 100 105 110
 ggg aat aca aca caa aca gaa agc gtt gaa tcc caa gag acc gga caa 384
 Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln
 115 120 125
 gcc gcg tct gaa acc tca cat cgt gat aac cct gcg tca cag cac 429
 Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
 130 135 140
 tagagtgtaa taagccgtcc gaa 452

<210> 936
 <211> 143
 <212> PRT

<213> Corynebacterium glutamicum

<400> 936

Gly Ile Thr Ala Asn Tyr Ala Phe Lys Gly Lys Lys Val Val Ala Trp
 1 5 10 15

Lys Asp Leu Ala Gly Ile Gly Phe Lys Gly Ala Arg Thr Phe Ala Arg
 20 25 30

Pro Thr Ser Asp Ala Glu Val Thr Leu Pro Gly Val Thr Phe Asn Ser
 35 40 45

Leu Pro Arg Leu Glu Ala Ala Ser His Gly Arg Ile Pro Asp Ala Ile
 50 55 60

Thr Ala Ser Lys Glu Ala Ala Asp Gly Lys Val Val Val Val Gln Glu
 65 70 75 80

Asp Gly Tyr Ser Val Met Met Ser Lys Glu Glu Tyr Leu Glu Arg Gln
 85 90 95

Lys Ala Leu Gly Lys Pro Val Gln Leu Asn Phe Asp Asp Asp Thr Asp
 100 105 110

Gly Asn Thr Thr Gln Thr Glu Ser Val Glu Ser Gln Glu Thr Gly Gln
 115 120 125

Ala Ala Ser Glu Thr Ser His Arg Asp Asn Pro Ala Ser Gln His
 130 135 140

<210> 937

<211> 630

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> RXN02014

<400> 937

agaggacaac aacatgagag cagacgcact aaaacgccgc gaacacatca taaccacaac 60

ctgcaatctc taccgcacac accatcacga ttcgctcacc atg gaa aac att gca 115
 Met Glu Asn Ile Ala
 1 5

gaa cag gca gga gtg ggt gtt gca act tta tac cga aac ttc ccc gat 163
 Glu Gln Ala Gly Val Gly Val Ala Thr Leu Tyr Arg Asn Phe Pro Asp
 10 15 20

cgc ttc aca ctg gac atg gca tgc gcc caa tac ctt ttc aac gtg gtg 211
 Arg Phe Thr Leu Asp Met Ala Cys Ala Gln Tyr Leu Phe Asn Val Val
 25 30 35

atc tcc ctc caa ctc caa gcc atc agc acc ttc ccc acc gac cca gaa 259
 Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
 40 45 50

ggc gtg tgg acc tcc ttc aac caa cta ctt ttc gac cgc ggc cta ggc 307

Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
55 60 65

tcc ctc gtc cca gca ctt gcc cca gaa tcc tta gac gac ctc ccc gac 355
Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
70 75 80 85

gag gtc tcc gcc ctg cgt cgc acc aca gag aaa aac acc aca aca ctc 403
Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
90 95 100

atc aac cta gcc aag cag cac gga ctc gta cac cac gac atc gcg ccg 451
Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
105 110 115

ggc acc tac atc gtc ggt ttg atc acc att tcc cgc cca cct atc acc 499
Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
120 125 130

gcg ctg gcg aca att tca gaa aac tcc cac aaa gca ctg ctt ggc ctt 547
Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
135 140 145

tat ttg tcc ggt ctt aaa cac ggc atg atg gct aac atc gga gaa cat 595
Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
150 155 160 165

gac gga aag tcc tgatctagca gtttcctttt tag 630
Asp Gly Lys Ser

<210> 938

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 938

Met Glu Asn Ile Ala Glu Gln Ala Gly Val Gly Val Ala Thr Leu Tyr
1 5 10 15

Arg Asn Phe Pro Asp Arg Phe Thr Leu Asp Met Ala Cys Ala Gln Tyr
20 25 30

Leu Phe Asn Val Val Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe
35 40 45

Pro Thr Asp Pro Glu Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe
50 55 60

Asp Arg Gly Leu Gly Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu
65 70 75 80

Asp Asp Leu Pro Asp Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys
85 90 95

Asn Thr Thr Thr Leu Ile Asn Leu Ala Lys Gln His Gly Leu Val His
100 105 110

His Asp Ile Ala Pro Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser
115 120 125

Arg Pro Pro Ile Thr Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys
 130 135 140

Ala Leu Leu Gly Leu Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala
 145 150 155 160

Asn Ile Gly Glu His Asp Gly Lys Ser
 165

<210> 939

<211> 419

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(396)

<223> FRXA02014

<400> 939

atc tcc ctc caa ctc caa gcc atc agc acc ttc ccc acc gac cca gaa 48
 Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
 1 5 10 15

ggc gtg tgg acc tcc ttc aac caa cta ctt ttc gac cgc ggc cta ggc 96
 Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
 20 25 30

tcc ctc gtc cca gca ctt gcc cca gaa tcc tta gac gac ctc ccc gac 144
 Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
 35 40 45

gag gtc tcc gcc ctg cgt cgc acc aca gag aaa aac acc aca aca ctc 192
 Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
 50 55 60

atc aac cta gcc aag cag cac gga ctc gta cac cac gac atc gcg ccg 240
 Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
 65 70 75 80

ggc acc tac atc gtc ggt ttg atc acc att tcc cgc cca cct atc acc 288
 Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
 85 90 95

gcg ctg gcg aca att tca gaa aac tcc cac aaa gca ctg ctt ggc ctt 336
 Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
 100 105 110

tat ttg tcc ggt ctt aaa cac ggc atg atg gct aac atc gga gaa cat 384
 Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
 115 120 125

gac gga aag tcc tgatctagca gtttcctttt tag 419
 Asp Gly Lys Ser
 130

<210> 940

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 940

Ile Ser Leu Gln Leu Gln Ala Ile Ser Thr Phe Pro Thr Asp Pro Glu
 1 5 10 15

Gly Val Trp Thr Ser Phe Asn Gln Leu Leu Phe Asp Arg Gly Leu Gly
 20 25 30

Ser Leu Val Pro Ala Leu Ala Pro Glu Ser Leu Asp Asp Leu Pro Asp
 35 40 45

Glu Val Ser Ala Leu Arg Arg Thr Thr Glu Lys Asn Thr Thr Thr Leu
 50 55 60

Ile Asn Leu Ala Lys Gln His Gly Leu Val His His Asp Ile Ala Pro
 65 70 75 80

Gly Thr Tyr Ile Val Gly Leu Ile Thr Ile Ser Arg Pro Pro Ile Thr
 85 90 95

Ala Leu Ala Thr Ile Ser Glu Asn Ser His Lys Ala Leu Leu Gly Leu
 100 105 110

Tyr Leu Ser Gly Leu Lys His Gly Met Met Ala Asn Ile Gly Glu His
 115 120 125

Asp Gly Lys Ser
 130

<210> 941

<211> 524

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(501)

<223> RXN02019

<400> 941

gaa att cct gct ggc acc aag gtt gag gcc tct gac ctt gga ctt cag 48
 Glu Ile Pro Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln
 1 5 10 15

gca atc cct act tcc cta ctg ccc agc acc tcc tac gat tcg att gac 96
 Ala Ile Pro Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp
 20 25 30

gat gta gtt ggg ctc gtt gcg gcc tcc aca tta agt tcc ggg gaa ata 144
 Asp Val Val Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile
 35 40 45

gcc aca aag cct cga ttc gtg ggc acc gaa ttg ata aac tcc att gcg 192
 Ala Thr Lys Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala
 50 55 60

aca aac gtc act gat agc tct ttg gtg gaa gaa att aac atg gtt cca 240
 Thr Asn Val Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro

65	70	75	80	
ctc agt ttg gct gaa cct tcc gtc atc ccc cta ctg cag cat ggg gac				288
Leu Ser Leu Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp				
	85	90	95	
acc att tcg gtt gtt tcc caa gac cca gac acc ggt ctc cca gag aac				336
Thr Ile Ser Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn				
	100	105	110	
att gct gca ggt gga aca gta att ctg gcg ggt ggt aca gac ccc tca				384
Ile Ala Ala Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser				
	115	120	125	
acc atc ttg att gcg ctt cca caa tca atc gct gaa aag gtt gca gca				432
Thr Ile Leu Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala				
	130	135	140	
caa tcg ctc aat acc cct ctg gcg gta gtc ctg acc gga gac aga gca				480
Gln Ser Leu Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala				
	145	150	155	160
gat aat tac aca acc gaa gaa tagttcccta ttcaaaaaaa agg				524
Asp Asn Tyr Thr Thr Glu Glu				
	165			
<210> 942				
<211> 167				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 942				
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Ala Ile Pro Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp				
	20	25	30	
Asp Val Val Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile				
	35	40	45	
Ala Thr Lys Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala				
	50	55	60	
Thr Asn Val Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro				
	65	70	75	80
Leu Ser Leu Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp				
	85	90	95	
Thr Ile Ser Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn				
	100	105	110	
Ile Ala Ala Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser				
	115	120	125	
Thr Ile Leu Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala				
	130	135	140	
Gln Ser Leu Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala				

145

150

155

160

Asp Asn Tyr Thr Thr Glu Glu
165

<210> 943

<211> 515

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(492)

<223> FRXA02019

<400> 943

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1 5 10 15

act tcc cta ctg ccc agc acc tcc tac gat tcg att gac gat gta gtt 96
Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp Asp Val Val
20 25 30

ggg ctc gtt gcg gcc tcc aca tta agt tcc ggg gaa ata gcc aca aag 144
Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile Ala Thr Lys
35 40 45

cct cga ttc gtg ggc acc gaa ttg ata aac tcc att gcg aca aac gtc 192
Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala Thr Asn Val
50 55 60

act gat agc tct ttg gtg gaa gaa att aac atg gtt cca ctc agt ttg 240
Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro Leu Ser Leu
65 70 75 80

gct gaa cct tcc gtc atc ccc cta ctg cag cat ggg gac acc att tcg 288
Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp Thr Ile Ser
85 90 95

gtt gtt tcc caa gac cca gac acc ggt ctc cca gag aac att gct gca 336
Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn Ile Ala Ala
100 105 110

ggt gga aca gta att ctg gcg ggt ggt aca gac ccc tca acc atc ttg 384
Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser Thr Ile Leu
115 120 125

att gcg ctt cca caa tca atc gct gaa aag gtt gca gca caa tcg ctc 432
Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala Gln Ser Leu
130 135 140

aat acc cct ctg gcg gta gtc ctg acc gga gac aga gca aat aat tac 480
Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala Asn Asn Tyr
145 150 155 160

aca acc gaa gaa tagttcccta ttcaaaaaaa agg 515
Thr Thr Glu Glu

<210> 944
 <211> 164
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 944

Ala Gly Thr Lys Val Glu Ala Ser Asp Leu Gly Leu Gln Ala Ile Pro
 1 5 10 15
 Thr Ser Leu Leu Pro Ser Thr Ser Tyr Asp Ser Ile Asp Asp Val Val
 20 25 30
 Gly Leu Val Ala Ala Ser Thr Leu Ser Ser Gly Glu Ile Ala Thr Lys
 35 40 45
 Pro Arg Phe Val Gly Thr Glu Leu Ile Asn Ser Ile Ala Thr Asn Val
 50 55 60
 Thr Asp Ser Ser Leu Val Glu Glu Ile Asn Met Val Pro Leu Ser Leu
 65 70 75 80
 Ala Glu Pro Ser Val Ile Pro Leu Leu Gln His Gly Asp Thr Ile Ser
 85 90 95
 Val Val Ser Gln Asp Pro Asp Thr Gly Leu Pro Glu Asn Ile Ala Ala
 100 105 110
 Gly Gly Thr Val Ile Leu Ala Gly Gly Thr Asp Pro Ser Thr Ile Leu
 115 120 125
 Ile Ala Leu Pro Gln Ser Ile Ala Glu Lys Val Ala Ala Gln Ser Leu
 130 135 140
 Asn Thr Pro Leu Ala Val Val Leu Thr Gly Asp Arg Ala Asn Asn Tyr
 145 150 155 160
 Thr Thr Glu Glu

<210> 945
 <211> 891
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(868)

<223> RXN02023

<400> 945

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 gacttccgaa atgtaactag agactagagg aggaaacacg atg gct cct aaa caa 115
 Met Ala Pro Lys Gln
 1 5
 act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa 163
 Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
 10 15 20

cgt	cg	cag	aca	gag	gg	act	ttt	gat	caa	cgc	ttg	cta	gaa	atg	cgc	211
Arg	Arg	Gln	Thr	Glu	Gly	Thr	Phe	Asp	Gln	Arg	Leu	Leu	Glu	Met	Arg	
			25					30					35			
gct	gat	cac	aat	tgg	aag	cac	gcc	gat	cca	tgg	cgt	gta	ctg	cgt	att	259
Ala	Asp	His	Asn	Trp	Lys	His	Ala	Asp	Pro	Trp	Arg	Val	Leu	Arg	Ile	
			40				45					50				
cag	tct	gag	ttt	gtg	gcg	gg	ttt	gat	gcc	ctc	cac	gag	atg	cca	aag	307
Gln	Ser	Glu	Phe	Val	Ala	Gly	Phe	Asp	Ala	Leu	His	Glu	Met	Pro	Lys	
			55				60					65				
gcc	gta	acc	gtc	ttt	gg	tcc	gca	cgc	att	aaa	gag	gat	cac	ccg	tac	355
Ala	Val	Thr	Val	Phe	Gly	Ser	Ala	Arg	Ile	Lys	Glu	Asp	His	Pro	Tyr	
						75				80					85	
tac	aag	gcg	gg	gta	gaa	ctt	gg	gaa	aag	ctc	gtt	gca	gcg	gac	tac	403
Tyr	Lys	Ala	Gly	Val	Glu	Leu	Gly	Glu	Lys	Leu	Val	Ala	Ala	Asp	Tyr	
				90					95					100		
gca	gtt	gtc	acc	gg	ggc	gg	cca	gg	ctg	atg	gaa	gcc	ccc	aat	aag	451
Ala	Val	Val	Thr	Gly	Gly	Gly	Pro	Gly	Leu	Met	Glu	Ala	Pro	Asn	Lys	
			105					110					115			
ggg	gca	agc	gag	gcc	aat	gg	tta	tca	gtt	gg	ctg	ggc	att	gag	ttg	499
Gly	Ala	Ser	Glu	Ala	Asn	Gly	Leu	Ser	Val	Gly	Leu	Gly	Ile	Glu	Leu	
			120				125					130				
cca	cat	gaa	cag	cat	ctg	aac	cct	tat	gtg	gat	ttg	gg	ctg	aac	ttc	547
Pro	His	Glu	Gln	His	Leu	Asn	Pro	Tyr	Val	Asp	Leu	Gly	Leu	Asn	Phe	
						140					145					
cg	tac	ttc	ttc	gca	cgc	aag	acc	atg	ttc	ctg	aaa	tac	tcc	cag	gct	595
Arg	Tyr	Phe	Phe	Ala	Arg	Lys	Thr	Met	Phe	Leu	Lys	Tyr	Ser	Gln	Ala	
					155					160					165	
ttt	gtg	tgt	ctg	cct	gg	gg	ttc	ggc	acg	ctc	gat	gag	ctt	ttc	gag	643
Phe	Val	Cys	Leu	Pro	Gly	Gly	Phe	Gly	Thr	Leu	Asp	Glu	Leu	Phe	Glu	
				170					175					180		
gtc	ctc	tgc	atg	gta	caa	acc	ggc	aag	gta	ccc	aac	ttt	ccc	atc	gtg	691
Val	Leu	Cys	Met	Val	Gln	Thr	Gly	Lys	Val	Pro	Asn	Phe	Pro	Ile	Val	
			185					190					195			
ctg	atc	ggc	act	gag	ttc	tgg	gca	gg	ttg	gtg	gat	tgg	atc	cgt	cac	739
Leu	Ile	Gly	Thr	Glu	Phe	Trp	Ala	Gly	Leu	Val	Asp	Trp	Ile	Arg	His	
			200				205					210				
cg	ctg	gta	gag	gaa	ggc	atg	atc	gat	gag	aag	gat	gtt	gac	cg	atg	787
Arg	Leu	Val	Glu	Glu	Gly	Met	Ile	Asp	Glu	Lys	Asp	Val	Asp	Arg	Met	
			215			220					225					
ttg	gtc	act	gat	gac	ctg	gat	cag	gcc	gtc	aaa	ttc	atc	gtc	gat	gca	

tgt

891

<210> 946

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 946

Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val
1 5 10 15

Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg
20 25 30

Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp
35 40 45

Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu
50 55 60

His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys
65 70 75 80

Glu Asp His Pro Tyr Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu
85 90 95

Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met
100 105 110

Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly
115 120 125

Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp
130 135 140

Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu
145 150 155 160

Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu
165 170 175

Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Pro
180 185 190

Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val
195 200 205

Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys
210 215 220

Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys
225 230 235 240

Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn
245 250 255

<210> 947

<211> 891

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(868)

<223> FRXA02023

<400> 947

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gacttccgaa atgtaactag agactagagg aggaaacacg atg gct cct aaa caa      115
                                     Met Ala Pro Lys Gln
                                     1                               5

act ccc agc cca gag aag aat cga aac ctg gtg gga cca gtt ctg caa      163
Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val Gly Pro Val Leu Gln
                                     10                               15                               20

cgt cgg cag aca gag ggt act ttt gat caa cgc ttg cta gaa atg cgc      211
Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg Leu Leu Glu Met Arg
                                     25                               30                               35

gct gat cac aat tgg aag cac gcc gat cca tgg cgt gta ctg cgt att      259
Ala Asp His Asn Trp Lys His Ala Asp Pro Trp Arg Val Leu Arg Ile
                                     40                               45                               50

cag tct gag ttt gtg gcg ggt ttt gat gcc ctc cac gag atg cca aag      307
Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu His Glu Met Pro Lys
                                     55                               60                               65

gcc gta acc gtc ttt ggt tcc gca cgc att aaa gag gat cac ccg tac      355
Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys Glu Asp His Pro Tyr
                                     70                               75                               80                               85

tac aag gcg ggt gta gaa ctt ggt gaa aag ctc gtt gct gct gac tac      403
Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu Val Ala Ala Asp Tyr
                                     90                               95                               100

gca gtt gtc acc ggt ggc ggt cca ggt ctg atg gaa gcc ccc aat aag      451
Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met Glu Ala Pro Asn Lys
                                     105                               110                               115

ggg gca agc gag gcc aat ggt tta tca gtt ggt ctg ggc att gag ttg      499
Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly Leu Gly Ile Glu Leu
                                     120                               125                               130

cca cat gaa cag cac ctg aac cct tat gtg gat ttg ggt ctg aac ttc      547
Pro His Glu Gln His Leu Asn Pro Tyr Val Asp Leu Gly Leu Asn Phe
                                     135                               140                               145

cgg tac ttc ttc gca cgc aag acc atg ttc ctg aaa tac tcc cag gct      595
Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu Lys Tyr Ser Gln Ala
                                     150                               155                               160                               165

ttt gtg tgt ctg cct ggc ggt ttc ggc acg ctc gat gag ctt ttc gag      643
Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu Asp Glu Leu Phe Glu
                                     170                               175                               180

gtc ctc tgc atg gta caa acc ggc aag gta acc aac ttt ccc atc gtg      691
Val Leu Cys Met Val Gln Thr Gly Lys Val Thr Asn Phe Pro Ile Val
                                     185                               190                               195

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ctg atc ggc act gag ttc tgg gca ggt ttg gtg gat tgg atc cgt cac 739
 Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val Asp Trp Ile Arg His
 200 205 210

cgc ctg gta gag gaa ggc atg atc gat gag aag gat gtt gac cgg atg 787
 Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys Asp Val Asp Arg Met
 215 220 225

ttg gtc act gat gac ctg gat cag gcc gtc aaa ttc atc gtc gat gca 835
 Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys Phe Ile Val Asp Ala
 230 235 240 245

cac gct gga ttg gac gta gcg cgt ctc cac aat taagcagtgg ctacattagg 888
 His Ala Gly Leu Asp Val Ala Arg Leu His Asn
 250 255

tgt 891

<210> 948

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 948

Met Ala Pro Lys Gln Thr Pro Ser Pro Glu Lys Asn Arg Asn Leu Val
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Gly Pro Val Leu Gln Arg Arg Gln Thr Glu Gly Thr Phe Asp Gln Arg
 20 25 30

Leu Leu Glu Met Arg Ala Asp His Asn Trp Lys His Ala Asp Pro Trp
 35 40 45

Arg Val Leu Arg Ile Gln Ser Glu Phe Val Ala Gly Phe Asp Ala Leu
 50 55 60

His Glu Met Pro Lys Ala Val Thr Val Phe Gly Ser Ala Arg Ile Lys
 65 70 75 80

Glu Asp His Pro Tyr Tyr Lys Ala Gly Val Glu Leu Gly Glu Lys Leu
 85 90 95

Val Ala Ala Asp Tyr Ala Val Val Thr Gly Gly Gly Pro Gly Leu Met
 100 105 110

Glu Ala Pro Asn Lys Gly Ala Ser Glu Ala Asn Gly Leu Ser Val Gly
 115 120 125

Leu Gly Ile Glu Leu Pro His Glu Gln His Leu Asn Pro Tyr Val Asp
 130 135 140

Leu Gly Leu Asn Phe Arg Tyr Phe Phe Ala Arg Lys Thr Met Phe Leu
 145 150 155 160

Lys Tyr Ser Gln Ala Phe Val Cys Leu Pro Gly Gly Phe Gly Thr Leu
 165 170 175

Asp Glu Leu Phe Glu Val Leu Cys Met Val Gln Thr Gly Lys Val Thr
 180 185 190

Asn Phe Pro Ile Val Leu Ile Gly Thr Glu Phe Trp Ala Gly Leu Val
 195 200 205

Asp Trp Ile Arg His Arg Leu Val Glu Glu Gly Met Ile Asp Glu Lys
 210 215 220

Asp Val Asp Arg Met Leu Val Thr Asp Asp Leu Asp Gln Ala Val Lys
 225 230 235 240

Phe Ile Val Asp Ala His Ala Gly Leu Asp Val Ala Arg Leu His Asn
 245 250 255

<210> 949

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXN02032

<400> 949

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gggtctatttt ttatgccag gcacggctca taggagaacc atg ccc ttt cta caa 115
 Met Pro Phe Leu Gln
 1 5

atc tct ctg ctt tcc atc ggt gtc gcc gcc gat gcg ttt gct tgt tcc 163
 Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp Ala Phe Ala Cys Ser
 10 15 20

gtt gtc cgc ggc acc gcc att caa gtc aac ctt ttc aaa cgc gca ctt 211
 Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu Phe Lys Arg Ala Leu
 25 30 35

gtt ctc gcg ggc atc ttt ggt gtc ttc caa gcg gca atg cct tta atc 259
 Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala Ala Met Pro Leu Ile
 40 45 50

ggc tgg ttc att ggc cgt ttc ttt gct gga atc acc ttc atc gct gaa 307
 Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile Thr Phe Ile Ala Glu
 55 60 65

att gat cac tgg atc gct ttt gca cta ttg ggt att gtc ggc acc aaa 355
 Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly Ile Val Gly Thr Lys
 70 75 80 85

atg atc tgg gat gcc ttc caa cct gaa gat gat gaa acc att gtc gat 403
 Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp Glu Thr Ile Val Asp
 90 95 100

gac ggc cgc gtt caa ttt aga cca gca att atc ctg ggg cta gcc acc 451
 Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile Leu Gly Leu Ala Thr
 105 110 115

agc att gac gca tta gcc gta ggc atg ggc ctg gca ttc gtg gaa gtt 499
 Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu Ala Phe Val Glu Val

120	125	130	
tcc atc ctc aaa gtg gca ctg	tcc atg ggc agc atc acc ttc gca ctt	547	
Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser Ile Thr Phe Ala Leu			
135	140	145	
tcg ctt gct ggc gcc tgg atc gga cac cat ggt gga gga aag ttt ggc	595		
Ser Leu Ala Gly Ala Trp Ile Gly His His Gly Gly Gly Lys Phe Gly			
150	155	160	
aag tgg gct acg att ctt ggc gga ata atc ttg atc gga atc ggc gca	643		
Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu Ile Gly Ile Gly Ala			
170	175	180	
aac atc gtc tac gaa cac ctc agc gcg taaccctcgg cgcattatcc	690		
Asn Ile Val Tyr Glu His Leu Ser Ala			
185	190		
tca		693	

<210> 950
 <211> 190
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 950
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 Ala Phe Ala Cys Ser Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu
 20 25 30
 Phe Lys Arg Ala Leu Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala
 35 40 45
 Ala Met Pro Leu Ile Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile
 50 55 60
 Thr Phe Ile Ala Glu Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly
 65 70 75 80
 Ile Val Gly Thr Lys Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp
 85 90 95
 Glu Thr Ile Val Asp Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile
 100 105 110
 Leu Gly Leu Ala Thr Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu
 115 120 125
 Ala Phe Val Glu Val Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser
 130 135 140
 Ile Thr Phe Ala Leu Ser Leu Ala Gly Ala Trp Ile Gly His His Gly
 145 150 155 160
 Gly Gly Lys Phe Gly Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu
 165 170 175
 Ile Gly Ile Gly Ala Asn Ile Val Tyr Glu His Leu Ser Ala

180

185

190

<210> 951
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 <212> DNA
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<220>
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 <222> (101)..(670)
 <223> FRXA02032

<400> 951

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ggctctatttt ttatgccag gcacggctca taggagaacc atg ccc ttt cta caa 115
                                         Met Pro Phe Leu Gln
                                         1      5

atc tct ctg ctt tcc atc ggt gtc gcc gcc gat gcg ttt gct tgt tcc 163
Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp Ala Phe Ala Cys Ser
              10                      15                      20

ggt gtc cgc ggc acc gcc att caa gtc aac ctt ttc aaa cgc gca ctt 211
Val Val Arg Gly Thr Ala Ile Gln Val Asn Leu Phe Lys Arg Ala Leu
              25                      30                      35

ggt ctc gcg ggc atc ttt ggt gtc ttc caa gcg gca atg cct tta atc 259
Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala Ala Met Pro Leu Ile
              40                      45                      50

ggc tgg ttc att ggc cgt ttc ttt gct gga atc acc ttc atc gct gaa 307
Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile Thr Phe Ile Ala Glu
              55                      60                      65

att gat cac tgg atc gct ttt gca cta ttg ggt att gtc ggc acc aaa 355
Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly Ile Val Gly Thr Lys
              70                      75                      80                      85

atg atc tgg gat gcc ttc caa cct gaa gat gat gaa acc att gtc gat 403
Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp Glu Thr Ile Val Asp
              90                      95                      100

gac ggc cgc gtt caa ttt aga cca gca att atc ctg ggg cta gcc acc 451
Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile Leu Gly Leu Ala Thr
              105                      110                      115

agc att gac gca tta gcc gta ggc atg ggc ctg gca ttc gtg gaa gtt 499
Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu Ala Phe Val Glu Val
              120                      125                      130

tcc atc ctc aaa gtg gca ctg tcc atg ggc agc atc acc ttc gca ctt 547
Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser Ile Thr Phe Ala Leu
              135                      140                      145

tcg ctt gct ggc gcc tgg atc gga cac cat ggt gga gga aag ttt ggc 595
Ser Leu Ala Gly Ala Trp Ile Gly His His Gly Gly Gly Lys Phe Gly
              150                      155                      160                      165

aag tgg gct acg att ctt ggc gga ata atc ttg atc gga atc ggc gca 643

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Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu Ile Gly Ile Gly Ala
170 175 180

aac atc gtc tac gaa cac ctc agc gcg taaccctcgg cgcattatcc 690
Asn Ile Val Tyr Glu His Leu Ser Ala
185 190

tca 693

<210> 952

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 952

Met Pro Phe Leu Gln Ile Ser Leu Leu Ser Ile Gly Val Ala Ala Asp
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20 25 30

Phe Lys Arg Ala Leu Val Leu Ala Gly Ile Phe Gly Val Phe Gln Ala
35 40 45

Ala Met Pro Leu Ile Gly Trp Phe Ile Gly Arg Phe Phe Ala Gly Ile
50 55 60

Thr Phe Ile Ala Glu Ile Asp His Trp Ile Ala Phe Ala Leu Leu Gly
65 70 75 80

Ile Val Gly Thr Lys Met Ile Trp Asp Ala Phe Gln Pro Glu Asp Asp
85 90 95

Glu Thr Ile Val Asp Asp Gly Arg Val Gln Phe Arg Pro Ala Ile Ile
100 105 110

Leu Gly Leu Ala Thr Ser Ile Asp Ala Leu Ala Val Gly Met Gly Leu
115 120 125

Ala Phe Val Glu Val Ser Ile Leu Lys Val Ala Leu Ser Met Gly Ser
130 135 140

Ile Thr Phe Ala Leu Ser Leu Ala Gly Ala Trp Ile Gly His His Gly
145 150 155 160

Gly Gly Lys Phe Gly Lys Trp Ala Thr Ile Leu Gly Gly Ile Ile Leu
165 170 175

Ile Gly Ile Gly Ala Asn Ile Val Tyr Glu His Leu Ser Ala
180 185 190

<210> 953

<211> 863

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(840)

<223> RXN02039

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1 5 10 15	
gca ccc ctt tgg ctc gtg ggc acg ctt gtg tgg ctg gcg gtg cag gcg	96
Ala Pro Leu Trp Leu Val Gly Thr Leu Val Trp Leu Ala Val Gln Ala	
20 25 30	
gtg atg cat gac ggc gag ctt tac cat gtg gaa gtt ccc acg att gcg	144
Val Met His Asp Gly Glu Leu Tyr His Val Glu Val Pro Thr Ile Ala	
35 40 45	
ctg gtc atc ggc ttt ggc gcg cag ctt ctg atc ggt gtg atg agt tat	192
Leu Val Ile Gly Phe Gly Ala Gln Leu Leu Ile Gly Val Met Ser Tyr	
50 55 60	
cta ctg ccg tcg acg atg ggt ggc ggc gcg agc gcg gtg cgg act gga	240
Leu Leu Pro Ser Thr Met Gly Gly Gly Ala Ser Ala Val Arg Thr Gly	
65 70 75 80	
acg cac att tta aac act gcg ggc ctg ttt agg tgg acg ctg atc aac	288
Thr His Ile Leu Asn Thr Ala Gly Leu Phe Arg Trp Thr Leu Ile Asn	
85 90 95	
ggt ggc ctg gcg att tgg ctg ctc acc gac aat tcg tgg ctg cgc gtc	336
Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp Asn Ser Trp Leu Arg Val	
100 105 110	
gtg gtg tct ctg ctg agt atc gga gcg ttg gca gtt ttt gtc att ctg	384
Val Val Ser Leu Leu Ser Ile Gly Ala Leu Ala Val Phe Val Ile Leu	
115 120 125	
ctg ccc aag gct gtg cgg gcg cag cgc gga gtg atc acc aaa aag cgc	432
Leu Pro Lys Ala Val Arg Ala Gln Arg Gly Val Ile Thr Lys Lys Arg	
130 135 140	
gaa cca att act ccg ccg gag gag cct cga ctc aat caa att acc gcg	480
Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg Leu Asn Gln Ile Thr Ala	
145 150 155 160	
gga atc tct gtg ctt gcc ctg att ttg gca gca ttc ggt ggg ctc aac	528
Gly Ile Ser Val Leu Ala Leu Ile Leu Ala Ala Phe Gly Gly Leu Asn	
165 170 175	
ccc ggt gtt gcg ccg gtg gca agc tca aat gaa gac gtc tat gct gtg	576
Pro Gly Val Ala Pro Val Ala Ser Ser Asn Glu Asp Val Tyr Ala Val	
180 185 190	
acc att acc gca ggt gac atg gtg ttt atc cct gat gtg att gaa gtg	624
Thr Ile Thr Ala Gly Asp Met Val Phe Ile Pro Asp Val Ile Glu Val	
195 200 205	
cct gct ggt aaa tca ctc gaa gtc acg atg ctc aac gaa gac gac atg	672
Pro Ala Gly Lys Ser Leu Glu Val Thr Met Leu Asn Glu Asp Asp Met	
210 215 220	
gtg cac gat ctg aaa ttt gcc aac ggt gtg caa acc gga cgt gtg gcg	720
Val His Asp Leu Lys Phe Ala Asn Gly Val Gln Thr Gly Arg Val Ala	

225

230

235

240

cca ggt gat gaa att acg gtg acc gtc ggc gat att tcc gaa gac atg 768
 Pro Gly Asp Glu Ile Thr Val Thr Val Gly Asp Ile Ser Glu Asp Met
 245 250 255

gac ggc tgg tgc acc atc gct ggg cac cgc gcg caa gga atg gat ctg 816
 Asp Gly Trp Cys Thr Ile Ala Gly His Arg Ala Gln Gly Met Asp Leu
 260 265 270

gaa gta aag gtt gcg gct ccg aat taaccaaggg ctgctgaaaa act 863
 Glu Val Lys Val Ala Ala Pro Asn
 275 280

<210> 954

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 954

Lys Ala Ser Ile Ser Asn Leu Ser Phe Trp Thr Ser Thr Ser Thr Thr
 1 5 10 15

Ala Pro Leu Trp Leu Val Gly Thr Leu Val Trp Leu Ala Val Gln Ala
 20 25 30

Val Met His Asp Gly Glu Leu Tyr His Val Glu Val Pro Thr Ile Ala
 35 40 45

Leu Val Ile Gly Phe Gly Ala Gln Leu Leu Ile Gly Val Met Ser Tyr
 50 55 60

Leu Leu Pro Ser Thr Met Gly Gly Gly Ala Ser Ala Val Arg Thr Gly
 65 70 75 80

Thr His Ile Leu Asn Thr Ala Gly Leu Phe Arg Trp Thr Leu Ile Asn
 85 90 95

Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp Asn Ser Trp Leu Arg Val
 100 105 110

Val Val Ser Leu Leu Ser Ile Gly Ala Leu Ala Val Phe Val Ile Leu
 115 120 125

Leu Pro Lys Ala Val Arg Ala Gln Arg Gly Val Ile Thr Lys Lys Arg
 130 135 140

Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg Leu Asn Gln Ile Thr Ala
 145 150 155 160

Gly Ile Ser Val Leu Ala Leu Ile Leu Ala Ala Phe Gly Gly Leu Asn
 165 170 175

Pro Gly Val Ala Pro Val Ala Ser Ser Asn Glu Asp Val Tyr Ala Val
 180 185 190

Thr Ile Thr Ala Gly Asp Met Val Phe Ile Pro Asp Val Ile Glu Val
 195 200 205

Pro Ala Gly Lys Ser Leu Glu Val Thr Met Leu Asn Glu Asp Asp Met

210	215	220
Val His Asp Leu Lys Phe Ala Asn Gly Val Gln Thr Gly Arg Val Ala		
225	230	235 240
Pro Gly Asp Glu Ile Thr Val Thr Val Gly Asp Ile Ser Glu Asp Met		
	245	250 255
Asp Gly Trp Cys Thr Ile Ala Gly His Arg Ala Gln Gly Met Asp Leu		
	260	265 270
Glu Val Lys Val Ala Ala Pro Asn		
275	280	

<210> 955

<211> 833

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(810)

<223> FRXA02039

<400> 955

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Thr Ser Thr Ser Thr Thr Ala Pro Leu Trp Leu Val Gly Thr Leu Val	
1 5 10 15	
tgg ctg gcg gtg cag gcg gtg atg cat gac ggc gag ctt tac cat gtg	96
Trp Leu Ala Val Gln Ala Val Met His Asp Gly Glu Leu Tyr His Val	
20 25 30	
gaa gtt ccc acg att gcg ctg gtc atc ggc ttt ggc gcg cag ctt ctg	144
Glu Val Pro Thr Ile Ala Leu Val Ile Gly Phe Gly Ala Gln Leu Leu	
35 40 45	
atc ggt gtg atg agt tat cta ctg ccg tcg acg atg ggt ggc ggc gcg	192
Ile Gly Val Met Ser Tyr Leu Leu Pro Ser Thr Met Gly Gly Gly Ala	
50 55 60	
agc gcg gtg cgg act gga acg cac att tta aac act gcg ggg ctg ttt	240
Ser Ala Val Arg Thr Gly Thr His Ile Leu Asn Thr Ala Gly Leu Phe	
65 70 75 80	
agg tgg acg ctg atc aac ggt ggc ctg gcg att tgg ctg ctc acc gac	288
Arg Trp Thr Leu Ile Asn Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp	
85 90 95	
aat tcg tgg ctg cgc gtc gtg gtg tct ctg ctg agt atc gga gcg ttg	336
Asn Ser Trp Leu Arg Val Val Val Ser Leu Leu Ser Ile Gly Ala Leu	
100 105 110	
gca gtt ttt gtc att ctg ctg ccc aag gct gtg cgg gcg cag cgc gga	384
Ala Val Phe Val Ile Leu Leu Pro Lys Ala Val Arg Ala Gln Arg Gly	
115 120 125	
gtg atc acc aaa aag cgc gaa cca att act ccg ccg gag gag cct cga	432
Val Ile Thr Lys Lys Arg Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg	
130 135 140	

ctc aat caa att acc gcg gga atc tct gtg ctt gcc ctg att ttg gca 480
 Leu Asn Gln Ile Thr Ala Gly Ile Ser Val Leu Ala Leu Ile Leu Ala
 145 150 155 160

gca ttc ggt ggg ctc aac ccc ggt gtt gcg ccg gtg gca agc tca aat 528
 Ala Phe Gly Gly Leu Asn Pro Gly Val Ala Pro Val Ala Ser Ser Asn
 165 170 175

gaa gac gtc tat gct gtg acc att acc gca ggt gac atg gtg ttt atc 576
 Glu Asp Val Tyr Ala Val Thr Ile Thr Ala Gly Asp Met Val Phe Ile
 180 185 190

cct gat gtg att gaa gtg cct gct ggt aaa tca ctc gaa gtc acg atg 624
 Pro Asp Val Ile Glu Val Pro Ala Gly Lys Ser Leu Glu Val Thr Met
 195 200 205

ctc aac gaa gac gac atg gtg cac gat ctg aaa ttt gcc aac ggt gtg 672
 Leu Asn Glu Asp Asp Met Val His Asp Leu Lys Phe Ala Asn Gly Val
 210 215 220

caa acc gga cgt gtg gcg cca ggt gat gaa att acg gtg acc gtc ggc 720
 Gln Thr Gly Arg Val Ala Pro Gly Asp Glu Ile Thr Val Thr Val Gly
 225 230 235 240

gat att tcc gaa gac atg gac ggc tgg tgc acc atc gct ggg cac cgc 768
 Asp Ile Ser Glu Asp Met Asp Gly Trp Cys Thr Ile Ala Gly His Arg
 245 250 255

gcg caa gga atg gat ctg gaa gta aag gtt gcg gct ccg aat 810
 Ala Gln Gly Met Asp Leu Glu Val Lys Val Ala Ala Pro Asn
 260 265 270

taaccaaggg ctgctgaaaa act 833

<210> 956

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 956

Thr Ser Thr Ser Thr Thr Ala Pro Leu Trp Leu Val Gly Thr Leu Val
 1 5 10 15

Trp Leu Ala Val Gln Ala Val Met His Asp Gly Glu Leu Tyr His Val
 20 25 30

Glu Val Pro Thr Ile Ala Leu Val Ile Gly Phe Gly Ala Gln Leu Leu
 35 40 45

Ile Gly Val Met Ser Tyr Leu Leu Pro Ser Thr Met Gly Gly Gly Ala
 50 55 60

Ser Ala Val Arg Thr Gly Thr His Ile Leu Asn Thr Ala Gly Leu Phe
 65 70 75 80

Arg Trp Thr Leu Ile Asn Gly Gly Leu Ala Ile Trp Leu Leu Thr Asp
 85 90 95

Asn Ser Trp Leu Arg Val Val Val Ser Leu Leu Ser Ile Gly Ala Leu

100	105	110
Ala Val Phe Val Ile Leu Leu Pro Lys Ala Val Arg Ala Gln Arg Gly 115 120 125		
Val Ile Thr Lys Lys Arg Glu Pro Ile Thr Pro Pro Glu Glu Pro Arg 130 135 140		
Leu Asn Gln Ile Thr Ala Gly Ile Ser Val Leu Ala Leu Ile Leu Ala 145 150 155 160		
Ala Phe Gly Gly Leu Asn Pro Gly Val Ala Pro Val Ala Ser Ser Asn 165 170 175		
Glu Asp Val Tyr Ala Val Thr Ile Thr Ala Gly Asp Met Val Phe Ile 180 185 190		
Pro Asp Val Ile Glu Val Pro Ala Gly Lys Ser Leu Glu Val Thr Met 195 200 205		
Leu Asn Glu Asp Asp Met Val His Asp Leu Lys Phe Ala Asn Gly Val 210 215 220		
Gln Thr Gly Arg Val Ala Pro Gly Asp Glu Ile Thr Val Thr Val Gly 225 230 235 240		
Asp Ile Ser Glu Asp Met Asp Gly Trp Cys Thr Ile Ala Gly His Arg 245 250 255		
Ala Gln Gly Met Asp Leu Glu Val Lys Val Ala Ala Pro Asn 260 265 270		

<210> 957
 <211> 1506
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1483)
 <223> RXN02044

<400> 957
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 tagttggtgc aaaccaataa tagctatagc cccaatacaa atg gtc acc cca atc 115
 Met Val Thr Pro Ile
 1 5
 atg ggg aat tcg aac tct atc ctg ggc att tac cgt cag aaa atc caa 163
 Met Gly Asn Ser Asn Ser Ile Leu Gly Ile Tyr Arg Gln Lys Ile Gln
 10 15 20
 aat cga cat ttg gtt tct acg ctt ttt agg gca tac ttc cca atc gtg 211
 Asn Arg His Leu Val Ser Thr Leu Phe Arg Ala Tyr Phe Pro Ile Val
 25 30 35
 acc gag ctg att att tta ttg att gtt atc gtg acg gcg ctc gcc ttc 259
 Thr Glu Leu Ile Ile Leu Leu Ile Val Ile Val Thr Ala Leu Ala Phe
 40 45 50

gat ttc aca aac gga ttc cac gac acc ggc aat gcg atg gcc aca tcc Asp Phe Thr Asn Gly Phe His Asp Thr Gly Asn Ala Met Ala Thr Ser 55 60 65	307
att gcc aca ggc gct cta aaa cct aaa gtc gcc gtg gca cta tcc gcc Ile Ala Thr Gly Ala Leu Lys Pro Lys Val Ala Val Ala Leu Ser Ala 70 75 80 85	355
tca ctg aac ctt gtt ggc gca ttc ctc tct gta gaa gtt gcg aca act Ser Leu Asn Leu Val Gly Ala Phe Leu Ser Val Glu Val Ala Thr Thr 90 95 100	403
gtt gcc aaa ggc gtt gtt gac ctc gac caa ttc gac cta agc aat gcc Val Ala Lys Gly Val Val Asp Leu Asp Gln Phe Asp Leu Ser Asn Ala 105 110 115	451
tgg gat tcc cac cag ctc ctg ctt gtc gtc ttc gcc ggc ctc att ggc Trp Asp Ser His Gln Leu Leu Leu Val Val Phe Ala Gly Leu Ile Gly 120 125 130	499
gcc atc gtc tgg aac ctt ctg acc tgg ctg cta ggc att cct tcc agc Ala Ile Val Trp Asn Leu Leu Thr Trp Leu Leu Gly Ile Pro Ser Ser 135 140 145	547
tcc tct cac gca ctt ttc ggt ggc ctc att ggc gcc gca att gct tca Ser Ser His Ala Leu Phe Gly Gly Leu Ile Gly Ala Ala Ile Ala Ser 150 155 160 165	595
ctc ggt ttc ggc gga gtg gtg tgg gaa ggt gtc ttg tcc aag atg atc Leu Gly Phe Gly Gly Val Val Trp Glu Gly Val Leu Ser Lys Met Ile 170 175 180	643
atc cca gca ttg gct gca cca gtt gtt gca ggt ctc gtg gcc gcc atc Ile Pro Ala Leu Ala Ala Pro Val Val Ala Gly Leu Val Ala Ala Ile 185 190 195	691
ggc act ttc gcc gtg tac agc atc aca aag gca gtt gga gac aac gag Gly Thr Phe Ala Val Tyr Ser Ile Thr Lys Ala Val Gly Asp Asn Glu 200 205 210	739
aag aac cgt tac ttc cgc tgg ggt cag atc ggc tcc gct tcc ttg gtt Lys Asn Arg Tyr Phe Arg Trp Gly Gln Ile Gly Ser Ala Ser Leu Val 215 220 225	787
tcc ctg gca cac ggc acc aac gat gcc cag aag acc atg ggc gtt atc Ser Leu Ala His Gly Thr Asn Asp Ala Gln Lys Thr Met Gly Val Ile 230 235 240 245	835
ttc ctt tcc ctg gtt gcc acc ggt cac ctg gga act gac gct gac atc Phe Leu Ser Leu Val Ala Thr Gly His Leu Gly Thr Asp Ala Asp Ile 250 255 260	883
cca ttc tgg gtc aag gct aca tgt gca ttg gca atc gca atc ggt acc Pro Phe Trp Val Lys Ala Thr Cys Ala Leu Ala Ile Ala Ile Gly Thr 265 270 275	931
tac ttg ggt ggt tgg cgc gtt atc cgc aca ctg ggc aaa ggc ttg gtt Tyr Leu Gly Gly Trp Arg Val Ile Arg Thr Leu Gly Lys Gly Leu Val 280 285 290	979

gag att gat tcc cct cag ggc atg gca gca gaa act tct tct gca gca 1027
 Glu Ile Asp Ser Pro Gln Gly Met Ala Ala Glu Thr Ser Ser Ala Ala
 295 300 305

atc att ttg act tct tcc cac ttc ggt atg gca ctg tcc acc act cac 1075
 Ile Ile Leu Thr Ser Ser His Phe Gly Met Ala Leu Ser Thr Thr His
 310 315 320 325

gtt gct act ggc tcc atc atg ggt acc ggc att gga cgt aaa ggg gcg 1123
 Val Ala Thr Gly Ser Ile Met Gly Thr Gly Ile Gly Arg Lys Gly Ala
 330 335 340

aag gtt cgt tgg tcc gtc gca gga cgc atg gca atg gcc tgg gtt atc 1171
 Lys Val Arg Trp Ser Val Ala Gly Arg Met Ala Met Ala Trp Val Ile
 345 350 355

acc ctc cct gcc tcc gcg atc gtt ggc gtt ttc tgc tgg tgg gta gct 1219
 Thr Leu Pro Ala Ser Ala Ile Val Gly Val Phe Cys Trp Trp Val Ala
 360 365 370

cac gga att ggt ctt atc agc tca gac ctc ctc gga gtc ctc gtt gca 1267
 His Gly Ile Gly Leu Ile Ser Ser Asp Leu Leu Gly Val Leu Val Ala
 375 380 385

ttc gcc att ctg gtc att ctg tct ggc tac att tac gcc cgt tcc cgt 1315
 Phe Ala Ile Leu Val Ile Leu Ser Gly Tyr Ile Tyr Ala Arg Ser Arg
 390 395 400 405

cgc gtg cct gtt gat cca agc aac gtc aac gct gac tgg aat gaa gaa 1363
 Arg Val Pro Val Asp Pro Ser Asn Val Asn Ala Asp Trp Asn Glu Glu
 410 415 420

tca aac agc gtg gaa cct gca aca cct tcc gcc ccg gct gct tct gag 1411
 Ser Asn Ser Val Glu Pro Ala Thr Pro Ser Ala Pro Ala Ser Glu
 425 430 435

att aca gaa gct cct gcc gct cca gcc gct caa gcc gtt caa gat ctc 1459
 Ile Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Ala Val Gln Asp Leu
 440 445 450

aac aac gag aat gag gta acc aag taatgaactt cgctactatt ttc 1506
 Asn Asn Glu Asn Glu Val Thr Lys
 455 460

<210> 958
 <211> 461
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 958
 Met Val Thr Pro Ile Met Gly Asn Ser Asn Ser Ile Leu Gly Ile Tyr
 1 5 10 15
 Arg Gln Lys Ile Gln Asn Arg His Leu Val Ser Thr Leu Phe Arg Ala
 20 25 30
 Tyr Phe Pro Ile Val Thr Glu Leu Ile Ile Leu Leu Ile Val Ile Val
 35 40 45
 Thr Ala Leu Ala Phe Asp Phe Thr Asn Gly Phe His Asp Thr Gly Asn

50	55	60
Ala Met Ala Thr Ser Ile	Ala Thr Gly Ala Leu Lys Pro Lys Val Ala	
65	70	75 80
Val Ala Leu Ser Ala Ser Leu Asn Leu Val Gly Ala Phe Leu Ser Val		
	85	90 95
Glu Val Ala Thr Thr Val Ala Lys Gly Val Val Asp Leu Asp Gln Phe		
	100	105 110
Asp Leu Ser Asn Ala Trp Asp Ser His Gln Leu Leu Leu Val Val Phe		
	115	120 125
Ala Gly Leu Ile Gly Ala Ile Val Trp Asn Leu Leu Thr Trp Leu Leu		
	130	135 140
Gly Ile Pro Ser Ser Ser Ser His Ala Leu Phe Gly Gly Leu Ile Gly		
	145	150 155 160
Ala Ala Ile Ala Ser Leu Gly Phe Gly Gly Val Val Trp Glu Gly Val		
	165	170 175
Leu Ser Lys Met Ile Ile Pro Ala Leu Ala Ala Pro Val Val Ala Gly		
	180	185 190
Leu Val Ala Ala Ile Gly Thr Phe Ala Val Tyr Ser Ile Thr Lys Ala		
	195	200 205
Val Gly Asp Asn Glu Lys Asn Arg Tyr Phe Arg Trp Gly Gln Ile Gly		
	210	215 220
Ser Ala Ser Leu Val Ser Leu Ala His Gly Thr Asn Asp Ala Gln Lys		
	225	230 235 240
Thr Met Gly Val Ile Phe Leu Ser Leu Val Ala Thr Gly His Leu Gly		
	245	250 255
Thr Asp Ala Asp Ile Pro Phe Trp Val Lys Ala Thr Cys Ala Leu Ala		
	260	265 270
Ile Ala Ile Gly Thr Tyr Leu Gly Gly Trp Arg Val Ile Arg Thr Leu		
	275	280 285
Gly Lys Gly Leu Val Glu Ile Asp Ser Pro Gln Gly Met Ala Ala Glu		
	290	295 300
Thr Ser Ser Ala Ala Ile Ile Leu Thr Ser Ser His Phe Gly Met Ala		
	305	310 315 320
Leu Ser Thr Thr His Val Ala Thr Gly Ser Ile Met Gly Thr Gly Ile		
	325	330 335
Gly Arg Lys Gly Ala Lys Val Arg Trp Ser Val Ala Gly Arg Met Ala		
	340	345 350
Met Ala Trp Val Ile Thr Leu Pro Ala Ser Ala Ile Val Gly Val Phe		
	355	360 365
Cys Trp Trp Val Ala His Gly Ile Gly Leu Ile Ser Ser Asp Leu Leu		
	370	375 380

Gly Val Leu Val Ala Phe Ala Ile Leu Val Ile Leu Ser Gly Tyr Ile
 385 390 395 400
 Tyr Ala Arg Ser Arg Arg Val Pro Val Asp Pro Ser Asn Val Asn Ala
 405 410 415
 Asp Trp Asn Glu Glu Ser Asn Ser Val Glu Pro Ala Thr Pro Ser Ala
 420 425 430
 Pro Ala Ala Ser Glu Ile Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln
 435 440 445
 Ala Val Gln Asp Leu Asn Asn Glu Asn Glu Val Thr Lys
 450 455 460

<210> 959
 <211> 384
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> RXN02045

<400> 959
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 Met Asn Phe Ala Thr
 1 5
 att ttc gga agc atc ttt gag gtc acc ctc gtg ggc att ttg ctc ggc 163
 Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val Gly Ile Leu Leu Gly
 10 15 20
 gca ggc ctt cca gcc ctt ttt gca tta gga atc cgc ttt gct cac agc 211
 Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile Arg Phe Ala His Ser
 25 30 35
 cct tct tcc aac ggc acc aac gct ctt gga aaa att gct tca acc atc 259
 Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys Ile Ala Ser Thr Ile
 40 45 50
 tgc ttt gcc atc att gcg gtt gct atc atc gct ggc att ctc tgg gtc 307
 Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala Gly Ile Leu Trp Val
 55 60 65
 acc aaa gca acg atc tac cag tac tct ggt ttc gac att ttc ggc act 355
 Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe Asp Ile Phe Gly Thr
 70 75 80 85
 gaa ggc taaaagcacc agctgcgaat aac 384
 Glu Gly

<210> 960
 <211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 960

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Met Asn Phe Ala Thr Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val
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Gly Ile Leu Leu Gly Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile
      20             25             30

Arg Phe Ala His Ser Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys
      35             40             45

Ile Ala Ser Thr Ile Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala
      50             55             60

Gly Ile Leu Trp Val Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe
      65             70             75             80

Asp Ile Phe Gly Thr Glu Gly
      85

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<210> 961

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> FRXA02045

<400> 961

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ccgttcaaga tctcaacaac gagaatgagg taaccaagta atg aac ttc gct act 115
                                         Met Asn Phe Ala Thr
                                         1             5

att ttc gga agc atc ttt gag gtc acc ctc gtg ggc att ttg ctc ggc 163
Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val Gly Ile Leu Leu Gly
      10             15             20

gca ggc ctt cca gcc ctt ttt gca tta gga atc cgc ttt gct cac agc 211
Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile Arg Phe Ala His Ser
      25             30             35

cct tct tcc aac ggc acc aac gct ctt gga aaa att gct tca acc atc 259
Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys Ile Ala Ser Thr Ile
      40             45             50

tgc ttt gcc atc att gcg gtt gct atc atc gct ggc att ctc tgg gtc 307
Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala Gly Ile Leu Trp Val
      55             60             65

acc aaa gca acg atc tac cag tac tct ggt ttc gac att ttc ggc act 355
Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe Asp Ile Phe Gly Thr
      70             75             80             85

gaa ggc taaaagcacc agctgcgaat aac 384

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Glu Gly

<210> 962

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 962

Met Asn Phe Ala Thr Ile Phe Gly Ser Ile Phe Glu Val Thr Leu Val
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Gly Ile Leu Leu Gly Ala Gly Leu Pro Ala Leu Phe Ala Leu Gly Ile
 20 25 30

Arg Phe Ala His Ser Pro Ser Ser Asn Gly Thr Asn Ala Leu Gly Lys
 35 40 45

Ile Ala Ser Thr Ile Cys Phe Ala Ile Ile Ala Val Ala Ile Ile Ala
 50 55 60

Gly Ile Leu Trp Val Thr Lys Ala Thr Ile Tyr Gln Tyr Ser Gly Phe
 65 70 75 80

Asp Ile Phe Gly Thr Glu Gly
 85

<210> 963

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXN02049

<400> 963

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 Val Arg Tyr Leu Thr 5
 1

ctg gcc aca atc atc gca ggt ctc tcc ggg ttc gtc gtc atc atc atc 163
 Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe Val Val Ile Ile Ile 20
 10 15

gct gcc tgg gcc ctt ggt gat tcc agc caa ctt tcc gaa gaa ttc acc 211
 Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu Ser Glu Glu Phe Thr 35
 25 30

gcc tac tgg ggt ctg ttc ttt gca gga acc gga gtg ctg act ggg ttg 259
 Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly Val Leu Thr Gly Leu 50
 40 45

acg cag gag acg acc cgc gcg gtg acg gcc ggt tct cgt ggt ggt tct 307
 Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly Ser Arg Gly Gly Ser 65
 55 60

cgt ggt ggg cgt gct ggt tct gtt gtt gga ttt agg ccg ttt ttg ttt 355
 Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe Arg Pro Phe Leu Phe
 70 75 80 85
 agc ttc gtg gtt gcg gcg ata gtg ctc gtg gtg ctt ggc gct tcg gcg 403
 Ser Phe Val Val Ala Ala Ile Val Leu Val Val Leu Gly Ala Ser Ala
 90 95 100
 ccg ctg tgg atc ggc cag ctt tta agt aat ttg caa ggt gtt ggt gtt 451
 Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu Gln Gly Val Gly Val
 105 110 115
 ggg cta ctt gct gta ggt ctt gct agc tac gcg atc caa gcg aca atc 499
 Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala Ile Gln Ala Thr Ile
 120 125 130
 tcc ggc att ttt gtc cgg ctg cca att gtg gaa aga gta tgc ctc gct 547
 Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu Arg Val Cys Leu Ala
 135 140 145
 gat ttc ttt gga cac cgg cgt gcg cat ggt ttt aac tgt tgc cgc ctg 595
 Asp Phe Phe Gly His Arg Arg Ala His Gly Phe Asn Cys Cys Arg Leu
 150 155 160 165
 gtt gct ggg tta tca att gct ggc gtt ctt gat cat cac cgt tgt ggg 643
 Val Ala Gly Leu Ser Ile Ala Gly Val Leu Asp His His Arg Cys Gly
 170 175 180
 atc aat atc ctg gct ggt cat cgt gct gtg ctt cgg ttc ggt gcg ttc 691
 Ile Asn Ile Leu Ala Gly His Arg Ala Val Leu Arg Phe Gly Ala Phe
 185 190 195
 cgt ttt ggg atc ggt tgc tgatgtttca cggggcgttt tca 732
 Arg Phe Gly Ile Gly Cys
 200

<210> 964
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 964
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 Val Val Ile Ile Ile Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu
 20 25 30
 Ser Glu Glu Phe Thr Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly
 35 40 45
 Val Leu Thr Gly Leu Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly
 50 55 60
 Ser Arg Gly Gly Ser Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe
 65 70 75 80
 Arg Pro Phe Leu Phe Ser Phe Val Val Ala Ala Ile Val Leu Val Val
 85 90 95

Leu Gly Ala Ser Ala Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu
 100 105 110
 Gln Gly Val Gly Val Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala
 115 120 125
 Ile Gln Ala Thr Ile Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu
 130 135 140
 Arg Val Cys Leu Ala Asp Phe Phe Gly His Arg Arg Ala His Gly Phe
 145 150 155 160
 Asn Cys Cys Arg Leu Val Ala Gly Leu Ser Ile Ala Gly Val Leu Asp
 165 170 175
 His His Arg Cys Gly Ile Asn Ile Leu Ala Gly His Arg Ala Val Leu
 180 185 190
 Arg Phe Gly Ala Phe Arg Phe Gly Ile Gly Cys
 195 200

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 <212> DNA
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<220>
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 <223> FRXA02049

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 atctggagtt gccggagttt ccttctggtg gtttggacta gtg cgc tat ctg acg 115
 Val Arg Tyr Leu Thr
 1 5
 ctg gcc aca atc atc gca ggt ctc tcc ggg ttc gtc gtc atc atc atc 163
 Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe Val Val Ile Ile Ile
 10 15 20
 gct gcc tgg gcc ctt ggt gat tcc agc caa ctt tcc gaa gaa ttc acc 211
 Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu Ser Glu Glu Phe Thr
 25 30 35
 gcc tac tgg ggt ctg ttc ttt gca gga acc gga gtg ctg act ggg ttg 259
 Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly Val Leu Thr Gly Leu
 40 45 50
 acg cag gag acg acc cgc gcg gtg acg gcc ggt tct cgt ggt ggt tct 307
 Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly Ser Arg Gly Gly Ser
 55 60 65
 cgt ggt ggg cgt gct ggt tct gtt gtt gga ttt agg ccg ttt ttg ttt 355
 Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe Arg Pro Phe Leu Phe
 70 75 80 85
 agc ttc gtg gtt gcg gcg ata gtg ctc gtg gtg ctt ggc gct tcg gcg 403

Ser Phe Val Val Ala Ala Ile Val Leu Val Val Leu Gly Ala Ser Ala
 90 95 100

ccg ctg tgg atc ggc cag ctt tta agt aat ttg caa ggt gtt ggt gtt 451
 Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu Gln Gly Val Gly Val
 105 110 115

ggg cta ctt gct gta ggt ctt gct agc tac gcg atc caa gcg aca atc 499
 Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala Ile Gln Ala Thr Ile
 120 125 130

tcc ggc att ttt gtc cgg ctg cca att gtg gaa aag agt atg cct cgc 547
 Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu Lys Ser Met Pro Arg
 135 140 145

tgattttcttt ggacaccggc gtg 570

<210> 966

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 966

Val Arg Tyr Leu Thr Leu Ala Thr Ile Ile Ala Gly Leu Ser Gly Phe
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Val Val Ile Ile Ile Ala Ala Trp Ala Leu Gly Asp Ser Ser Gln Leu
 20 25 30

Ser Glu Glu Phe Thr Ala Tyr Trp Gly Leu Phe Phe Ala Gly Thr Gly
 35 40 45

Val Leu Thr Gly Leu Thr Gln Glu Thr Thr Arg Ala Val Thr Ala Gly
 50 55 60

Ser Arg Gly Gly Ser Arg Gly Gly Arg Ala Gly Ser Val Val Gly Phe
 65 70 75 80

Arg Pro Phe Leu Phe Ser Phe Val Val Ala Ala Ile Val Leu Val Val
 85 90 95

Leu Gly Ala Ser Ala Pro Leu Trp Ile Gly Gln Leu Leu Ser Asn Leu
 100 105 110

Gln Gly Val Gly Val Gly Leu Leu Ala Val Gly Leu Ala Ser Tyr Ala
 115 120 125

Ile Gln Ala Thr Ile Ser Gly Ile Phe Val Arg Leu Pro Ile Val Glu
 130 135 140

Lys Ser Met Pro Arg
 145

<210> 967

<211> 918

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(895)

<223> RXN02050

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cggctgccaa ttgtggaaag agtatgcctc gctgatttct ttg gac acc ggc gtg 115
                                   Leu Asp Thr Gly Val
                                   1           5

cgc atg gtt tta act gtt gcc gcc tgg ttg ctg ggt tat caa ttg ctg 163
Arg Met Val Leu Thr Val Ala Ala Trp Leu Leu Gly Tyr Gln Leu Leu
              10              15              20

gcg ttc ttg atc atc acc gtt gtg gga tca ata tcc tgg ctg gtc atc 211
Ala Phe Leu Ile Ile Thr Val Val Gly Ser Ile Ser Trp Leu Val Ile
              25              30              35

gtg ctg tgc ttc ggt tgc gtg cgt tcc gtt ttg gga tgc gtt gct gat 259
Val Leu Cys Phe Gly Ser Val Arg Ser Val Leu Gly Ser Val Ala Asp
              40              45              50

gtt tca cgg ggc gtt ttc atc cga cag gct ctg ctt gcg atg gca gca 307
Val Ser Arg Gly Val Phe Ile Arg Gln Ala Leu Leu Ala Met Ala Ala
              55              60              65

tcc ggc gcc acg gca gtg ctg att act ggt ttc ccg acc ctg ctg aaa 355
Ser Gly Ala Thr Ala Val Leu Ile Thr Gly Phe Pro Thr Leu Leu Lys
              70              75              80              85

ttc acg aac cct tca gcg gtt gca gga ggg gtt tgc atg gcc gct gtt 403
Phe Thr Asn Pro Ser Ala Val Ala Gly Gly Val Ser Met Ala Ala Val
              90              95              100

tcc tac gcc gtc atc ctg acc cgc gct ccc ctg ctg gtt ccg ctg cag 451
Ser Tyr Ala Val Ile Leu Thr Arg Ala Pro Leu Leu Val Pro Leu Gln
              105              110              115

caa ttc caa tgc gcg atc atc gtt cgt ttt gtc aaa ggt acg tcc ggt 499
Gln Phe Gln Ser Ala Ile Ile Val Arg Phe Val Lys Gly Thr Ser Gly
              120              125              130

cca ttg aaa act ttg gcg ggt ccg ttg gca att gtg tgg gca gtc gga 547
Pro Leu Lys Thr Leu Ala Gly Pro Leu Ala Ile Val Trp Ala Val Gly
              135              140              145

ctt gtt gga gct ggt ctt gca tgg tta gtt ggc cca tgg atc ctg gac 595
Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly Pro Trp Ile Leu Asp
              150              155              160              165

gtt gta ctc caa aag gaa ctc ttc gcg gtc cct ggc tgg cta ctc gcg 643
Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro Gly Trp Leu Leu Ala
              170              175              180

atg ctc acc tta ggc gcc acc acc acc gct tca ttg atg gtg tcc ggc 691
Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser Leu Met Val Ser Gly
              185              190              195

tgc gcg gcg atc gcc ttt gaa cgt cac ggg atc tat ctc acc gga tgg 739
Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile Tyr Leu Thr Gly Trp

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200	205	210	
ggt ggt gcc act gtt gtt gcc gtc gga ttc ttg ctg gga cct ttt gat			787
Val Val Ala Thr Val Val Ala Val Gly Phe Leu Leu Gly Pro Phe Asp			
215	220	225	
ttg ggc gtc gct gct ggc ctt gcg ctc att gtt ggc cca ctc tgc ggt			835
Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val Gly Pro Leu Cys Gly			
230	235	240	245
ttg ctg gta cac atg gga gcg ttt gtt ggt ggg gat cgg aat cgg gtt			883
Leu Leu Val His Met Gly Ala Phe Val Gly Gly Asp Arg Asn Arg Val			
250	255	260	
ttg act gcg gga tagtttggtt tgattggggg att			918
Leu Thr Ala Gly			
265			

<210> 968
 <211> 265
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 968
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 Gly Tyr Gln Leu Leu Ala Phe Leu Ile Ile Thr Val Val Gly Ser Ile
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 Ser Trp Leu Val Ile Val Leu Cys Phe Gly Ser Val Arg Ser Val Leu
 35 40 45
 Gly Ser Val Ala Asp Val Ser Arg Gly Val Phe Ile Arg Gln Ala Leu
 50 55 60
 Leu Ala Met Ala Ala Ser Gly Ala Thr Ala Val Leu Ile Thr Gly Phe
 65 70 75 80
 Pro Thr Leu Leu Lys Phe Thr Asn Pro Ser Ala Val Ala Gly Gly Val
 85 90 95
 Ser Met Ala Ala Val Ser Tyr Ala Val Ile Leu Thr Arg Ala Pro Leu
 100 105 110
 Leu Val Pro Leu Gln Gln Phe Gln Ser Ala Ile Ile Val Arg Phe Val
 115 120 125
 Lys Gly Thr Ser Gly Pro Leu Lys Thr Leu Ala Gly Pro Leu Ala Ile
 130 135 140
 Val Trp Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly
 145 150 155 160
 Pro Trp Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro
 165 170 175
 Gly Trp Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser
 180 185 190

Leu Met Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile
 195 200 205
 Tyr Leu Thr Gly Trp Val Val Ala Thr Val Val Ala Val Gly Phe Leu
 210 215 220
 Leu Gly Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val
 225 230 235 240
 Gly Pro Leu Cys Gly Leu Leu Val His Met Gly Ala Phe Val Gly Gly
 245 250 255
 Asp Arg Asn Arg Val Leu Thr Ala Gly
 260 265

<210> 969
 <211> 495
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(472)
 <223> FRXA02050

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 aaaggtaccg tccggtccat tgaaaacttt ggcggggtccg ttg gca att gtg tgg 115
 Leu Ala Ile Val Trp
 1 5
 gca gtc gga ctt gtt gga gct ggt ctt gca tgg tta gtt ggc cca tgg 163
 Ala Val Gly Leu Val Gly Ala Gly Leu Ala Trp Leu Val Gly Pro Trp
 10 15 20
 atc ctg gac gtt gta ctc caa aag gaa ctc ttc gcg gtc cct ggc tgg 211
 Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe Ala Val Pro Gly Trp
 25 30 35
 cta ctc gcg atg ctc acc tta ggc gcc acc acc acc gct tca ttg atg 259
 Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr Thr Ala Ser Leu Met
 40 45 50
 gtg tcc ggc tgc gcg gcg atc gcc ttt gaa cgt cac ggg atc tat ctc 307
 Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg His Gly Ile Tyr Leu
 55 60 65
 acc gga tgg gtt gtt gcc act gtt gtt gcc gtc gga ttc ttg ctg gga 355
 Thr Gly Trp Val Val Ala Thr Val Val Ala Val Gly Phe Leu Leu Gly
 70 75 80 85
 cct ttt gat ttg ggc gtc gct gct ggc ctt gcg ctc att gtt ggc cca 403
 Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala Leu Ile Val Gly Pro
 90 95 100
 ctc tgc ggt ttg ctg gta cac atg gga gcg ttt gtt ggt ggg gat cgg 451
 Leu Cys Gly Leu Leu Val His Met Gly Ala Phe Val Gly Gly Asp Arg
 105 110 115

aat cgg gtt ttg act gcg gga tagtttggtt tgattggggg att
 Asn Arg Val Leu Thr Ala Gly
 120

495

<210> 970
 <211> 124
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 970
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 Leu Val Gly Pro Trp Ile Leu Asp Val Val Leu Gln Lys Glu Leu Phe
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 Ala Val Pro Gly Trp Leu Leu Ala Met Leu Thr Leu Gly Ala Thr Thr
 35 40 45
 Thr Ala Ser Leu Met Val Ser Gly Cys Ala Ala Ile Ala Phe Glu Arg
 50 55 60
 His Gly Ile Tyr Leu Thr Gly Trp Val Val Ala Thr Val Val Ala Val
 65 70 75 80
 Gly Phe Leu Leu Gly Pro Phe Asp Leu Gly Val Ala Ala Gly Leu Ala
 85 90 95
 Leu Ile Val Gly Pro Leu Cys Gly Leu Leu Val His Met Gly Ala Phe
 100 105 110
 Val Gly Gly Asp Arg Asn Arg Val Leu Thr Ala Gly
 115 120

<210> 971
 <211> 618
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(595)
 <223> RXN02059

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 gtaaatgtga actgaaaaag tgaaaaggaa gatgataaag atg act caa cca cgg 115
 Met Thr Gln Pro Arg
 1 5
 ccc gat gcc gca tct gtg tcg ctg gaa aag aag cgc cca gaa gga tgg 163
 Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys Arg Pro Glu Gly Trp
 10 15 20
 cca gtg gga agc ttt gaa aca tac cca gaa gcc caa gca gca gtg gat 211
 Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala Gln Ala Ala Val Asp
 25 30 35


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ttg ctc agt gat aat gca ttc ccc gtc acc gaa ttg acc att gtt ggt 259
Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu Leu Thr Ile Val Gly
      40                      45                      50

gtg gac ctg att gaa gtg gaa cgc gtt aca ggt cgt ctc acg tgg ggt 307
Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly Arg Leu Thr Trp Gly
      55                      60                      65

cgt gtg att gcc gga gga atg gca tct ggc gca tgg ttg ggt ctg ttc 355
Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala Trp Leu Gly Leu Phe
      70                      75                      80                      85

ttt ggc att gtc atg gcc ttg atg tct gga ttc tgg ttc tct tcc atc 403
Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe Trp Phe Ser Ser Ile
      90                      95                      100

gca gcg gga ata ggt atg ggt ttg gtg ttt ggc att gtc ggt gca gca 451
Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly Ile Val Gly Ala Ala
      105                      110                      115

gtt cct tat gct gct tcc aaa ggc aag cgg gac ttt acc tct tca act 499
Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp Phe Thr Ser Ser Thr
      120                      125                      130

caa att gtg gcg ggg cgc tat gat gtg att tgt tcc cca gaa cgt gct 547
Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys Ser Pro Glu Arg Ala
      135                      140                      145

cgg gaa gct cga gac atg att gcc ctg aaa act cga gat ctc cgc caa 595
Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr Arg Asp Leu Arg Gln
      150                      155                      160                      165

taagttaaac taacgcctat gaa 618

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<210> 972

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 972

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Arg Pro Glu Gly Trp Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala
      20                      25                      30

Gln Ala Ala Val Asp Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu
      35                      40                      45

Leu Thr Ile Val Gly Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly
      50                      55                      60

Arg Leu Thr Trp Gly Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala
      65                      70                      75                      80

Trp Leu Gly Leu Phe Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe
      85                      90                      95

Trp Phe Ser Ser Ile Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly
      100                      105                      110

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Ile Val Gly Ala Ala Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp
 115 120 125

Phe Thr Ser Ser Thr Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys
 130 135 140

Ser Pro Glu Arg Ala Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr
 145 150 155 160

Arg Asp Leu Arg Gln
 165

<210> 973
 <211> 618
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(595)
 <223> FRXA02059

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gtaaatgtga actgaaaaag tgaaaaggaa gatgataaag atg act caa cca cgg 115
 Met Thr Gln Pro Arg
 1 5

ccc gat gcc gca tct gtg tcg ctg gaa aag aag cgc cca gaa gga tgg 163
 Pro Asp Ala Ala Ser Val Ser Leu Glu Lys Lys Arg Pro Glu Gly Trp
 10 15 20

cca gtg gga agc ttt gaa aca tac cca gaa gcc caa gca gca gtg gat 211
 Pro Val Gly Ser Phe Glu Thr Tyr Pro Glu Ala Gln Ala Ala Val Asp
 25 30 35

ttg ctc agt gat aat gca ttc ccc gtc acc gaa ttg acc att gtt ggt 259
 Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu Leu Thr Ile Val Gly
 40 45 50

gtg gac ctg att gaa gtg gaa cgc gtt aca ggt cgt ctc acg tgg ggt 307
 Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly Arg Leu Thr Trp Gly
 55 60 65

cgt gtg att gcc gga gga atg gca tct ggc gca tgg ttg ggt ctg ttc 355
 Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala Trp Leu Gly Leu Phe
 70 75 80 85

ttt ggc att gtc atg gcc ttg atg tct gga ttc tgg ttc tct tcc atc 403
 Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe Trp Phe Ser Ser Ile
 90 95 100

gca gcg gga ata ggt atg ggt ttg gtg ttt ggc att gtc ggt gca gca 451
 Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly Ile Val Gly Ala Ala
 105 110 115

gtt cct tat gct gct tcc aaa ggc aag cgg gac ttt acc tct tca act 499
 Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp Phe Thr Ser Ser Thr

120	125	130	
caa att gtg gcg ggg cgc tat gat gtg att tgt tcc cca gaa cgt gct			547
Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys Ser Pro Glu Arg Ala			
135	140	145	
cgg gaa gct cga gac atg att gcc ctg aaa act cga gat ctc cgc caa			595
Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr Arg Asp Leu Arg Gln			
150	155	160	165
taagttaaac taacgcctat gaa			618

<210> 974
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 974
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 Gln Ala Ala Val Asp Leu Leu Ser Asp Asn Ala Phe Pro Val Thr Glu
 35 40 45
 Leu Thr Ile Val Gly Val Asp Leu Ile Glu Val Glu Arg Val Thr Gly
 50 55 60
 Arg Leu Thr Trp Gly Arg Val Ile Ala Gly Gly Met Ala Ser Gly Ala
 65 70 75 80
 Trp Leu Gly Leu Phe Phe Gly Ile Val Met Ala Leu Met Ser Gly Phe
 85 90 95
 Trp Phe Ser Ser Ile Ala Ala Gly Ile Gly Met Gly Leu Val Phe Gly
 100 105 110
 Ile Val Gly Ala Ala Val Pro Tyr Ala Ala Ser Lys Gly Lys Arg Asp
 115 120 125
 Phe Thr Ser Ser Thr Gln Ile Val Ala Gly Arg Tyr Asp Val Ile Cys
 130 135 140
 Ser Pro Glu Arg Ala Arg Glu Ala Arg Asp Met Ile Ala Leu Lys Thr
 145 150 155 160
 Arg Asp Leu Arg Gln
 165

<210> 975
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(592)

<223> RXN02066

<400> 975

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                                         Met Phe Asn Ser Asp
                                         1 5
acc acc gcg aat ctc caa gct aaa agt cga gat cgt gca gga tct aaa 163
Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp Arg Ala Gly Ser Lys
              10              15              20
gca aag cgc agc agg cca agt ttt gat tca gta gcg cgg gat gtt ttg 211
Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val Ala Arg Asp Val Leu
              25              30              35
gat gtt cga aca aaa aca gca caa gtt aaa aac aag gct aaa gag ttt 259
Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn Lys Ala Lys Glu Phe
              40              45              50
tcc tct gtt gat cac ctt tca gca gac gcc gca gcc atg ttt gta gac 307
Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala Ala Met Phe Val Asp
              55              60              65
aat gaa ctg tcc cgt ggc gcc atg cat cgc gcc agg ctg cac att gtg 355
Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala Arg Leu His Ile Val
              70              75              80              85
cac tgc gct gaa tgt agg gaa gag att aac cgt cag cgg gaa acc gtt 403
His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg Gln Arg Glu Thr Val
              90              95              100
gat tat ctc cgc tca gag tgc aaa aac gaa gaa gtg tcc gcc cca atg 451
Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu Val Ser Ala Pro Met
              105              110              115
gac ctc aaa gca cgg ctt gcc agc ctc gcc act gag tgc atg cct ggc 499
Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr Glu Cys Met Pro Gly
              120              125              130
cct ggc gca gag aat tta gca atg cag cgc cca gag tct ttt gtg gct 547
Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro Glu Ser Phe Val Ala
              135              140              145
aaa gtt gag tcc gta gtg cgc gca gtt cgt aag aac caa ggc cgc 592
Lys Val Glu Ser Val Val Arg Ala Val Arg Lys Asn Gln Gly Arg
              150              155              160
taatttttaa tccttattta cat 615

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<210> 976

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 976

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 Ala Arg Asp Val Leu Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn
 35 40 45
 Lys Ala Lys Glu Phe Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala
 50 55 60
 Ala Met Phe Val Asp Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala
 65 70 75 80
 Arg Leu His Ile Val His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg
 85 90 95
 Gln Arg Glu Thr Val Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu
 100 105 110
 Val Ser Ala Pro Met Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr
 115 120 125
 Glu Cys Met Pro Gly Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro
 130 135 140
 Glu Ser Phe Val Ala Lys Val Glu Ser Val Val Arg Ala Val Arg Lys
 145 150 155 160
 Asn Gln Gly Arg

<210> 977

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> FRXA02066

<400> 977

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acatccttga aagtcgagac acaggaggtc atcggaagat atg ttc aat tcc gac 115
 Met Phe Asn Ser Asp
 1 5

acc acc gcg aat ctc caa gct aaa agt cga gat cgt gca gga tct aaa 163
 Thr Thr Ala Asn Leu Gln Ala Lys Ser Arg Asp Arg Ala Gly Ser Lys
 10 15 20

gca aag cgc agc agg cca agt ttt gat tca gta gcg cgg gat gtt ttg 211
 Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val Ala Arg Asp Val Leu
 25 30 35

gat gtt cga aca aaa aca gca caa gtt aaa aac aag gct aaa gag ttt 259
 Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn Lys Ala Lys Glu Phe
 40 45 50

tcc tct gtt gat cac ctt tca gca gac gcc gca gcc atg ttt gta gac 307

Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala Ala Met Phe Val Asp
 55 60 65
 aat gaa ctg tcc cgt ggc gcc atg cat cgc gcc agg ctg cac att gtg 355
 Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala Arg Leu His Ile Val
 70 75 80 85
 cac tgc gct gaa tgt agg gaa gag att aac cgt cag cgg gaa acc gtt 403
 His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg Gln Arg Glu Thr Val
 90 95 100
 gat tat ctc cgc tca gag tgc aaa aac gaa gaa gtg tcc gcc cca atg 451
 Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu Val Ser Ala Pro Met
 105 110 115
 gac ctc aaa gca cgg ctt gcc agc ctc gcc act gag tgc atg cct ggc 499
 Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr Glu Cys Met Pro Gly
 120 125 130
 cct ggc gca gag aat tta gca atg cag cgc cca gag tct ttt gtg gct 547
 Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro Glu Ser Phe Val Ala
 135 140 145
 aaa gtt gag tcc gta gtg cgc gca gtt cgt aag aac caa ggc cgc 592
 Lys Val Glu Ser Val Val Arg Ala Val Arg Lys Asn Gln Gly Arg
 150 155 160
 taatttttaa tccttattta cat 615

<210> 978

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 978

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Arg Ala Gly Ser Lys Ala Lys Arg Ser Arg Pro Ser Phe Asp Ser Val
 20 25 30

Ala Arg Asp Val Leu Asp Val Arg Thr Lys Thr Ala Gln Val Lys Asn
 35 40 45

Lys Ala Lys Glu Phe Ser Ser Val Asp His Leu Ser Ala Asp Ala Ala
 50 55 60

Ala Met Phe Val Asp Asn Glu Leu Ser Arg Gly Ala Met His Arg Ala
 65 70 75 80

Arg Leu His Ile Val His Cys Ala Glu Cys Arg Glu Glu Ile Asn Arg
 85 90 95

Gln Arg Glu Thr Val Asp Tyr Leu Arg Ser Glu Cys Lys Asn Glu Glu
 100 105 110

Val Ser Ala Pro Met Asp Leu Lys Ala Arg Leu Ala Ser Leu Ala Thr
 115 120 125

Glu Cys Met Pro Gly Pro Gly Ala Glu Asn Leu Ala Met Gln Arg Pro

130 135 140
 Glu Ser Phe Val Ala Lys Val Glu Ser Val Val Arg Ala Val Arg Lys
 145 150 155 160
 Asn Gln Gly Arg

<210> 979
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(556)
 <223> RXN02067

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 Val Gly Trp Gly Glu
 1 5
 atc ttc ctc tta gtc gtt gtg ggc ctt gtt gtc atc ggc ccg gaa cgg 163
 Ile Phe Leu Leu Val Val Val Gly Leu Val Val Ile Gly Pro Glu Arg
 10 15 20
 ttg cct cgt ttg atc cag gac gca cgc gct gcg ctg ctc gct gca cgt 211
 Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala Leu Leu Ala Ala Arg
 25 30 35
 acc gct atc gac aat gca aag cag tcg ttg gac agt gat ttt ggt tcg 259
 Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp Ser Asp Phe Gly Ser
 40 45 50
 gaa ttt gat gaa atc cga aag cca cta acc cag gtt gca cag tac agc 307
 Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln Val Ala Gln Tyr Ser
 55 60 65
 cgg atg agc ccc aag acg gcc atc act aag gcg tta ttt gat aat gat 355
 Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala Leu Phe Asp Asn Asp
 70 75 80 85
 tcc tcg ttc ctg gat gac ttt gat cca aag aag atc atg gcc gaa gga 403
 Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys Ile Met Ala Glu Gly
 90 95 100
 aca gaa ggc gaa gct cag cgc aac aag cag gca gct gac aac aat gcg 451
 Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala Ala Asp Asn Asn Ala
 105 110 115
 aat gtg gtg gaa cgt cca gct gat ggt tcc acc gca cgc cca acg caa 499
 Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr Ala Arg Pro Thr Gln
 120 125 130
 aac gat cca aaa gac ggc ccg aat tac tca ggt ggc gtc tct tgg acc 547
 Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly Gly Val Ser Trp Thr
 135 140 145

gat att att tagcttttat ttaacgccaa gcc
 Asp Ile Ile
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579

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 <211> 152
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 980
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 Leu Leu Ala Ala Arg Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp
 35 40 45
 Ser Asp Phe Gly Ser Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln
 50 55 60
 Val Ala Gln Tyr Ser Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala
 65 70 75 80
 Leu Phe Asp Asn Asp Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys
 85 90 95
 Ile Met Ala Glu Gly Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala
 100 105 110
 Ala Asp Asn Asn Ala Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr
 115 120 125
 Ala Arg Pro Thr Gln Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly
 130 135 140
 Gly Val Ser Trp Thr Asp Ile Ile
 145 150

<210> 981
 <211> 579
 <212> DNA
 <213> Corynebacterium glutamicum

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 Val Gly Trp Gly Glu
 1 5
 atc ttc ctc tta gtc gtt gtg ggc ctt gtt gtc atc ggc ccg gaa cgg 163

Ile Phe Leu Leu Val Val Val Gly Leu Val Val Ile Gly Pro Glu Arg
 10 15 20
 ttg cct cgt ttg atc cag gac gca cgc gct gcg ctg ctc gct gca cgt 211
 Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala Leu Leu Ala Ala Arg
 25 30 35
 acc gct atc gac aat gca aag cag tcg ttg gac agt gat ttt ggt tcg 259
 Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp Ser Asp Phe Gly Ser
 40 45 50
 gaa ttt gat gaa atc cga aag cca cta acc cag gtt gca cag tac agc 307
 Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln Val Ala Gln Tyr Ser
 55 60 65
 cgg atg agc ccc aag acg gcc atc act aag gcg tta ttt gat aat gat 355
 Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala Leu Phe Asp Asn Asp
 70 75 80 85
 tcc tcg ttc ctg gat gac ttt gat cca aag aag atc atg gcc gaa gga 403
 Ser Ser Phe Leu Asp Asp Phe Asp Pro Lys Lys Ile Met Ala Glu Gly
 90 95 100
 aca gaa ggc gaa gct cag cgc aac aag cag gca gct gac aac aat gcg 451
 Thr Glu Gly Glu Ala Gln Arg Asn Lys Gln Ala Ala Asp Asn Asn Ala
 105 110 115
 aat gtg gtg gaa cgt cca gct gat ggt tcc acc gca cgc cca acg caa 499
 Asn Val Val Glu Arg Pro Ala Asp Gly Ser Thr Ala Arg Pro Thr Gln
 120 125 130
 aac gat cca aaa gac ggc ccg aat tac tca ggt ggc gtc tct tgg acc 547
 Asn Asp Pro Lys Asp Gly Pro Asn Tyr Ser Gly Gly Val Ser Trp Thr
 135 140 145
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 Asp Ile Ile
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<210> 982

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 982

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 Ile Gly Pro Glu Arg Leu Pro Arg Leu Ile Gln Asp Ala Arg Ala Ala
 20 25 30
 Leu Leu Ala Ala Arg Thr Ala Ile Asp Asn Ala Lys Gln Ser Leu Asp
 35 40 45
 Ser Asp Phe Gly Ser Glu Phe Asp Glu Ile Arg Lys Pro Leu Thr Gln
 50 55 60
 Val Ala Gln Tyr Ser Arg Met Ser Pro Lys Thr Ala Ile Thr Lys Ala
 65 70 75 80

gtg agt gac gct cgt cga gaa gca aac agc gtc acc gag cgc gcc cag 499
Val Ser Asp Ala Arg Arg Glu Ala Asn Ser Val Thr Glu Arg Ala Gln
120 125 130

gct gaa tct gag cgc ctg gtc aac tcc ggc aat gat gcg tat cgc cgc 547
Ala Glu Ser Glu Arg Leu Val Asn Ser Gly Asn Asp Ala Tyr Arg Arg
135 140 145

gcg gtt gct gaa ggc cag gcc gag cag gat cgc ctg gtc agc gag gca 595
Ala Val Ala Glu Gly Gln Ala Glu Gln Asp Arg Leu Val Ser Glu Ala
150 155 160 165

gaa gtg gtg cgt cgc tcc acg gaa gaa gca cac cgc att gtg gat gca 643
Glu Val Val Arg Arg Ser Thr Glu Glu Ala His Arg Ile Val Asp Ala
170 175 180

gcg cac gct gac tcc aac aag ctg cgc aat gaa tgc gat gac tac gtg 691
Ala His Ala Asp Ser Asn Lys Leu Arg Asn Glu Cys Asp Asp Tyr Val
185 190 195

gat acc aag ttg gca gag ttt gaa acc tcg ctg tcc acc acg ttg cgt 739
Asp Thr Lys Leu Ala Glu Phe Glu Thr Ser Leu Ser Thr Thr Leu Arg
200 205 210

tct gtc act gct gat cgt tcc gca cta cgc cga gga gct gga gct act 787
Ser Val Thr Ala Asp Arg Ser Ala Leu Arg Arg Gly Ala Gly Ala Thr
215 220 225

ggc cgc gag ctg cgc gat gag caa ccg gca gcg cgt ggt gaa tat gag 835
Gly Arg Glu Leu Arg Asp Glu Gln Pro Ala Ala Arg Gly Glu Tyr Glu
230 235 240 245

cgg gac tac gag cgt gat tat gaa cga ggc tac gaa cgc gac gat cga 883
Arg Asp Tyr Glu Arg Asp Tyr Glu Arg Gly Tyr Glu Arg Asp Asp Arg
250 255 260

gac tac tagtttccaa gaaaccattt agg 912
Asp Tyr

<210> 984

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 984

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20 25 30

Glu Val Leu Ala Leu Leu Asp Asp Leu Arg Asp Ala Leu Pro Val Glu
35 40 45

Leu Asp Asp Ala Gln Asp Val Leu Asp His Arg Asp Gly Val Ile Arg
50 55 60

Glu Ala Glu Glu Lys Ala Ile Ala Leu Val Asp Asp Ala Glu Asn Glu
65 70 75 80

Ala Arg Asn Leu Leu Ala Arg Ala Thr Glu Glu Ser Asp Ala Met Val
85 90 95

Glu Asp Ala Thr Lys His Ala His Ser Val Val Ala Lys Ala Asn Asp
100 105 110

Thr Ala Asp Arg Ile Val Ser Asp Ala Arg Arg Glu Ala Asn Ser Val
115 120 125

Thr Glu Arg Ala Gln Ala Glu Ser Glu Arg Leu Val Asn Ser Gly Asn
130 135 140

Asp Ala Tyr Arg Arg Ala Val Ala Glu Gly Gln Ala Glu Gln Asp Arg
145 150 155 160

Leu Val Ser Glu Ala Glu Val Val Arg Arg Ser Thr Glu Glu Ala His
165 170 175

Arg Ile Val Asp Ala Ala His Ala Asp Ser Asn Lys Leu Arg Asn Glu
180 185 190

Cys Asp Asp Tyr Val Asp Thr Lys Leu Ala Glu Phe Glu Thr Ser Leu
195 200 205

Ser Thr Thr Leu Arg Ser Val Thr Ala Asp Arg Ser Ala Leu Arg Arg
210 215 220

Gly Ala Gly Ala Thr Gly Arg Glu Leu Arg Asp Glu Gln Pro Ala Ala
225 230 235 240

Arg Gly Glu Tyr Glu Arg Asp Tyr Glu Arg Asp Tyr Glu Arg Gly Tyr
245 250 255

Glu Arg Asp Asp Arg Asp Tyr
260

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<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(634)
<223> RXN02076

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Met Lys Ser Pro Phe
1 5

att ttt gat gtc gcc gca ctc ctt cgt gga agt gcc ctt ccg gaa cac 163
Ile Phe Asp Val Ala Ala Leu Leu Arg Gly Ser Ala Leu Pro Glu His
10 15 20

ctc acc caa tca ggt cca agc ccg acc cgc att ggt ccg gaa atg atc 211
Leu Thr Gln Ser Gly Pro Ser Pro Thr Arg Ile Gly Pro Glu Met Ile

25	30	35	
gcg atc ccc gag ggc gga aaa gtt atc gta gaa gcc cag atc att cca			259
Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu Ala Gln Ile Ile Pro			
40	45	50	
ctc ggt gga ggc ctg gcc gtc gaa gca gat atc gaa gcg cag ctt ctg			307
Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile Glu Ala Gln Leu Leu			
55	60	65	
gga cag tgc tcc cgc tgc ctc cgc gaa ctc acc cca acc aag acg ctg			355
Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr Pro Thr Lys Thr Leu			
70	75	80	85
cac gtc tct gag gtt ttt gct gcc gat cca gac ttt gtt act ggt gaa			403
His Val Ser Glu Val Phe Ala Ala Asp Pro Asp Phe Val Thr Gly Glu			
90	95	100	
gat gca gca gat gac gaa gat gag ctg cca atg gtt aac caa gac cag			451
Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met Val Asn Gln Asp Gln			
105	110	115	
att gat ctg ctt cag tct gtc att gat gaa gct ggt ctg acc ttg ccg			499
Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala Gly Leu Thr Leu Pro			
120	125	130	
ttt aac cct gtc tgc gaa gaa ctt ggg tac ggc gca tgc cag gat gat			547
Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly Ala Cys Gln Asp Asp			
135	140	145	
gaa acg cca gct cct gac ggt gtc tct gaa gaa gta gaa gac gag gaa			595
Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu Val Glu Asp Glu Glu			
150	155	160	165
aag gtc gat ccg cgc tgg gct ggt ttg gag aag ttc ctg tgagcaggaa			644
Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys Phe Leu			
170	175		
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<210> 986

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 986

Met	Lys	Ser	Pro	Phe	Ile	Phe	Asp	Val	Ala	Ala	Leu	Leu	Arg	Gly	Ser
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Ala	Leu	Pro	Glu	His	Leu	Thr	Gln	Ser	Gly	Pro	Ser	Pro	Thr	Arg	Ile
	20						25						30		

Gly	Pro	Glu	Met	Ile	Ala	Ile	Pro	Glu	Gly	Gly	Lys	Val	Ile	Val	Glu
	35						40					45			

Ala	Gln	Ile	Ile	Pro	Leu	Gly	Gly	Gly	Leu	Ala	Val	Glu	Ala	Asp	Ile
	50					55					60				

Glu	Ala	Gln	Leu	Leu	Gly	Gln	Cys	Ser	Arg	Cys	Leu	Arg	Glu	Leu	Thr
65					70					75					80

His Val Ser Glu Val Phe Ala Ala Asp Pro Asp Phe Val Thr Gly Glu
 90 95 100
 gat gca gca gat gac gaa gat gag ctg cca atg gtt aac caa gac cag 451
 Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met Val Asn Gln Asp Gln
 105 110 115
 att gat ctg ctt cag tct gtc att gat gaa gct ggt ctg acc ttg ccg 499
 Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala Gly Leu Thr Leu Pro
 120 125 130
 ttt aac cct gtc tgc gaa gaa ctt ggg tac ggc gca tgc cag gat gat 547
 Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly Ala Cys Gln Asp Asp
 135 140 145
 gaa acg cca gct cct gac ggt gtc tct gaa gaa gta gaa gac gag gaa 595
 Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu Val Glu Asp Glu Glu
 150 155 160 165
 aag gtc gat ccg cgc tgg gct ggt ttg gag aag ttc ctg tgagcaggaa 644
 Lys Val Asp Pro Arg Trp Ala Gly Leu Glu Lys Phe Leu
 170 175
 aaagaatcgc ctc 657

<210> 988
 <211> 178
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 988
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 20 25 30
 Gly Pro Glu Met Ile Ala Ile Pro Glu Gly Gly Lys Val Ile Val Glu
 35 40 45
 Ala Gln Ile Ile Pro Leu Gly Gly Gly Leu Ala Val Glu Ala Asp Ile
 50 55 60
 Glu Ala Gln Leu Leu Gly Gln Cys Ser Arg Cys Leu Arg Glu Leu Thr
 65 70 75 80
 Pro Thr Lys Thr Leu His Val Ser Glu Val Phe Ala Ala Asp Pro Asp
 85 90 95
 Phe Val Thr Gly Glu Asp Ala Ala Asp Asp Glu Asp Glu Leu Pro Met
 100 105 110
 Val Asn Gln Asp Gln Ile Asp Leu Leu Gln Ser Val Ile Asp Glu Ala
 115 120 125
 Gly Leu Thr Leu Pro Phe Asn Pro Val Cys Glu Glu Leu Gly Tyr Gly
 130 135 140
 Ala Cys Gln Asp Asp Glu Thr Pro Ala Pro Asp Gly Val Ser Glu Glu
 145 150 155 160

Phe Leu

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<223> RXN02094
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Met Ala Glu His Asn																
1 5																
gcc atc atc acg gat gca gta cat tcc gac ccc gct gtt tta gaa gac											163					
Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro Ala Val Leu Glu Asp																
10 15 20																
aac gcc ggg ttc agc gga aag tac cta atc cgt gcc ctg gac aag gca											211					
Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg Ala Leu Asp Lys Ala																
25 30 35																
gct cat atg caa aca ggt gcc atc gag gga tac att tct tgg ctt cgg											259					
Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr Ile Ser Trp Leu Arg																
40 45 50																
aag cac aat cct gag aaa aca ccg gcg cag ctg cag gta ctc gtc gac											307					
Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu Gln Val Leu Val Asp																
55 60 65																
aag cat ttt atg cgc ctt gcc acc ggc tct ggc gct ggt gtg ggc atg											355					
Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly Ala Gly Val Gly Met																
70 75 80 85																
gct gcg gcc gtg cca ggc att ggc ttt gtc acg ggt gct ctt gcc gtt											403					
Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr Gly Ala Leu Ala Val																
90 95 100																
ggt gct gaa tcg ttg gtg ttt ttg gat gct gct gcg ttt tac acc atg											451					
Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala Ala Phe Tyr Thr Met																
105 110 115																
gca tcc gcg cac ctg cgt ggc atc gac atc cgc cat cct gaa cgc cga											499					
Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg His Pro Glu Arg Arg																
120 125 130																
cgt ggt ttg att ttg gtg gtt ctg ctg ggc acc gca ggc aaa gcc att											547					
Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr Ala Gly Lys Ala Ile																
135 140 145																

gtt gac gca ggc gtc ggt gat tta tcc aag aaa aac cac gcg ccg ggc 595
Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys Asn His Ala Pro Gly
150 155 160 165

att gcg att tcc cgg ttt aat atc ggt ggc ttg atg gaa gtc aac ggc 643
Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu Met Glu Val Asn Gly
170 175 180

cga ctg atg cgc tac gca gtg aag gaa gta agc aag cgt ttc cgt tcg 691
Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser Lys Arg Phe Arg Ser
185 190 195

gca ttg att ggc aaa att ctg ccg ttt ggt atc ggt gcg gtg ctg ggc 739
Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile Gly Ala Val Leu Gly
200 205 210

acg atg gcc aac cgc aaa att gcc aag agg act gtc gga aac gca tac 787
Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr Val Gly Asn Ala Tyr
215 220 225

gac tct ctt ggt cct ctc ccc acc cat ttt taagtactca agacccttcc 837
Asp Ser Leu Gly Pro Leu Pro Thr His Phe
230 235

aac 840

<210> 990
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 990
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20 25 30

Ala Leu Asp Lys Ala Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr
35 40 45

Ile Ser Trp Leu Arg Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu
50 55 60

Gln Val Leu Val Asp Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly
65 70 75 80

Ala Gly Val Gly Met Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr
85 90 95

Gly Ala Leu Ala Val Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala
100 105 110

Ala Phe Tyr Thr Met Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg
115 120 125

His Pro Glu Arg Arg Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr
130 135 140

Ala Gly Lys Ala Ile Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys

145	150	155	160
Asn His Ala Pro Gly Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu			
	165	170	175
Met Glu Val Asn Gly Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser			
	180	185	190
Lys Arg Phe Arg Ser Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile			
	195	200	205
Gly Ala Val Leu Gly Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr			
	210	215	220
Val Gly Asn Ala Tyr Asp Ser Leu Gly Pro Leu Pro Thr His Phe			
225	230	235	

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> FRXA02094

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 Met Ala Glu His Asn
 1 5
 gcc atc atc acg gat gca gta cat tcc gac ccc gct gtt tta gaa gac 163
 Ala Ile Ile Thr Asp Ala Val His Ser Asp Pro Ala Val Leu Glu Asp
 10 15 20
 aac gcc ggg ttc agc gga aag tac cta atc cgt gcc ctg gac aag gca 211
 Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg Ala Leu Asp Lys Ala
 25 30 35
 gct cat atg caa aca ggt gcc atc gag gga tac att tct tgg ctt cgg 259
 Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr Ile Ser Trp Leu Arg
 40 45 50
 aag cac aat cct gag aaa aca ccg gcg cag ctg cag gta ctc gtc gac 307
 Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu Gln Val Leu Val Asp
 55 60 65
 aag cat ttt atg cgc ctt gcc acc ggc tct ggc gct ggt gtg ggc atg 355
 Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly Ala Gly Val Gly Met
 70 75 80 85
 gct gcg gcc gtg cca ggc att ggc ttt gtc acg ggt gct ctt gcc gtt 403
 Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr Gly Ala Leu Ala Val
 90 95 100
 ggt gct gaa tcg ttg gtg ttt ttg gat gct gct gcg ttt tac acc atg 451
 Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala Ala Phe Tyr Thr Met

105	110	115	
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Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg His Pro Glu Arg Arg			
120	125	130	
cgt ggt ttg att ttg gtg gtt ctg ctg ggc acc gca ggc aaa gcc att			547
Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr Ala Gly Lys Ala Ile			
135	140	145	
gtt gac gca ggc gtc ggt gat tta tcc aag aaa aac cac gcg ccg ggc			595
Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys Asn His Ala Pro Gly			
150	155	160	165
att gcg att tcc cgg ttt aat atc ggt ggc ttg atg gaa gtc aac ggc			643
Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu Met Glu Val Asn Gly			
170	175	180	
cga ctg atg cgc tac gca gtg aag gaa gta agc aag cgt ttc cgt tcg			691
Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser Lys Arg Phe Arg Ser			
185	190	195	
gca ttg att ggc aaa att ctg ccg ttt ggt atc ggt gcg gtg ctg ggc			739
Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile Gly Ala Val Leu Gly			
200	205	210	
acg atg gcc aac cgc aaa att gcc aag agg act gtc gga aac gca tac			787
Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr Val Gly Asn Ala Tyr			
215	220	225	
gac tct ctt ggt cct ctc ccc acc cat ttt taagtactca agacccttcc			837
Asp Ser Leu Gly Pro Leu Pro Thr His Phe			
230	235		
aac			840

<210> 992
 <211> 239
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 992
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 Ala Val Leu Glu Asp Asn Ala Gly Phe Ser Gly Lys Tyr Leu Ile Arg
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 Ala Leu Asp Lys Ala Ala His Met Gln Thr Gly Ala Ile Glu Gly Tyr
 35 40 45
 Ile Ser Trp Leu Arg Lys His Asn Pro Glu Lys Thr Pro Ala Gln Leu
 50 55 60
 Gln Val Leu Val Asp Lys His Phe Met Arg Leu Ala Thr Gly Ser Gly
 65 70 75 80
 Ala Gly Val Gly Met Ala Ala Ala Val Pro Gly Ile Gly Phe Val Thr
 85 90 95

Gly Ala Leu Ala Val Gly Ala Glu Ser Leu Val Phe Leu Asp Ala Ala
100 105 110

Ala Phe Tyr Thr Met Ala Ser Ala His Leu Arg Gly Ile Asp Ile Arg
115 120 125

His Pro Glu Arg Arg Arg Gly Leu Ile Leu Val Val Leu Leu Gly Thr
130 135 140

Ala Gly Lys Ala Ile Val Asp Ala Gly Val Gly Asp Leu Ser Lys Lys
145 150 155 160

Asn His Ala Pro Gly Ile Ala Ile Ser Arg Phe Asn Ile Gly Gly Leu
165 170 175

Met Glu Val Asn Gly Arg Leu Met Arg Tyr Ala Val Lys Glu Val Ser
180 185 190

Lys Arg Phe Arg Ser Ala Leu Ile Gly Lys Ile Leu Pro Phe Gly Ile
195 200 205

Gly Ala Val Leu Gly Thr Met Ala Asn Arg Lys Ile Ala Lys Arg Thr
210 215 220

Val Gly Asn Ala Tyr Asp Ser Leu Gly Pro Leu Pro Thr His Phe
225 230 235

<210> 993

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXN02104

<400> 993

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Met Ser Asn Ser Pro
1 5

acc gac gtt tca acg agc gca cct cga att atg atc gcg cca gat tcc 163
Thr Asp Val Ser Thr Ser Ala Pro Arg Ile Met Ile Ala Pro Asp Ser
10 15 20

tac aaa gga acc gct acc gca tca gaa gct gcg caa tac tta ggc gaa 211
Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala Gln Tyr Leu Gly Glu
25 30 35

ggc gtg ttg gaa att ttg ccc aac gcc tcc att acg ttg gca ccc atg 259
Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile Thr Leu Ala Pro Met
40 45 50

gcc gac ggt ggc gaa gga aca tcc tca gtt ttc ggc ggg cag gtc ata 307
Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe Gly Gly Gln Val Ile
55 60 65

aca tta ccc acg aca aat gcc gcg gga cgc ctc acc gaa gcc agc tac	355
Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu Thr Glu Ala Ser Tyr	
70 75 80 85	
acc tta gat tcc gaa aca aac act gcc tac att gac atc gcc gca gcc	403
Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile Asp Ile Ala Ala Ala	
90 95 100	
tcc ggt ttg ccc gcc gtt gca gac gat cta gtc ccc acc acc ggc gat	451
Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val Pro Thr Thr Gly Asp	
105 110 115	
acc tac ggc acc ggc gtt ttg atc gca gac gcg gtc acc cgt ggc gca	499
Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala Val Thr Arg Gly Ala	
120 125 130	
act cgc att gct tta ggc ctt ggc gga tca gcc aca act gac gcc ggc	547
Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala Thr Thr Asp Ala Gly	
135 140 145	
tca gga att ctc atc gcc ctc ggc gcc gtc cca cgc aac aaa gag ggc	595
Ser Gly Ile Leu Ile Ala Leu Gly Ala Val Pro Arg Asn Lys Glu Gly	
150 155 160 165	
tac gca cta cga acc ggt ggc gcc gac ctc atc aac ctc gat tac atc	643
Tyr Ala Leu Arg Thr Gly Gly Ala Asp Leu Ile Asn Leu Asp Tyr Ile	
170 175 180	
gat acc gcc gaa ctc aac atc ccc gca gcc gcc gtc gaa tgg atc ctg	691
Asp Thr Ala Glu Leu Asn Ile Pro Ala Ala Ala Val Glu Trp Ile Leu	
185 190 195	
ctc acc gat gtc gac gcc ccc gcc acc ggc ccg cag ggc gcg gcc acc	739
Leu Thr Asp Val Asp Ala Pro Ala Thr Gly Pro Gln Gly Ala Ala Thr	
200 205 210	
gta ttc ggg ccc caa aaa ggt gcc acc gaa aaa gac att tcg ctt ctc	787
Val Phe Gly Pro Gln Lys Gly Ala Thr Glu Lys Asp Ile Ser Leu Leu	
215 220 225	
gac gcc gcc ctc cac cac gcc tgc gcc caa ctg gaa gtt gat ggc aca	835
Asp Ala Ala Leu His His Ala Cys Ala Gln Leu Glu Val Asp Gly Thr	
230 235 240 245	
aag cca ggt atg ggc gca gcc ggg ggc att gca atc gga ctg acg tgg	883
Lys Pro Gly Met Gly Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp	
250 255 260	
ctg tcc acc ctc atg cac ggc aac gac caa cag atc cat atc ctc ccc	931
Leu Ser Thr Leu Met His Gly Asn Asp Gln Gln Ile His Ile Leu Pro	
265 270 275	
ggc gcg cca ctg att gcc cgc tcc aac gga atc gag gat gcg ctg cca	979
Gly Ala Pro Leu Ile Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro	
280 285 290	
gaa act gac ttg ttg atc acc ggt gaa ggc cga cta gat tcc caa tcg	1027
Glu Thr Asp Leu Leu Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser	
295 300 305	
ttc acc gga aag gtt gtg ggc acc ctc cac ggt tta gct aaa gcc cac	1075

Phe Thr Gly Lys Val Val Gly Thr Leu His Gly Leu Ala Lys Ala His
 310 315 320 325
 gat gtg gat ctc gct gtt gcg gcc ggc atc gtg gaa ggc ggt att ccc 1123
 Asp Val Asp Leu Ala Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro
 330 335 340
 gat gat ttc cta gcg gta gaa atg att aaa tcc tcc gac gtt gca gca 1171
 Asp Asp Phe Leu Ala Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala
 345 350 355
 caa tta cgt gat gca ggc cga agg atc gct caa gaa tac gta gct caa 1219
 Gln Leu Arg Asp Ala Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln
 360 365 370
 aac tagcgaagga tctccacagt cca 1245
 Asn

<210> 994
 <211> 374
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 994
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 Gln Tyr Leu Gly Glu Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile
 35 40 45
 Thr Leu Ala Pro Met Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe
 50 55 60
 Gly Gly Gln Val Ile Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu
 65 70 75 80
 Thr Glu Ala Ser Tyr Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile
 85 90 95
 Asp Ile Ala Ala Ala Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val
 100 105 110
 Pro Thr Thr Gly Asp Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala
 115 120 125
 Val Thr Arg Gly Ala Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala
 130 135 140
 Thr Thr Asp Ala Gly Ser Gly Ile Leu Ile Ala Leu Gly Ala Val Pro
 145 150 155 160
 Arg Asn Lys Glu Gly Tyr Ala Leu Arg Thr Gly Gly Ala Asp Leu Ile
 165 170 175
 Asn Leu Asp Tyr Ile Asp Thr Ala Glu Leu Asn Ile Pro Ala Ala Ala
 180 185 190

Val Glu Trp Ile Leu Leu Thr Asp Val Asp Ala Pro Ala Thr Gly Pro
 195 200 205
 Gln Gly Ala Ala Thr Val Phe Gly Pro Gln Lys Gly Ala Thr Glu Lys
 210 215 220
 Asp Ile Ser Leu Leu Asp Ala Ala Leu His His Ala Cys Ala Gln Leu
 225 230 235 240
 Glu Val Asp Gly Thr Lys Pro Gly Met Gly Ala Ala Gly Gly Ile Ala
 245 250 255
 Ile Gly Leu Thr Trp Leu Ser Thr Leu Met His Gly Asn Asp Gln Gln
 260 265 270
 Ile His Ile Leu Pro Gly Ala Pro Leu Ile Ala Arg Ser Asn Gly Ile
 275 280 285
 Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu Ile Thr Gly Glu Gly Arg
 290 295 300
 Leu Asp Ser Gln Ser Phe Thr Gly Lys Val Val Gly Thr Leu His Gly
 305 310 315 320
 Leu Ala Lys Ala His Asp Val Asp Leu Ala Val Ala Ala Gly Ile Val
 325 330 335
 Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala Val Glu Met Ile Lys Ser
 340 345 350
 Ser Asp Val Ala Ala Gln Leu Arg Asp Ala Gly Arg Arg Ile Ala Gln
 355 360 365
 Glu Tyr Val Ala Gln Asn
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<210> 995
 <211> 443
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(420)
 <223> FRXA02104

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 gca gcc ggg ggc att gca atc gga ctg acg tgg ctg tcc acc ctc atg 96
 Ala Ala Gly Gly Ile Ala Ile Gly Leu Thr Trp Leu Ser Thr Leu Met
 20 25 30
 cac ggc aac gac caa cag atc cat atc ctc ccc ggc gcg cca ctg att 144
 His Gly Asn Asp Gln Gln Ile His Ile Leu Pro Gly Ala Pro Leu Ile
 35 40 45

gcc cgc tcc aac gga atc gag gat gcg ctg cca gaa act gac ttg ttg 192
Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu
50 55 60

atc acc ggt gaa ggc cga cta gat tcc caa tcg ttc acc gga aag gtt 240
Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser Phe Thr Gly Lys Val
65 70 75 80

gtg ggc acc ctc cac ggt tta gct aaa gcc cac gat gtg gat ctc gct 288
Val Gly Thr Leu His Gly Leu Ala Lys Ala His Asp Val Asp Leu Ala
85 90 95

gtt gcg gcc ggc atc gtg gaa ggc ggt att ccc gat gat ttc cta gcg 336
Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala
100 105 110

gta gaa atg att aaa tcc tcc gac gtt gca gca caa tta cgt gat gca 384
Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala Gln Leu Arg Asp Ala
115 120 125

ggc cga agg atc gct caa gaa tac gta gct caa aac tagcgaagga 430
Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln Asn
130 135 140

tctccacagt cca 443

<210> 996
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 996
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20 25 30

His Gly Asn Asp Gln Gln Ile His Ile Leu Pro Gly Ala Pro Leu Ile
35 40 45

Ala Arg Ser Asn Gly Ile Glu Asp Ala Leu Pro Glu Thr Asp Leu Leu
50 55 60

Ile Thr Gly Glu Gly Arg Leu Asp Ser Gln Ser Phe Thr Gly Lys Val
65 70 75 80

Val Gly Thr Leu His Gly Leu Ala Lys Ala His Asp Val Asp Leu Ala
85 90 95

Val Ala Ala Gly Ile Val Glu Gly Gly Ile Pro Asp Asp Phe Leu Ala
100 105 110

Val Glu Met Ile Lys Ser Ser Asp Val Ala Ala Gln Leu Arg Asp Ala
115 120 125

Gly Arg Arg Ile Ala Gln Glu Tyr Val Ala Gln Asn
130 135 140

<213> Corynebacterium glutamicum

<400> 998

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Ile Ala Pro Asp Ser Tyr Lys Gly Thr Ala Thr Ala Ser Glu Ala Ala
          20           25           30

Gln Tyr Leu Gly Glu Gly Val Leu Glu Ile Leu Pro Asn Ala Ser Ile
          35           40           45

Thr Leu Ala Pro Met Ala Asp Gly Gly Glu Gly Thr Ser Ser Val Phe
          50           55           60

Gly Gly Gln Val Ile Thr Leu Pro Thr Thr Asn Ala Ala Gly Arg Leu
          65           70           75           80

Thr Glu Ala Ser Tyr Thr Leu Asp Ser Glu Thr Asn Thr Ala Tyr Ile
          85           90           95

Asp Ile Ala Ala Ala Ser Gly Leu Pro Ala Val Ala Asp Asp Leu Val
          100          105          110

Pro Thr Thr Gly Asp Thr Tyr Gly Thr Gly Val Leu Ile Ala Asp Ala
          115          120          125

Val Thr Arg Gly Ala Thr Arg Ile Ala Leu Gly Leu Gly Gly Ser Ala
          130          135          140

Thr Thr Asp Ala Gly Ser Gly
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<210> 999

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(442)

<223> RXN02107

<400> 999

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acgccaccga ggagtggact aagcgagttc aatagtttct atg gat ctg cac aag 115
                                     Met Asp Leu His Lys
                                     1           5

gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt 163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
          10           15           20

cct ttc gga ccc gag cac gaa gtg tac aaa gtg cgg ggc aag gta ttt 211
Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val Arg Gly Lys Val Phe
          25           30           35

ttg ctg ctc acg ata cta aat gat gag ccg att atc acg ctg aaa tca 259
Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile Ile Thr Leu Lys Ser

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40	45	50	
gac ccc gag att ggc gct tca cta cgc agt ggc ttc ccc acc atc cag			307
Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly Phe Pro Thr Ile Gln			
55	60	65	
gct gga tat cac atg aac aaa gtg cac tgg ctg agc att agc gat ggt			355
Ala Gly Tyr His Met Asn Lys Val His Trp Leu Ser Ile Ser Asp Gly			
70	75	80	85
gaa cgg atc acg aaa gac ttc atc gaa ggt ctc gtg gaa gag tcc tat			403
Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu Val Glu Glu Ser Tyr			
90	95	100	
gaa ctg gta att tcc acc ttg ccg aag tat aaa agg cct taacttggtt			452
Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys Arg Pro			
105	110		
gcttgccgggt ggc			465

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1000
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 20 25 30
 Arg Gly Lys Val Phe Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile
 35 40 45
 Ile Thr Leu Lys Ser Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly
 50 55 60
 Phe Pro Thr Ile Gln Ala Gly Tyr His Met Asn Lys Val His Trp Leu
 65 70 75 80
 Ser Ile Ser Asp Gly Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu
 85 90 95
 Val Glu Glu Ser Tyr Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys
 100 105 110
 Arg Pro

<210> 1001
 <211> 465
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(442)
 <223> FRXA02107

<400> 1001

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                                         Met Asp Leu His Lys
                                         1 5

gta gct gca gcg cac gcg gcg act ctt ccc ctg agc acc aaa gag ttt 163
Val Ala Ala Ala His Ala Ala Thr Leu Pro Leu Ser Thr Lys Glu Phe
                        10 15 20

cct ttc gga ccc gag cac gaa gtg tac aaa gtg cgg ggc aag gta ttt 211
Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val Arg Gly Lys Val Phe
                        25 30 35

ttg ctg ctc acg ata cta aat gat gag ccg att atc acg ctg aaa tca 259
Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile Ile Thr Leu Lys Ser
                        40 45 50

gac ccc gag att ggc gct tca cta cgc agt ggc ttc ccc acc atc cag 307
Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly Phe Pro Thr Ile Gln
                        55 60 65

gct gga tat cac atg aac aaa gtg cac tgg ctg agc att agc gat ggt 355
Ala Gly Tyr His Met Asn Lys Val His Trp Leu Ser Ile Ser Asp Gly
                        70 75 80 85

gaa cgg atc acg aaa gac ttc atc gaa ggt ctc gtg gaa gag tcc tat 403
Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu Val Glu Glu Ser Tyr
                        90 95 100

gaa ctg gta att tcc acc ttg ccg aag tat aaa agg cct taacttggtt 452
Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys Arg Pro
                        105 110

gcttgccgggt ggc 465

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<210> 1002

<211> 114

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1002

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Ser Thr Lys Glu Phe Pro Phe Gly Pro Glu His Glu Val Tyr Lys Val
 20 25 30

Arg Gly Lys Val Phe Leu Leu Leu Thr Ile Leu Asn Asp Glu Pro Ile
 35 40 45

Ile Thr Leu Lys Ser Asp Pro Glu Ile Gly Ala Ser Leu Arg Ser Gly
 50 55 60

Phe Pro Thr Ile Gln Ala Gly Tyr His Met Asn Lys Val His Trp Leu
 65 70 75 80

Ser Ile Ser Asp Gly Glu Arg Ile Thr Lys Asp Phe Ile Glu Gly Leu

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85

90

95

Val Glu Glu Ser Tyr Glu Leu Val Ile Ser Thr Leu Pro Lys Tyr Lys
 100 105 110

Arg Pro

<210> 1003

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXN02108

<400> 1003

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agtataaaag gccttaactt gggtgcttgc ggggtggcaag atg ggt gat atg aaa 115
 Met Gly Asp Met Lys
 1 5

att acc cgc cac atc cat gca tgc gtt gag atc tca cag gga aac gat 163
 Ile Thr Arg His Ile His Ala Cys Val Glu Ile Ser Gln Gly Asn Asp
 10 15 20

cga atc att att gat ccc ggt act ttt ggc gcc cca gat tta tgt ggc 211
 Arg Ile Ile Ile Asp Pro Gly Thr Phe Gly Ala Pro Asp Leu Cys Gly
 25 30 35

gcg acc atc ctg gtc acc cac aat cat gcc gat cac gtt gat ccc gag 259
 Ala Thr Ile Leu Val Thr His Asn His Ala Asp His Val Asp Pro Glu
 40 45 50

ttg ctc aag ccc ggc atg acg att tac gcg cct cga tca gta gca cat 307
 Leu Leu Lys Pro Gly Met Thr Ile Tyr Ala Pro Arg Ser Val Ala His
 55 60 65

tca att cca gta gaa tgc cac atc gtg gaa cac ggc cga aac ttt acc 355
 Ser Ile Pro Val Glu Cys His Ile Val Glu His Gly Arg Asn Phe Thr
 70 75 80 85

gtt ggg tcc cta tcc gtt gag gtt ctt ggt tct gaa cat gcg atg ctc 403
 Val Gly Ser Leu Ser Val Glu Val Leu Gly Ser Glu His Ala Met Leu
 90 95 100

acc cat tcc atg ccg atc gcg gaa aac gtt gga tac tta atc aac ggc 451
 Thr His Ser Met Pro Ile Ala Glu Asn Val Gly Tyr Leu Ile Asn Gly
 105 110 115

cga gtg ctc cac ccc ggc gat acc ttc caa ccc att aaa gat gtc gaa 499
 Arg Val Leu His Pro Gly Asp Thr Phe Gln Pro Ile Lys Asp Val Glu
 120 125 130

ctc gcc ctg gtt cct gtc aac ggc ccc tgg gtg aaa atg ctg gat gtg 547
 Leu Ala Leu Val Pro Val Asn Gly Pro Trp Val Lys Met Leu Asp Val
 135 140 145

gaa ggc tat ttg aag aaa ttt cca cca aag cgt ttc atc ggc att cac 595
 Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys Arg Phe Ile Gly Ile His
 150 155 160 165
 gat ggc att gtt aat gat cgc ggt ttg gcg atc aac aag aag ttc tta 643
 Asp Gly Ile Val Asn Asp Arg Gly Leu Ala Ile Asn Lys Lys Phe Leu
 170 175 180
 acg cat ctt ggt gaa acc tat ggc tcg gaa tac tcg ccg ctt gaa gag 691
 Thr His Leu Gly Glu Thr Tyr Gly Ser Glu Tyr Ser Pro Leu Glu Glu
 185 190 195
 gga gag tcg ttg gaa att tagattcttg gtttagattc ttg 732
 Gly Glu Ser Leu Glu Ile
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<210> 1004

<211> 203

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1004

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 20 25 30
 Pro Asp Leu Cys Gly Ala Thr Ile Leu Val Thr His Asn His Ala Asp
 35 40 45
 His Val Asp Pro Glu Leu Leu Lys Pro Gly Met Thr Ile Tyr Ala Pro
 50 55 60
 Arg Ser Val Ala His Ser Ile Pro Val Glu Cys His Ile Val Glu His
 65 70 75 80
 Gly Arg Asn Phe Thr Val Gly Ser Leu Ser Val Glu Val Leu Gly Ser
 85 90 95
 Glu His Ala Met Leu Thr His Ser Met Pro Ile Ala Glu Asn Val Gly
 100 105 110
 Tyr Leu Ile Asn Gly Arg Val Leu His Pro Gly Asp Thr Phe Gln Pro
 115 120 125
 Ile Lys Asp Val Glu Leu Ala Leu Val Pro Val Asn Gly Pro Trp Val
 130 135 140
 Lys Met Leu Asp Val Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys Arg
 145 150 155 160
 Phe Ile Gly Ile His Asp Gly Ile Val Asn Asp Arg Gly Leu Ala Ile
 165 170 175
 Asn Lys Lys Phe Leu Thr His Leu Gly Glu Thr Tyr Gly Ser Glu Tyr
 180 185 190
 Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu Ile

195

200

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<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(535)
<223> FRXA02108

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MetThrIleTyrAla
15
cctcga tcagta gca cat tca att cca gta gaa tgc cac atc gtg gaa163
Pro Arg Ser Val Ala His Ser Ile Pro Val Glu Cys His Ile Val Glu
101520
cacggc cga aac ttt acc gtt ggg tcc cta tcc gtt gag gtt ctt ggt211
His Gly Arg Asn Phe Thr Val Gly Ser Leu Ser Val Glu Val Leu Gly
253035
tctgaa cat gcg atg ctc acc cat tcc atg ccg atc gcg gaa aac gtt259
Ser Glu His Ala Met Leu Thr His Ser Met Pro Ile Ala Glu Asn Val
404550
gga tac tta atc aac ggc cga gtg ctc cac ccc ggc gat acc ttc caa307
Gly Tyr Leu Ile Asn Gly Arg Val Leu His Pro Gly Asp Thr Phe Gln
556065
ccc att aaa gat gtc gaa ctc gcc ctg gtt cct gtc aac ggc ccc tgg355
Pro Ile Lys Asp Val Glu Leu Ala Leu Val Pro Val Asn Gly Pro Trp
70758085
gtg aaa atg ctg gat gtg gaa ggc tat ttg aag aaa ttt cca cca aag403
Val Lys Met Leu Asp Val Glu Gly Tyr Leu Lys Lys Phe Pro Pro Lys
9095100
cgt ttc atc ggc att cac gat ggc att gtt aat gat cgc ggt ttg gcg451
Arg Phe Ile Gly Ile His Asp Gly Ile Val Asn Asp Arg Gly Leu Ala
105110115
atc aac aag aag ttc tta acg cat ctt ggt gaa acc tat ggc tcg gaa499
Ile Asn Lys Lys Phe Leu Thr His Leu Gly Glu Thr Tyr Gly Ser Glu
120125130
tac tcg ccg ctt gaa gag gga gag tcg ttg gaa att tagattcttg545
Tyr Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu Ile
135140145
gttttagattc ttg558

<210> 1006
<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 1006

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Cys His Ile Val Glu His Gly Arg Asn Phe Thr Val Gly Ser Leu Ser
20 25 30
Val Glu Val Leu Gly Ser Glu His Ala Met Leu Thr His Ser Met Pro
35 40 45
Ile Ala Glu Asn Val Gly Tyr Leu Ile Asn Gly Arg Val Leu His Pro
50 55 60
Gly Asp Thr Phe Gln Pro Ile Lys Asp Val Glu Leu Ala Leu Val Pro
65 70 75 80
Val Asn Gly Pro Trp Val Lys Met Leu Asp Val Glu Gly Tyr Leu Lys
85 90 95
Lys Phe Pro Pro Lys Arg Phe Ile Gly Ile His Asp Gly Ile Val Asn
100 105 110
Asp Arg Gly Leu Ala Ile Asn Lys Lys Phe Leu Thr His Leu Gly Glu
115 120 125
Thr Tyr Gly Ser Glu Tyr Ser Pro Leu Glu Glu Gly Glu Ser Leu Glu
130 135 140
Ile
145

<210> 1007

<211> 509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(486)

<223> RXN02114

<400> 1007

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ctt ggc ggc atc gcc att ggt att tgg ctg ctc ggt ggt gtg ctc ggt 96
Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
20 25 30
ggg ttg gtt atc cgc aag ccg ggt gcc gca att ttc gtt gaa gta gtg 144
Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
35 40 45
gcc gca tgt gtc tct gca gcg ctt gct tca cag ttt ggt atc tcc acc 192
Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
50 55 60

att tac tcc ggc ttg gcg cag gga atc ggc gct gaa atc atc ttc gcg 240
 Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65 70 75 80
 ctg ttc ctc tac cgt cgc tac agc ctg ccc acc acc atg ctt gca ggt 288
 Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
 85 90 95
 atg ggc gca ggt ggc ggc gca att ttc ctg gaa atg ttc ttc tac gga 336
 Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
 100 105 110
 aac ctc gca aag acg atg tcc ttc aac atc atc tat tcc acc act gtc 384
 Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
 115 120 125
 ctt att tcc ggt gcg atc ctt gcc ggc ctg ctc agc tgg tac ctg gtc 432
 Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
 130 135 140
 cgc gcg ttg gcg agg act ggt gca ctt gat cgt ttc gcc gct ggc cgc 480
 Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
 145 150 155 160
 gag gta taaatgacca ccgcacttgg aac 509
 Glu Val

<210> 1008

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 1008

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 Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
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 Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
 35 40 45
 Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
 50 55 60
 Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65 70 75 80
 Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
 85 90 95
 Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
 100 105 110
 Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
 115 120 125
 Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val

130 135 140
 Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
 145 150 155 160

Glu Val

<210> 1009
 <211> 509
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(486)
 <223> FRXA02114

<400> 1009
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 Ser Ile Gly Tyr Ala Trp Thr Thr Ala Phe His Ala Leu Thr Pro Gly
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 ctt ggc ggc atc gcc att ggt att tgg ctg ctc ggt ggt gtg ctc ggt 96
 Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
 20 25 30
 ggg ttg gtt atc cgc aag ccg ggt gcc gca att ttc gtt gaa gta gtg 144
 Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
 35 40 45
 gcc gca tgt gtc tct gca gcg ctt gct tca cag ttt ggt atc tcc acc 192
 Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
 50 55 60
 att tac tcc ggc ttg gcg cag gga atc ggc gct gaa atc atc ttc gcg 240
 Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65 70 75 80
 ctg ttc ctc tac cgt cgc tac agc ctg ccc acc acc atg ctt gca ggt 288
 Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
 85 90 95
 atg ggc gca ggt ggc ggc gca att ttc ctg gaa atg ttc ttc tac gga 336
 Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
 100 105 110
 aac ctc gca aag acg atg tcc ttc aac atc atc tat tcc acc act gtc 384
 Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
 115 120 125
 ctt att tcc ggt gcg atc ctt gcc ggc ctg ctc agc tgg tac ctg gtc 432
 Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
 130 135 140
 cgc gcg ttg gcg agg act ggt gca ctt gat cgt ttc gcc gct ggc cgc 480
 Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
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Glu Val

<210> 1010

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 1010

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Leu Gly Gly Ile Ala Ile Gly Ile Trp Leu Leu Gly Gly Val Leu Gly
 20 25 30

Gly Leu Val Ile Arg Lys Pro Gly Ala Ala Ile Phe Val Glu Val Val
 35 40 45

Ala Ala Cys Val Ser Ala Ala Leu Ala Ser Gln Phe Gly Ile Ser Thr
 50 55 60

Ile Tyr Ser Gly Leu Ala Gln Gly Ile Gly Ala Glu Ile Ile Phe Ala
 65 70 75 80

Leu Phe Leu Tyr Arg Arg Tyr Ser Leu Pro Thr Thr Met Leu Ala Gly
 85 90 95

Met Gly Ala Gly Gly Gly Ala Ile Phe Leu Glu Met Phe Phe Tyr Gly
 100 105 110

Asn Leu Ala Lys Thr Met Ser Phe Asn Ile Ile Tyr Ser Thr Thr Val
 115 120 125

Leu Ile Ser Gly Ala Ile Leu Ala Gly Leu Leu Ser Trp Tyr Leu Val
 130 135 140

Arg Ala Leu Ala Arg Thr Gly Ala Leu Asp Arg Phe Ala Ala Gly Arg
 145 150 155 160

Glu Val

<210> 1011

<211> 828

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(805)

<223> RXN02121

<400> 1011

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tgggatacct tcgagacaaa cttccgaaag ctccgcaacc atg atc acc tca cca 115
 Met Ile Thr Ser Pro
 1 5

ttt gag cgc gag ctg aag ctg ctc aac gag ggg gaa ctg ggt att gtc Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly Glu Leu Gly Ile Val 10 15 20	163
cag cag ttg gtg gaa tca agc aac atc gga ttc atc gtc gat ctt gaa Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe Ile Val Asp Leu Glu 25 30 35	211
tta gat ggc gat tat ggg tgg gcg gtc tac aaa ccg gaa ttg ggg gag Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys Pro Glu Leu Gly Glu 40 45 50	259
caa ccc ctg tgg gat ttc cct cct ggc ctg tac aaa cgt gaa cgt gca Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr Lys Arg Glu Arg Ala 55 60 65	307
gcc ttt gtg atc agt gag ttt ttg ggt tgg aac atc gtg cct cca acg Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn Ile Val Pro Pro Thr 70 75 80 85	355
gtg atc atg cac gat gcc ccg gct ggt gtg ggc tcg gtg cag tgg ttt Val Ile Met His Asp Ala Pro Ala Gly Val Gly Ser Val Gln Trp Phe 90 95 100	403
att gaa aac aat ggc gaa cac tat ttt cca ctg ttt gac acc cgc gct Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu Phe Asp Thr Arg Ala 105 110 115	451
gac ctg cat ccg cag ttt gtc cgc atg gct gtg ttt gat ctg ttg tgc Asp Leu His Pro Gln Phe Val Arg Met Ala Val Phe Asp Leu Leu Cys 120 125 130	499
aac aac act gac cgc aaa gcg ggc cat gtg ttg tta gac ggc gat cat Asn Asn Thr Asp Arg Lys Ala Gly His Val Leu Leu Asp Gly Asp His 135 140 145	547
att tgg ggc atc gat cac ggg ttg tgt ttt tcc gtc gaa ccg aag ctg Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser Val Glu Pro Lys Leu 150 155 160 165	595
cgc acg gtg att tgg gat ttc gca ggc tgc acc att cca gat gac ttg Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr Ile Pro Asp Asp Leu 170 175 180	643
gtg aca gat gtt gag cag ctt ttg gag gac gtc ccg gaa gaa ctt cat Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val Pro Glu Glu Leu His 185 190 195	691
cag ctt ctt cat ccc gca gaa att gat gcg ctg cag cgc cgt gcc tca Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu Gln Arg Arg Ala Ser 200 205 210	739
aga atc agc agg tta ccg ttc ctt ccg cag gcg aaa tcg cat cgt caa Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala Lys Ser His Arg Gln 215 220 225	787
ttc cct tgg cca ctt gtt tgagtaggct ggccggcagg tgc Phe Pro Trp Pro Leu Val 230 235	828

<210> 1012
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 1012
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Glu Leu Gly Ile Val Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe
20 25 30
Ile Val Asp Leu Glu Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys
35 40 45
Pro Glu Leu Gly Glu Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr
50 55 60
Lys Arg Glu Arg Ala Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn
65 70 75 80
Ile Val Pro Pro Thr Val Ile Met His Asp Ala Pro Ala Gly Val Gly
85 90 95
Ser Val Gln Trp Phe Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu
100 105 110
Phe Asp Thr Arg Ala Asp Leu His Pro Gln Phe Val Arg Met Ala Val
115 120 125
Phe Asp Leu Leu Cys Asn Asn Thr Asp Arg Lys Ala Gly His Val Leu
130 135 140
Leu Asp Gly Asp His Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser
145 150 155 160
Val Glu Pro Lys Leu Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr
165 170 175
Ile Pro Asp Asp Leu Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val
180 185 190
Pro Glu Glu Leu His Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu
195 200 205
Gln Arg Arg Ala Ser Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala
210 215 220
Lys Ser His Arg Gln Phe Pro Trp Pro Leu Val
225 230 235

<210> 1013
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(805)
<223> FRXA02121

<400> 1013

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tgggatacct tcgagacaaa cttccgaaag ctccgcaacc atg atc acc tca cca 115
Met Ile Thr Ser Pro
1 5

ttt gag cgc gag ctg aag ctg ctc aac gag ggg gaa ctg ggt att gtc 163
Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly Glu Leu Gly Ile Val
10 15 20

cag cag ttg gtg gaa tca agc aac atc gga ttc atc gtc gat ctt gaa 211
Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe Ile Val Asp Leu Glu
25 30 35

tta gat ggc gat tat ggg tgg gcg gtc tac aaa ccg gaa ttg ggg gag 259
Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys Pro Glu Leu Gly Glu
40 45 50

caa ccc ctg tgg gat ttc cct cct ggc ctg tac aaa cgt gaa cgt gca 307
Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr Lys Arg Glu Arg Ala
55 60 65

gcc ttt gtg atc agt gag ttt ttg ggt tgg aac atc gtg cct cca acg 355
Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn Ile Val Pro Pro Thr
70 75 80 85

gtg atc atg cac gat gcc ccg gct ggt gtg ggc tcg gtg cag tgg ttt 403
Val Ile Met His Asp Ala Pro Ala Gly Val Gly Ser Val Gln Trp Phe
90 95 100

att gaa aac aat ggc gaa cac tat ttt cca ctg ttt gac acc cgc gct 451
Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu Phe Asp Thr Arg Ala
105 110 115

gac ctg cat ccg cag ttt gtc cgc atg gct gtg ttt gat ctg ttg tgc 499
Asp Leu His Pro Gln Phe Val Arg Met Ala Val Phe Asp Leu Leu Cys
120 125 130

aac aac act gac cgg aaa tcg ggc cat gtg ttg cta gac ggc gat cat 547
Asn Asn Thr Asp Arg Lys Ser Gly His Val Leu Leu Asp Gly Asp His
135 140 145

att tgg ggc atc gat cac ggg ttg tgt ttt tcc gtc gaa ccg aag ctg 595
Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser Val Glu Pro Lys Leu
150 155 160 165

cgc acg gtg att tgg gat ttc gca ggc tgc acc att cca gat gac ttg 643
Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr Ile Pro Asp Asp Leu
170 175 180

gtg aca gat gtt gag cag ctt ttg gag gac gtc ccg gaa gaa ctt cat 691
Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val Pro Glu Glu Leu His
185 190 195

cag ctt ctt cat ccc gca gaa att gat gcg ctg cag cgc cgt gcc tca 739
Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu Gln Arg Arg Ala Ser
200 205 210

aga atc agc agg tta ccg ttc ctt ccg cag gcg aaa tcg cat cgt caa 787

Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala Lys Ser His Arg Gln
 215 220 225

ttc cct tgg cca ctt gtt tgagtaggct ggcgggcagg tgc
 Phe Pro Trp Pro Leu Val
 230 235

828

<210> 1014

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

Met Ile Thr Ser Pro Phe Glu Arg Glu Leu Lys Leu Leu Asn Glu Gly
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Glu Leu Gly Ile Val Gln Gln Leu Val Glu Ser Ser Asn Ile Gly Phe
 20 25 30

Ile Val Asp Leu Glu Leu Asp Gly Asp Tyr Gly Trp Ala Val Tyr Lys
 35 40 45

Pro Glu Leu Gly Glu Gln Pro Leu Trp Asp Phe Pro Pro Gly Leu Tyr
 50 55 60

Lys Arg Glu Arg Ala Ala Phe Val Ile Ser Glu Phe Leu Gly Trp Asn
 65 70 75 80

Ile Val Pro Pro Thr Val Ile Met His Asp Ala Pro Ala Gly Val Gly
 85 90 95

Ser Val Gln Trp Phe Ile Glu Asn Asn Gly Glu His Tyr Phe Pro Leu
 100 105 110

Phe Asp Thr Arg Ala Asp Leu His Pro Gln Phe Val Arg Met Ala Val
 115 120 125

Phe Asp Leu Leu Cys Asn Asn Thr Asp Arg Lys Ser Gly His Val Leu
 130 135 140

Leu Asp Gly Asp His Ile Trp Gly Ile Asp His Gly Leu Cys Phe Ser
 145 150 155 160

Val Glu Pro Lys Leu Arg Thr Val Ile Trp Asp Phe Ala Gly Cys Thr
 165 170 175

Ile Pro Asp Asp Leu Val Thr Asp Val Glu Gln Leu Leu Glu Asp Val
 180 185 190

Pro Glu Glu Leu His Gln Leu Leu His Pro Ala Glu Ile Asp Ala Leu
 195 200 205

Gln Arg Arg Ala Ser Arg Ile Ser Arg Leu Pro Phe Leu Pro Gln Ala
 210 215 220

Lys Ser His Arg Gln Phe Pro Trp Pro Leu Val
 225 230 235

<210> 1015

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<400> 1016
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Ala Ser Lys Ala Lys Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu
          20          25          30
Ser Leu Arg Ile Ala Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr
          35          40          45

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Gln Leu Tyr Phe Asp Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile
 50 55 60

Val Gly Gly Val Arg Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu
 65 70 75 80

Leu Gly Ala Gln Ile Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe
 85 90 95

Thr Ile Asp Asn Pro Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser
 100 105 110

Phe Asn

<210> 1017

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(442)

<223> FRXA02138

<400> 1017

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 Met Thr Ala Pro Ser
 1 5

acc aac acc ggt gtt atc ttg acc gag tcc gca gcg tcc aaa gct aag 163
 Thr Asn Thr Gly Val Ile Leu Thr Glu Ser Ala Ala Ser Lys Ala Lys
 10 15 20

gca ctc atc gat cag gaa ggc cgc gac gac ctc tct ctg cgt atc gcc 211
 Ala Leu Ile Asp Gln Glu Gly Arg Asp Asp Leu Ser Leu Arg Ile Ala
 25 30 35

gtt cag cct ggc ggc tgc tct ggc ctt cgt tac cag ctt tac ttc gac 259
 Val Gln Pro Gly Gly Cys Ser Gly Leu Arg Tyr Gln Leu Tyr Phe Asp
 40 45 50

gac cgc acc ctt gat ggc gat aag gaa gac atc gtc ggt ggc gtt cgc 307
 Asp Arg Thr Leu Asp Gly Asp Lys Glu Asp Ile Val Gly Gly Val Arg
 55 60 65

ctt gtc gtt gac aag atg agc acc cca tac ttg ctc ggc gct cag atc 355
 Leu Val Val Asp Lys Met Ser Thr Pro Tyr Leu Leu Gly Ala Gln Ile
 70 75 80 85

gac ttc gct gac acc atc gag cag cag ggc ttc acc atc gac aac cca 403
 Asp Phe Ala Asp Thr Ile Glu Gln Gln Gly Phe Thr Ile Asp Asn Pro
 90 95 100

aac gca ggc agc tct tgc gct tgt ggt gac tcc ttc aac taaagagatt 452
 Asn Ala Gly Ser Ser Cys Ala Cys Gly Asp Ser Phe Asn
 105 110

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465

<210> 1018

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 1018

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			20					25					30		

Ser	Leu	Arg	Ile	Ala	Val	Gln	Pro	Gly	Gly	Cys	Ser	Gly	Leu	Arg	Tyr
		35					40					45			

Gln	Leu	Tyr	Phe	Asp	Asp	Arg	Thr	Leu	Asp	Gly	Asp	Lys	Glu	Asp	Ile
	50					55					60				

Val	Gly	Gly	Val	Arg	Leu	Val	Val	Asp	Lys	Met	Ser	Thr	Pro	Tyr	Leu
65					70					75					80

Leu	Gly	Ala	Gln	Ile	Asp	Phe	Ala	Asp	Thr	Ile	Glu	Gln	Gln	Gly	Phe
				85					90					95	

Thr	Ile	Asp	Asn	Pro	Asn	Ala	Gly	Ser	Ser	Cys	Ala	Cys	Gly	Asp	Ser
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Phe Asn

<210> 1019

<211> 1311

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS.

<222> (101)..(1288)

<223> RXN02151

<400> 1019

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atc	gcc	aag	gga	ata	tcc	atc	cta	ggt	gtc	gtg	tta	cta	cac	gtg	tcg	163
Ile	Ala	Lys	Gly	Ile	Ser	Ile	Leu	Gly	Val	Val	Leu	Leu	His	Val	Ser	
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Leu	Ala	Ile	Pro	Gly	Gly	Gln	Asp	Thr	Met	Met	Ser	His	Leu	Asn	Ala	
			25					30					35			

ctg	ctt	gat	cca	ctt	cgg	atg	cca	tta	ttt	ttt	atg	gtg	agt	gga	ttt	259
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Leu	Leu	Asp	Pro	Leu	Arg	Met	Pro	Leu	Phe	Phe	Met	Val	Ser	Gly	Phe		
		40					45					50					
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Phe	Ala	Val	Lys	Val	Leu	Asn	Gln	Ser	Phe	Gly	Glu	Leu	Phe	Arg	Gly		
	55					60					65						
cga	ctg	tgg	ttc	tac	ctg	gtt	cca	tat	ttg	ctg	tgg	act	cca	gtg	aat	355	
Arg	Leu	Trp	Phe	Tyr	Leu	Val	Pro	Tyr	Leu	Leu	Trp	Thr	Pro	Val	Asn		
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Leu	Tyr	Leu	His	Arg	Leu	Glu	Gly	Thr	Val	Phe	Thr	Gly	Arg	Ala	Pro		
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gga	aca	tgg	gaa	tgg	tac	agc	ggc	tcg	atg	ctc	tcg	gcc	acc	aat	atg	451	
Gly	Thr	Trp	Glu	Trp	Tyr	Ser	Gly	Ser	Met	Leu	Ser	Ala	Thr	Asn	Met		
			105				110						115				
tac	tgg	ttc	ctc	tac	ttc	ttg	gtc	atc	ttc	aac	cta	ttt	tta	tgg	gca	499	
Tyr	Trp	Phe	Leu	Tyr	Phe	Leu	Val	Ile	Phe	Asn	Leu	Phe	Leu	Trp	Ala		
	120						125					130					
acg	aga	aaa	ctc	cca	gct	tgg	gca	att	gtg	gcg	ttg	gtg	gcc	tca	ctg	547	
Thr	Arg	Lys	Leu	Pro	Ala	Trp	Ala	Ile	Val	Ala	Leu	Val	Ala	Ser	Leu		
	135					140					145						
tgg	cta	ctt	atg	ccg	gct	tat	agc	gag	att	gag	att	cta	cgc	aag	tcc	595	
Trp	Leu	Leu	Met	Pro	Ala	Tyr	Ser	Glu	Ile	Glu	Ile	Leu	Arg	Lys	Ser		
	150			155				160						165			
att	att	tac	ttg	cct	aca	ttc	ctc	att	ggc	gct	tac	ttc	cgc	cca	ctg	643	
Ile	Ile	Tyr	Leu	Pro	Thr	Phe	Leu	Ile	Gly	Ala	Tyr	Phe	Arg	Pro	Leu		
				170				175						180			
att	tcg	cgt	ttt	gca	gaa	gcc	gca	aca	agg	cca	aaa	gca	ata	gtg	ttt	691	
Ile	Ser	Arg	Phe	Ala	Glu	Ala	Ala	Thr	Arg	Pro	Lys	Ala	Ile	Val	Phe		
			185					190					195				
gca	gcg	gtc	ctt	tat	gtc	tcg	gga	ctt	gct	ttg	ggc	gtg	atc	tca	aat	739	
Ala	Ala	Val	Leu	Tyr	Val	Ser	Gly	Leu	Ala	Leu	Gly	Val	Ile	Ser	Asn		
		200					205					210					
ggg	ctg	cgc	gac	agc	gaa	aac	cat	ggc	gca	agc	gtg	ctg	tgg	ctg	atg	787	
Gly	Leu	Arg	Asp	Ser	Glu	Asn	His	Gly	Ala	Ser	Val	Leu	Trp	Leu	Met		
	215					220					225						
aac	ctc	cgc	gat	act	ttt	gct	cat	gca	ctc	ggc	ggc	aac	ctc	act	gga	835	
Asn	Leu	Arg	Asp	Thr	Phe	Ala	His	Ala	Leu	Gly	Gly	Asn	Leu	Thr	Gly		
	230				235					240					245		
ttc	gat	atg	gat	cac	ctt	cct	gga	atg	atc	att	cgg	att	gtt	tcc	ctg	883	
Phe	Asp	Met	Asp	His	Leu	Pro	Gly	Met	Ile	Ile	Arg	Ile	Val	Ser	Leu		
				250				255						260			
cct	gca	gga	att	gtg	ttg	tgc	gta	tgg	ctt	ggc	cga	ata	aag	cca	gta	931	
Pro	Ala	Gly	Ile	Val	Leu	Cys	Val	Trp	Leu	Gly	Arg	Ile	Lys	Pro	Val		
			265					270					275				
ggg	gag	ttt	ttg	aaa	ctt	att	ggt	agg	cac	acc	ctt	ccc	atc	tac	att	979	
Gly	Glu	Phe	Leu	Lys	Leu	Ile	Gly	Arg	His	Thr	Leu	Pro	Ile	Tyr	Ile		

280	285	290	
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Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly Phe Gly Leu Arg Trp			
295	300	305	
aat ttc atg gag att gat aac ttc tct gac agt ttg tgg cac cac acc			1075
Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser Leu Trp His His Thr			
310	315	320	325
aat acg tgg atg gtc atc gcg ttt gcc tgc gcg atg ctc ggc ggg tac			1123
Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala Met Leu Gly Gly Tyr			
	330	335	340
ctg acc tat ctg atc tcg cga gtt cca gtg ctg gga tgg act ctt gtt			1171
Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu Gly Trp Thr Leu Val			
	345	350	355
ccc cct aaa ctg cca gaa cca gat aaa act cca gct aaa gca caa gct			1219
Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro Ala Lys Ala Gln Ala			
	360	365	370
gat tct cac gtt aaa gct cag tct gcg aag cct atg aat gct tct acc			1267
Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro Met Asn Ala Ser Thr			
	375	380	385
tct tct aag acg tac ggt ata taactgaagc ataacctgtg tga			1311
Ser Ser Lys Thr Tyr Gly Ile			
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<210> 1020

<211> 396

<212> PRT

<213> Corynebacterium glutamicum

<400> 1020

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Ser His Leu Asn Ala Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe			
	35	40	45
Met Val Ser Gly Phe Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly			
	50	55	60
Glu Leu Phe Arg Gly Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu			
	65	70	75
Trp Thr Pro Val Asn Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe			
	85	90	95
Thr Gly Arg Ala Pro Gly Thr Trp Glu Trp Tyr Ser Gly Ser Met Leu			
	100	105	110
Ser Ala Thr Asn Met Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn			
	115	120	125

Leu Phe Leu Trp Ala Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala
 130 135 140
 Leu Val Ala Ser Leu Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu
 145 150 155 160
 Ile Leu Arg Lys Ser Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala
 165 170 175
 Tyr Phe Arg Pro Leu Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro
 180 185 190
 Lys Ala Ile Val Phe Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu
 195 200 205
 Gly Val Ile Ser Asn Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser
 210 215 220
 Val Leu Trp Leu Met Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly
 225 230 235 240
 Gly Asn Leu Thr Gly Phe Asp Met Asp His Leu Pro Gly Met Ile Ile
 245 250 255
 Arg Ile Val Ser Leu Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly
 260 265 270
 Arg Ile Lys Pro Val Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr
 275 280 285
 Leu Pro Ile Tyr Ile Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly
 290 295 300
 Phe Gly Leu Arg Trp Asn Phe Met Glu Ile Asp Asn Phe Ser Asp Ser
 305 310 315 320
 Leu Trp His His Thr Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala
 325 330 335
 Met Leu Gly Gly Tyr Leu Thr Tyr Leu Ile Ser Arg Val Pro Val Leu
 340 345 350
 Gly Trp Thr Leu Val Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro
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 Met Asn Ala Ser Thr Ser Ser Lys Thr Tyr Gly Ile
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<211> 1311

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1288)

<223> FRXA02151

<400> 1021

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atc gcc aag gga ata tcc atc cta ggt gtc gtg tta cta cac gtg tcg 163
Ile Ala Lys Gly Ile Ser Ile Leu Gly Val Val Leu Leu His Val Ser
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ttg gca att cca ggt ggc cag gac acc atg atg tcc cac ctg aac gca 211
Leu Ala Ile Pro Gly Gly Gln Asp Thr Met Met Ser His Leu Asn Ala
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Leu Leu Asp Pro Leu Arg Met Pro Leu Phe Phe Met Val Ser Gly Phe
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Phe Ala Val Lys Val Leu Asn Gln Ser Phe Gly Glu Leu Phe Arg Gly
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cga ctg tgg ttc tac ctg gtt cca tat ttg ctg tgg act cca gtg aat 355
Arg Leu Trp Phe Tyr Leu Val Pro Tyr Leu Leu Trp Thr Pro Val Asn
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ctt tat cta cac cgc ctc gag ggc aca gtt ttt acc ggt aga gca ccg 403
Leu Tyr Leu His Arg Leu Glu Gly Thr Val Phe Thr Gly Arg Ala Pro
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Tyr Trp Phe Leu Tyr Phe Leu Val Ile Phe Asn Leu Phe Leu Trp Ala
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Thr Arg Lys Leu Pro Ala Trp Ala Ile Val Ala Leu Val Ala Ser Leu
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Trp Leu Leu Met Pro Ala Tyr Ser Glu Ile Glu Ile Leu Arg Lys Ser
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Ile Ile Tyr Leu Pro Thr Phe Leu Ile Gly Ala Tyr Phe Arg Pro Leu
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att tcg cgt ttt gca gaa gcc gca aca agg cca aaa gca ata gtg ttt 691
Ile Ser Arg Phe Ala Glu Ala Ala Thr Arg Pro Lys Ala Ile Val Phe
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gca gcg gtc ctt tat gtc tcg gga ctt gct ttg ggc gtg atc tca aat 739
Ala Ala Val Leu Tyr Val Ser Gly Leu Ala Leu Gly Val Ile Ser Asn
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Gly Leu Arg Asp Ser Glu Asn His Gly Ala Ser Val Leu Trp Leu Met
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 aac ctc cgc gat act ttt gct cat gca ctc ggc ggc aac ctc act gga 835
 Asn Leu Arg Asp Thr Phe Ala His Ala Leu Gly Gly Asn Leu Thr Gly
 230 235 240 245
 ttc gat atg gat cac ctt cct gga atg atc att cgg att gtt tcc ctg 883
 Phe Asp Met Asp His Leu Pro Gly Met Ile Ile Arg Ile Val Ser Leu
 250 255 260
 cct gca gga att gtg ttg tgc gta tgg ctt ggc cga ata aag cca gta 931
 Pro Ala Gly Ile Val Leu Cys Val Trp Leu Gly Arg Ile Lys Pro Val
 265 270 275
 ggg gag ttt ttg aaa ctt att ggt agg cac acc ctt ccc atc tac att 979
 Gly Glu Phe Leu Lys Leu Ile Gly Arg His Thr Leu Pro Ile Tyr Ile
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 ggg cat gca aca gga cta tcg ctg att ttt ggt ttc ggc ttg cgc tgg 1027
 Gly His Ala Thr Gly Leu Ser Leu Ile Phe Gly Phe Gly Leu Arg Trp
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 aat acg tgg atg gtc atc gcg ttt gcc tgc gcg atg ctc ggc ggg tac 1123
 Asn Thr Trp Met Val Ile Ala Phe Ala Cys Ala Met Leu Gly Gly Tyr
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 Pro Pro Lys Leu Pro Glu Pro Asp Lys Thr Pro Ala Lys Ala Gln Ala
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 gat tct cac gtt aaa gct cag tct gcg aag cct atg aat gct tct acc 1267
 Asp Ser His Val Lys Ala Gln Ser Ala Lys Pro Met Asn Ala Ser Thr
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<211> 396

<212> PRT

<213> Corynebacterium glutamicum

<400> 1022

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Trp	Thr	Pro	Val	Asn	Leu	Tyr	Leu	His	Arg	Leu	Glu	Gly	Thr	Val	Phe	
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Tyr	Phe	Arg	Pro	Leu	Ile	Ser	Arg	Phe	Ala	Glu	Ala	Ala	Thr	Arg	Pro	
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Lys	Ala	Ile	Val	Phe	Ala	Ala	Val	Leu	Tyr	Val	Ser	Gly	Leu	Ala	Leu	
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Gly	Val	Ile	Ser	Asn	Gly	Leu	Arg	Asp	Ser	Glu	Asn	His	Gly	Ala	Ser	
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<220>

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<222> (101)..(946)

<223> RXN02169

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aac cgc cga ggc ttc tta aaa gcc acc aca gga ctt gcc act atc ggc 163
 Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly Leu Ala Thr Ile Gly
 10 15 20

gct gcc agc atg ttt atg cca aag gcc aac gcc ctt gga gca atc aag 211
 Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala Leu Gly Ala Ile Lys
 25 30 35

ggc acc gtc atc gac tac gca gca ggc gtc ccc agc gca gca tcc att 259
 Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro Ser Ala Ala Ser Ile
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aaa aat gca ggg cac ctt gga gct gtc cgt tac gtg tca cag cga cgc 307
 Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr Val Ser Gln Arg Arg
 55 60 65

ccc ggc act gaa tcc tgg atg atc ggc aag cca gtc aca ctg gca gaa 355
 Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro Val Thr Leu Ala Glu
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acc cga gct ttt gaa caa aac ggc ctc aaa acc gca tcc gtc tat caa 403
 Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr Ala Ser Val Tyr Gln
 90 95 100

tac gga aag gca gag acc gcc gat tgg aag aac ggc gcc gca gga gcg 451
 Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn Gly Ala Ala Gly Ala
 105 110 115

gca acc cac gct cca cag gca att gcg ctt cac gtg gca gct ggt ggc 499
 Ala Thr His Ala Pro Gln Ala Ile Ala Leu His Val Ala Ala Gly Gly
 120 125 130

cct aaa aat cgc ccc atc tac gtg gcg atc gac gac aac cca agc tgg 547
 Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp Asp Asn Pro Ser Trp
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tct gaa tac acc aat cag att cgc ccc tac ctc cag gca ttc aat gtt 595
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 170 175 180

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 Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly Glu Phe Phe Trp Met
 185 190 195

 cac aac tgg gga tca gaa gga aag atc cac cca cgc acc acc atc cac 739
 His Asn Trp Gly Ser Glu Gly Lys Ile His Pro Arg Thr Thr Ile His
 200 205 210

 cag atc cgc att gat aag gac acc ctc gac gga gtc ggc atc gac atg 787
 Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly Val Gly Ile Asp Met
 215 220 225

 aac aat gtc tat gca gac gac tgg ggt cag tgg acc cca ggc aac gcg 835
 Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp Thr Pro Gly Asn Ala
 230 235 240 245

 gtt gac gat gcc atc ccc acc att cct gga aac tcc aac acg gga aca 883
 Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn Ser Asn Thr Gly Thr
 250 255 260

 ggt act gga att gat gct gac acc atc aac caa gta atc aag att ctt 931
 Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln Val Ile Lys Ile Leu
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 Gly Thr Leu Ser Ser
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<211> 282

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

 Ser Ala Ala Ser Ile Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr
 50 55 60

 Val Ser Gln Arg Arg Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro
 65 70 75 80

 Val Thr Leu Ala Glu Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr
 85 90 95

Ala Ser Val Tyr Gln Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn
 100 105 110

Gly Ala Ala Gly Ala Ala Thr His Ala Pro Gln Ala Ile Ala Leu His
 115 120 125

Val Ala Ala Gly Gly Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp
 130 135 140

Asp Asn Pro Ser Trp Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu
 145 150 155 160

Gln Ala Phe Asn Val Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val
 165 170 175

Tyr Gly Asn Tyr Asn Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly
 180 185 190

Glu Phe Phe Trp Met His Asn Trp Gly Ser Glu Gly Lys Ile His Pro
 195 200 205

Arg Thr Thr Ile His Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly
 210 215 220

Val Gly Ile Asp Met Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp
 225 230 235 240

Thr Pro Gly Asn Ala Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn
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Ser Asn Thr Gly Thr Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln
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 <223> FRXA02169

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 Leu Asp Met Gln Ile
 1 5

aac cgc cga ggc ttc tta aaa gcc acc aca gga ctt gcc act atc gcc 163
 Asn Arg Arg Gly Phe Leu Lys Ala Thr Thr Gly Leu Ala Thr Ile Gly
 10 15 20

gct gcc agc atg ttt atg cca aag gcc aac gcc ctt gga gca atc aag 211
 Ala Ala Ser Met Phe Met Pro Lys Ala Asn Ala Leu Gly Ala Ile Lys
 25 30 35

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Gly Thr Val Ile Asp Tyr Ala Ala Gly Val Pro Ser Ala Ala Ser Ile	
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Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr Val Ser Gln Arg Arg	
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Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr Ala Ser Val Tyr Gln	
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Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn Gly Ala Ala Gly Ala	
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Ala Thr His Ala Pro Gln Ala Ile Ala Leu His Val Ala Ala Gly Gly	
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Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp Asp Asn Pro Ser Trp	
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Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val Tyr Gly Asn Tyr Asn	
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Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly Glu Phe Phe Trp Met	
185 190 195	
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His Asn Trp Gly Ser Glu Gly Lys Ile His Pro Arg Thr Thr Ile His	
200 205 210	
cag atc cgc att gat aag gac acc ctc gac gga gtc ggc atc gac atg	787
Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly Val Gly Ile Asp Met	
215 220 225	
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Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp Thr Pro Gly Asn Ala	
230 235 240 245	
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Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn Ser Asn Thr Gly Thr	
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Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln Val Ile Lys Ile Leu	
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969

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<212> PRT

<213> Corynebacterium glutamicum

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Ser Ala Ala Ser Ile Lys Asn Ala Gly His Leu Gly Ala Val Arg Tyr
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Val Ser Gln Arg Arg Pro Gly Thr Glu Ser Trp Met Ile Gly Lys Pro
65 70 75 80

Val Thr Leu Ala Glu Thr Arg Ala Phe Glu Gln Asn Gly Leu Lys Thr
85 90 95

Ala Ser Val Tyr Gln Tyr Gly Lys Ala Glu Thr Ala Asp Trp Lys Asn
100 105 110

Gly Ala Ala Gly Ala Ala Thr His Ala Pro Gln Ala Ile Ala Leu His
115 120 125

Val Ala Ala Gly Gly Pro Lys Asn Arg Pro Ile Tyr Val Ala Ile Asp
130 135 140

Asp Asn Pro Ser Trp Ser Glu Tyr Thr Asn Gln Ile Arg Pro Tyr Leu
145 150 155 160

Gln Ala Phe Asn Val Ala Leu Ser Ala Ala Gly Tyr Gln Leu Gly Val
165 170 175

Tyr Gly Asn Tyr Asn Val Ile Asn Trp Ala Ile Ala Asp Gly Leu Gly
180 185 190

Glu Phe Phe Trp Met His Asn Trp Gly Ser Glu Gly Lys Ile His Pro
195 200 205

Arg Thr Thr Ile His Gln Ile Arg Ile Asp Lys Asp Thr Leu Asp Gly
210 215 220

Val Gly Ile Asp Met Asn Asn Val Tyr Ala Asp Asp Trp Gly Gln Trp
225 230 235 240

Thr Pro Gly Asn Ala Val Asp Asp Ala Ile Pro Thr Ile Pro Gly Asn
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Ser Asn Thr Gly Thr Gly Thr Gly Ile Asp Ala Asp Thr Ile Asn Gln
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<211> 1581

<212> DNA

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<222> (101)..(1558)

<223> RXN02180

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 Met Thr Ser Gly Lys
 1 5
 tca acg agt act agg gga gcc cta gac cgg tat ttc aaa atc tcg gag 163
 Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr Phe Lys Ile Ser Glu
 10 15 20
 cga gga tca agc att ggc acg gaa atc cgt gca ggt gtg gtc aca ttc 211
 Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala Gly Val Val Thr Phe
 25 30 35
 ttc gcg atg gcc tac atc atc atc ctc aac ccc ttg atc ctt ggc acc 259
 Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro Leu Ile Leu Gly Thr
 40 45 50
 acc cct gac gta gag ggc aac acc cta ggc atc gca cag gtt gca gcg 307
 Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile Ala Gln Val Ala Ala
 55 60 65
 gca aca gcg ctt gcc gct ggt gtc atg acc atc gcg ttt ggt ttg att 355
 Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile Ala Phe Gly Leu Ile
 70 75 80 85
 gcg cgt tat cca ttc ggc att gct gct ggc ctg gga att aac acc atg 403
 Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu Gly Ile Asn Thr Met
 90 95 100
 gtc gcc gtg aca ctg gtt tca ggt gag ggc ctg acc tgg ccg gaa gca 451
 Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu Thr Trp Pro Glu Ala
 105 110 115
 atg gga ctt gtg gtc ctt gac ggt gtg gtc att gtt att ttg gct gtg 499
 Met Gly Leu Val Val Leu Asp Gly Val Val Ile Val Ile Leu Ala Val
 120 125 130
 tcc ggc ttc cgt gtt gct gtg ttc cgt gcg atc cca gca tcc atg aag 547
 Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile Pro Ala Ser Met Lys
 135 140 145
 gcg gcc atc agc gtg ggt atc ggc ctg ttc atc gcc atg atc ggc ctc 595
 Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile Ala Met Ile Gly Leu
 150 155 160 165

gtg gat gca ggc ttt gtt cgc cgt att cca gat gct gcc ggt act act	643
Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp Ala Ala Gly Thr Thr	
170 175 180	
gtg cca gtg act ttg ggc att gat ggt tcc att gcg tct tgg cca acg	691
Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile Ala Ser Trp Pro Thr	
185 190 195	
ttc gtg ttc gtt gtc ggt gtt ctt ctc tgt ggc atc ctt gtt gtc cgt	739
Phe Val Phe Val Val Gly Val Leu Leu Cys Gly Ile Leu Val Val Arg	
200 205 210	
cga gtt cgc ggt gga ctg ttt atc ggc att ttg gga acc acc att ttg	787
Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu Gly Thr Thr Ile Leu	
215 220 225	
gcg atc atc gca gaa gca atc ttt gat tcc ggt gcg tcc ttt gaa aat	835
Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly Ala Ser Phe Glu Asn	
230 235 240 245	
ggg gaa gca aac gca gaa ggc tgg tca ctc gcc gtt cct ggt ctc cca	883
Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala Val Pro Gly Leu Pro	
250 255 260	
gac tcc ttc ggt ggc atc ccg gat ctt tcc atc gtc ggc gca gtt gat	931
Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile Val Gly Ala Val Asp	
265 270 275	
ttg atc ggt gcg ttc agc cgc atc ggt gtg gtc gcc gcg acc ttg ctg	979
Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val Ala Ala Thr Leu Leu	
280 285 290	
atc ttt acc ctg gtc ctt gca aac ttc ttc gac gcc atg ggc acc atg	1027
Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp Ala Met Gly Thr Met	
295 300 305	
acc gct ctt ggt aag cag ggc aac ttg gtt gat gat gaa ggc aac ctt	1075
Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp Asp Glu Gly Asn Leu	
310 315 320 325	
cca gac att aag aag gca ctg gtt gtg gaa ggc gca ggt gcc att gtc	1123
Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly Ala Gly Ala Ile Val	
330 335 340	
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Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val Phe Ala Asp Ser Ser	
345 350 355	
gca ggt gtt gca gac ggc gca cga acc ggc ctt gcc aac gtg gtc acc	1219
Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu Ala Asn Val Val Thr	
360 365 370	
ggc tcc ttg ttc ttg gct gcc atg ttc ttg acc cca ctg tat gaa atc	1267
Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr Pro Leu Tyr Glu Ile	
375 380 385	
gtc ccc atc gaa gca gca gca cca gtg ctt gta gtt gtt ggc gcg atg	1315
Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val Val Val Gly Ala Met	
390 395 400 405	

atg atg ggg cag gtt acc gag att gat ttc tcc aag ttc tac atc gca 1363
 Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser Lys Phe Tyr Ile Ala
 410 415 420

ttc cca gcg ttc ttg acc att gtg atc atg cct ttc acc tac tcc att 1411
 Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro Phe Thr Tyr Ser Ile
 425 430 435

gca aac ggc att ggc gtt gga ttc atc atg tac gcc atc atg gct gca 1459
 Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr Ala Ile Met Ala Ala
 440 445 450

gcg gca ggc aaa gca aag caa gtg cac tgg ctg atg tgg ctg gtc gct 1507
 Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu Met Trp Leu Val Ala
 455 460 465

gga ctc ttc gtc gtg ttc ttc gcg att gat ccc atc atg gaa gct gtc 1555
 Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro Ile Met Glu Ala Val
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<210> 1028

<211> 486

<212> PRT

<213> Corynebacterium glutamicum

<400> 1028

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Phe Lys Ile Ser Glu Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala
 20 25 30

Gly Val Val Thr Phe Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro
 35 40 45

Leu Ile Leu Gly Thr Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile
 50 55 60

Ala Gln Val Ala Ala Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile
 65 70 75 80

Ala Phe Gly Leu Ile Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu
 85 90 95

Gly Ile Asn Thr Met Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu
 100 105 110

Thr Trp Pro Glu Ala Met Gly Leu Val Val Leu Asp Gly Val Val Ile
 115 120 125

Val Ile Leu Ala Val Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile
 130 135 140

Pro Ala Ser Met Lys Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile
 145 150 155 160

Ala Met Ile Gly Leu Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp
165 170 175

Ala Ala Gly Thr Thr Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile
180 185 190

Ala Ser Trp Pro Thr Phe Val Phe Val Val Gly Val Leu Leu Cys Gly
195 200 205

Ile Leu Val Val Arg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu
210 215 220

Gly Thr Thr Ile Leu Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly
225 230 235 240

Ala Ser Phe Glu Asn Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala
245 250 255

Val Pro Gly Leu Pro Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile
260 265 270

Val Gly Ala Val Asp Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val
275 280 285

Ala Ala Thr Leu Leu Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp
290 295 300

Ala Met Gly Thr Met Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp
305 310 315 320

Asp Glu Gly Asn Leu Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly
325 330 335

Ala Gly Ala Ile Val Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val
340 345 350

Phe Ala Asp Ser Ser Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu
355 360 365

Ala Asn Val Val Thr Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr
370 375 380

Pro Leu Tyr Glu Ile Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val
385 390 395 400

Val Val Gly Ala Met Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser
405 410 415

Lys Phe Tyr Ile Ala Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro
420 425 430

Phe Thr Tyr Ser Ile Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr
435 440 445

Ala Ile Met Ala Ala Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu
450 455 460

Met Trp Leu Val Ala Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro
465 470 475 480

Ile Met Glu Ala Val Gly

485

<210> 1029
 <211> 1581
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1558)
 <223> FRXA02180

<400> 1029

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                                         Met Thr Ser Gly Lys
                                         1           5

tca acg agt act agg gga gcc cta gac cgg tat ttc aaa atc tcg gag 163
Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr Phe Lys Ile Ser Glu
                        10                15                20

cga gga tca agc att ggc acg gaa atc cgt gca ggt gtg gtc aca ttc 211
Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala Gly Val Val Thr Phe
                        25                30                35

ttc gcg atg gcc tac atc atc atc ctc aac ccc ttg atc ctt ggc acc 259
Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro Leu Ile Leu Gly Thr
                        40                45                50

acc cct gac gta gag ggc aac acc cta ggc atc gca cag gtt gca gcg 307
Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile Ala Gln Val Ala Ala
                        55                60                65

gca aca gcg ctt gcc gct ggt gtc atg acc atc gcg ttt ggt ttg att 355
Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile Ala Phe Gly Leu Ile
                        70                75                80                85

gcg cgt tat cca ttc ggc att gct gct ggc ctg gga att aac acc atg 403
Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu Gly Ile Asn Thr Met
                        90                95                100

gtc gcc gtg aca ctg gtt tca ggt gag ggc ctg acc tgg ccg gaa gca 451
Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu Thr Trp Pro Glu Ala
                        105                110                115

atg gga ctt gtg gtc ctt gac ggt gtg gtc att gtt att ttg gct gtg 499
Met Gly Leu Val Val Leu Asp Gly Val Val Ile Val Ile Leu Ala Val
                        120                125                130

tcc ggc ttc cgt gtt gct gtg ttc cgt gcg atc cca gca tcc atg aag 547
Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile Pro Ala Ser Met Lys
                        135                140                145

gcg gcc atc agc gtg ggt atc ggc ctg ttc atc gcc atg atc ggc ctc 595
Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile Ala Met Ile Gly Leu
                        150                155                160                165

gtg gat gca ggc ttt gtt cgc cgt att cca gat gct gcc ggt act act 643

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Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp Ala Ala Gly Thr Thr	
170 175 180	
gtg cca gtg act ttg ggc att gat ggt tcc att gcg tct tgg cca acg	691
Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile Ala Ser Trp Pro Thr	
185 190 195	
ttc gtg ttc gtt gtc ggt gtt ctt ctc tgt ggc atc ctt gtt gtc cgt	739
Phe Val Phe Val Val Gly Val Leu Leu Cys Gly Ile Leu Val Val Arg	
200 205 210	
cga gtt cgc ggt gga ctg ttt atc ggc att ttg gga acc acc att ttg	787
Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu Gly Thr Thr Ile Leu	
215 220 225	
gcg atc atc gca gaa gca atc ttt gat tcc ggt gcg tcc ttt gaa aat	835
Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly Ala Ser Phe Glu Asn	
230 235 240 245	
ggt gaa gca aac gca gaa ggc tgg tca ctc gcc gtt cct ggt ctc cca	883
Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala Val Pro Gly Leu Pro	
250 255 260	
gac tcc ttc ggt ggc atc ccg gat ctt tcc atc gtc ggc gca gtt gat	931
Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile Val Gly Ala Val Asp	
265 270 275	
ttg atc ggt gcg ttc agc cgc atc ggt gtg gtc gcc gcg acc ttg ctg	979
Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val Ala Ala Thr Leu Leu	
280 285 290	
atc ttt acc ctg gtc ctt gca aac ttc ttc gac gcc atg ggc acc atg	1027
Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp Ala Met Gly Thr Met	
295 300 305	
acc gct ctt ggt aag cag ggc aac ttg gtt gat gat gaa ggc aac ctt	1075
Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp Asp Glu Gly Asn Leu	
310 315 320 325	
cca gac att aag aag gca ctg gtt gtg gaa ggc gca ggt gcc att gtc	1123
Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly Ala Gly Ala Ile Val	
330 335 340	
ggt ggt gct ttc tct gca tcc tcc aac acc gtg ttc gct gac tct tct	1171
Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val Phe Ala Asp Ser Ser	
345 350 355	
gca ggt gtt gca gac ggc gca cga acc ggc ctt gcc aac gtg gtc acc	1219
Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu Ala Asn Val Val Thr	
360 365 370	
ggc tcc ttg ttc ttg gct gcc atg ttc ttg acc cca ctg tat gaa atc	1267
Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr Pro Leu Tyr Glu Ile	
375 380 385	
gtc ccc atc gaa gca gca gca cca gtg ctt gta gtt gtt ggc gcg atg	1315
Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val Val Val Gly Ala Met	
390 395 400 405	
atg atg ggg cag gtt acc gag att gat ttc tcc aag ttc tac atc gca	1363
Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser Lys Phe Tyr Ile Ala	

410	415	420	
ttc cca gcg ttc ttg acc att gtg atc atg cct ttc acc tac tcc att			1411
Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro Phe Thr Tyr Ser Ile			
425	430	435	
gca aac ggc att ggc gtt gga ttc atc atg tac gcc atc atg gct gca			1459
Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr Ala Ile Met Ala Ala			
440	445	450	
gcg gca ggc aaa gca aag caa gtg cac tgg ctg atg tgg ctg gtc gct			1507
Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu Met Trp Leu Val Ala			
455	460	465	
gga ctc ttc gtc gtg ttc ttc gcg att gat ccc atc atg gaa gct gtc			1555
Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro Ile Met Glu Ala Val			
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Gly			

<210> 1030

<211> 486

<212> PRT

<213> Corynebacterium glutamicum

<400> 1030

Met Thr Ser Gly Lys Ser Thr Ser Thr Arg Gly Ala Leu Asp Arg Tyr			
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Phe Lys Ile Ser Glu Arg Gly Ser Ser Ile Gly Thr Glu Ile Arg Ala			
20	25	30	
Gly Val Val Thr Phe Phe Ala Met Ala Tyr Ile Ile Ile Leu Asn Pro			
35	40	45	
Leu Ile Leu Gly Thr Thr Pro Asp Val Glu Gly Asn Thr Leu Gly Ile			
50	55	60	
Ala Gln Val Ala Ala Ala Thr Ala Leu Ala Ala Gly Val Met Thr Ile			
65	70	75	80
Ala Phe Gly Leu Ile Ala Arg Tyr Pro Phe Gly Ile Ala Ala Gly Leu			
85	90	95	
Gly Ile Asn Thr Met Val Ala Val Thr Leu Val Ser Gly Glu Gly Leu			
100	105	110	
Thr Trp Pro Glu Ala Met Gly Leu Val Val Leu Asp Gly Val Val Ile			
115	120	125	
Val Ile Leu Ala Val Ser Gly Phe Arg Val Ala Val Phe Arg Ala Ile			
130	135	140	
Pro Ala Ser Met Lys Ala Ala Ile Ser Val Gly Ile Gly Leu Phe Ile			
145	150	155	160
Ala Met Ile Gly Leu Val Asp Ala Gly Phe Val Arg Arg Ile Pro Asp			
165	170	175	

Ala Ala Gly Thr Thr Val Pro Val Thr Leu Gly Ile Asp Gly Ser Ile
180 185 190

Ala Ser Trp Pro Thr Phe Val Phe Val Val Gly Val Leu Leu Cys Gly
195 200 205

Ile Leu Val Val Arg Arg Val Arg Gly Gly Leu Phe Ile Gly Ile Leu
210 215 220

Gly Thr Thr Ile Leu Ala Ile Ile Ala Glu Ala Ile Phe Asp Ser Gly
225 230 235 240

Ala Ser Phe Glu Asn Gly Glu Ala Asn Ala Glu Gly Trp Ser Leu Ala
245 250 255

Val Pro Gly Leu Pro Asp Ser Phe Gly Gly Ile Pro Asp Leu Ser Ile
260 265 270

Val Gly Ala Val Asp Leu Ile Gly Ala Phe Ser Arg Ile Gly Val Val
275 280 285

Ala Ala Thr Leu Leu Ile Phe Thr Leu Val Leu Ala Asn Phe Phe Asp
290 295 300

Ala Met Gly Thr Met Thr Ala Leu Gly Lys Gln Gly Asn Leu Val Asp
305 310 315 320

Asp Glu Gly Asn Leu Pro Asp Ile Lys Lys Ala Leu Val Val Glu Gly
325 330 335

Ala Gly Ala Ile Val Gly Gly Ala Phe Ser Ala Ser Ser Asn Thr Val
340 345 350

Phe Ala Asp Ser Ser Ala Gly Val Ala Asp Gly Ala Arg Thr Gly Leu
355 360 365

Ala Asn Val Val Thr Gly Ser Leu Phe Leu Ala Ala Met Phe Leu Thr
370 375 380

Pro Leu Tyr Glu Ile Val Pro Ile Glu Ala Ala Ala Pro Val Leu Val
385 390 395 400

Val Val Gly Ala Met Met Met Gly Gln Val Thr Glu Ile Asp Phe Ser
405 410 415

Lys Phe Tyr Ile Ala Phe Pro Ala Phe Leu Thr Ile Val Ile Met Pro
420 425 430

Phe Thr Tyr Ser Ile Ala Asn Gly Ile Gly Val Gly Phe Ile Met Tyr
435 440 445

Ala Ile Met Ala Ala Ala Ala Gly Lys Ala Lys Gln Val His Trp Leu
450 455 460

Met Trp Leu Val Ala Gly Leu Phe Val Val Phe Phe Ala Ile Asp Pro
465 470 475 480

Ile Met Glu Ala Val Gly
485

gct gag gtt gag tct tac tac aac gct ttc gtc ggc taaatctagc 689
Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val Gly
185 190

tgcaactttttt aaa 702

<210> 1032

<211> 193

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1032

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Ala Ser Thr Ile Ala Phe Gly Ala Ala Thr Ile Met Ala Pro Ser
20 25 30

Ala Ser Ala Ala Pro Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu
35 40 45

Ser Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly
50 55 60

Leu Gln Phe Ser Ala Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe
65 70 75 80

Ala Thr Tyr Ala Tyr Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala
85 90 95

Glu Arg Thr Leu Ala Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser
100 105 110

Ala Ser Leu Gly Leu Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala
115 120 125

Thr Thr Ser Thr Pro Glu Pro Ala Ala Ala Pro Ala Val Ala Glu
130 135 140

Tyr Asn Ala Pro Ala Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn
145 150 155 160

Thr Ile Lys Ser Thr Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr
165 170 175

Gly Ile Thr Val Pro Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val
180 185 190

Gly

<210> 1033

<211> 702

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(679)

<223> FRXA02185

<400> 1033

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cagctaacct cgacggcgac aaatgagagg aaaacttttc atg gga cgt cac tcc 115
                               Met Gly Arg His Ser
                               1 5

act aag act agc tcc gcg ttc acc aag ctc gca gct tcc acc atc gct 163
Thr Lys Thr Ser Ser Ala Phe Thr Lys Leu Ala Ala Ser Thr Ile Ala
          10          15          20

ttc ggt gct gct gca acc atc atg gct cct tct gca tct gct gca cct 211
Phe Gly Ala Ala Ala Thr Ile Met Ala Pro Ser Ala Ser Ala Ala Pro
          25          30          35

gat tcc gac tgg gat cgc ctc gca cag tgc gag tcc ggt ggt aac tgg 259
Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp
          40          45          50

gca atc aac acc ggt aac ggc tac cac ggt ggt ctg cag ttc tcc gct 307
Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly Leu Gln Phe Ser Ala
          55          60          65

agc acc tgg gct gct tac ggc ggc cag gag ttc gct acc tac gca tac 355
Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe Ala Thr Tyr Ala Tyr
          70          75          80          85

cag gca acc cgt gag cag cag atc gct gtt gca gag cgc acc ttg gct 403
Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala Glu Arg Thr Leu Ala
          90          95          100

ggt cag ggc tgg ggc gca tgg cct gct tgc tcc gct tcc ctt gga ctg 451
Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser Ala Ser Leu Gly Leu
          105          110          115

aac tcc gct cca acc cag cgt gac ctc tcc gct acc acc tcc acc cca 499
Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala Thr Thr Ser Thr Pro
          120          125          130

gag cca gct gca gct gca cca gct gtt gct gag tac aac gct cct gca 547
Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu Tyr Asn Ala Pro Ala
          135          140          145

gcc aac atc gca gtt ggc tcc acc gac ttg aac acc atc aag tcc acc 595
Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn Thr Ile Lys Ser Thr
          150          155          160          165

tac ggc gct gtc acc ggc acc ctc gct cag tac ggc atc acc gtt cca 643
Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr Gly Ile Thr Val Pro
          170          175          180

gct gag gtt gag tct tac tac aac gct ttc gtc ggc taaatctagc 689
Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val Gly
          185          190

tgcacttttt aaa 702

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<210> 1034
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 1034
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20 25 30
Ala Ser Ala Ala Pro Asp Ser Asp Trp Asp Arg Leu Ala Gln Cys Glu
35 40 45
Ser Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Tyr His Gly Gly
50 55 60
Leu Gln Phe Ser Ala Ser Thr Trp Ala Ala Tyr Gly Gly Gln Glu Phe
65 70 75 80
Ala Thr Tyr Ala Tyr Gln Ala Thr Arg Glu Gln Gln Ile Ala Val Ala
85 90 95
Glu Arg Thr Leu Ala Gly Gln Gly Trp Gly Ala Trp Pro Ala Cys Ser
100 105 110
Ala Ser Leu Gly Leu Asn Ser Ala Pro Thr Gln Arg Asp Leu Ser Ala
115 120 125
Thr Thr Ser Thr Pro Glu Pro Ala Ala Ala Ala Pro Ala Val Ala Glu
130 135 140
Tyr Asn Ala Pro Ala Ala Asn Ile Ala Val Gly Ser Thr Asp Leu Asn
145 150 155 160
Thr Ile Lys Ser Thr Tyr Gly Ala Val Thr Gly Thr Leu Ala Gln Tyr
165 170 175
Gly Ile Thr Val Pro Ala Glu Val Glu Ser Tyr Tyr Asn Ala Phe Val
180 185 190

Gly

<210> 1035
<211> 321
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(298)
<223> RXN02186

<400> 1035
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Met Tyr Asp Met Ala

1

5

aac gta gag aag aag cac ttc gtc gat ccg gca tgg ccg gag cac aat 163
 Asn Val Glu Lys Lys His Phe Val Asp Pro Ala Trp Pro Glu His Asn
 10 15 20

cca gct gac gga cac gtc gtt act gaa ctc atc tcc aag gtc gca ggc 211
 Pro Ala Asp Gly His Val Val Thr Glu Leu Ile Ser Lys Val Ala Gly
 25 30 35

gcg tcc agc cca tgg ggc gat gac aag gaa ttc cca gtt tct gca gaa 259
 Ala Ser Ser Pro Trp Gly Asp Asp Lys Glu Phe Pro Val Ser Ala Glu
 40 45 50

gag acc gga tac gtt cac ccg tac acc cgg atc aac cgc taagaaactt 308
 Glu Thr Gly Tyr Val His Pro Tyr Thr Arg Ile Asn Arg
 55 60 65

aaaaaagagg caa 321

<210> 1036

<211> 66

<212> PRT

<213> Corynebacterium glutamicum

<400> 1036

Met Tyr Asp Met Ala Asn Val Glu Lys Lys His Phe Val Asp Pro Ala
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Trp Pro Glu His Asn Pro Ala Asp Gly His Val Val Thr Glu Leu Ile
 20 25 30

Ser Lys Val Ala Gly Ala Ser Ser Pro Trp Gly Asp Asp Lys Glu Phe
 35 40 45

Pro Val Ser Ala Glu Glu Thr Gly Tyr Val His Pro Tyr Thr Arg Ile
 50 55 60

Asn Arg
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<210> 1037

<211> 342

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(319)

<223> FRXA02186

<400> 1037

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 Leu Phe Pro Glu Phe
 1 5

gaa aga atg tat gac atg gca aac gta gag aag aag cac ttc gtc gat 163

Glu Arg Met Tyr Asp Met Ala Asn Val Glu Lys Lys His Phe Val Asp
 10 15 20

ccg gca tgg ccg gag cac aat cca gct gac gga cac gtc gtt act gaa 211
 Pro Ala Trp Pro Glu His Asn Pro Ala Asp Gly His Val Val Thr Glu
 25 30 35

ctc atc tcc aag gtc gca ggc gcg tcc agc cca tgg ggc gat gac aag 259
 Leu Ile Ser Lys Val Ala Gly Ala Ser Ser Pro Trp Gly Asp Asp Lys
 40 45 50

gaa ttc cca gtt tct gca gaa gag acc gga tac gtt cac ccg tac acc 307
 Glu Phe Pro Val Ser Ala Glu Glu Thr Gly Tyr Val His Pro Tyr Thr
 55 60 65

cgg atc aac cgc taagaaactt aaaaaagagg caa 342
 Arg Ile Asn Arg
 70

<210> 1038
 <211> 73
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1038
 Leu Phe Pro Glu Phe Glu Arg Met Tyr Asp Met Ala Asn Val Glu Lys
 1 5 10 15

Lys His Phe Val Asp Pro Ala Trp Pro Glu His Asn Pro Ala Asp Gly
 20 25 30

His Val Val Thr Glu Leu Ile Ser Lys Val Ala Gly Ala Ser Ser Pro
 35 40 45

Trp Gly Asp Asp Lys Glu Phe Pro Val Ser Ala Glu Glu Thr Gly Tyr
 50 55 60

Val His Pro Tyr Thr Arg Ile Asn Arg
 65 70

<210> 1039
 <211> 898
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(898)
 <223> RXN02207

<400> 1039
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ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115
 Met Arg Arg Arg Ser
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala

10	15	20	
ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met 25 30 35			211
ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly 40 45 50			259
caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly 55 60 65			307
gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val 70 75 80 85			355
tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln 90 95 100			403
tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala 105 110 115			451
gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu 120 125 130			499
cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp 135 140 145			547
cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg 150 155 160 165			595
gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln 170 175 180			643
ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr 185 190 195			691
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg 200 205 210			739
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly 215 220 225			787
ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile 230 235 240 245			835
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro 250 255 260			883

cac cga cga gga acc
His Arg Arg Gly Thr
265

898

<210> 1040
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 1040
Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
1 5 10 15
Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
20 25 30
Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
35 40 45
Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
50 55 60
Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
65 70 75 80
Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
85 90 95
Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
100 105 110
Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
115 120 125
Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
130 135 140
Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145 150 155 160
Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
165 170 175
Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
180 185 190
Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
195 200 205
Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
210 215 220
Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
225 230 235 240
Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu
245 250 255
Gln Asn Asp Arg Pro His Arg Arg Gly Thr

260

265

<210> 1041

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> FRXA02207

<400> 1041

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gggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115
                                   Met Arg Arg Arg Ser
                                   1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163
Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
              10              15              20

ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg 211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
              25              30              35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc 259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
              40              45              50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt 307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly
              55              60              65

gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc 355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val
              70              75              80              85

tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa 403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln
              90              95              100

tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc 451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala
              105              110              115

gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg 499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu
              120              125              130

cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat 547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp
              135              140              145

cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc 595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg
              150              155              160              165

gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag 643

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Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln
 170 175 180
 ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc 691
 Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr
 185 190 195
 tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt 739
 Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg
 200 205 210
 gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt 787
 Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly
 215 220 225
 ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att 835
 Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile
 230 235 240 245
 gcc atc tac aac gct gat gat gtc 859
 Ala Ile Tyr Asn Ala Asp Asp Val
 250

<210> 1042

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 1042

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
 1 5 10 15
 Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr
 20 25 30
 Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
 35 40 45
 Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
 50 55 60
 Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
 65 70 75 80
 Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
 85 90 95
 Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
 100 105 110
 Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
 115 120 125
 Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
 130 135 140
 Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
 145 150 155 160
 Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala

165	170	175
Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp 180	185	190
Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp 195	200	205
Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val 210	215	220
Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu 225	230	235
Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val 245	250	

<210> 1043

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN02223

<400> 1043

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tccaccacaa actctagaga tttggggtag aaacgaagac atg agc acc tac caa	115
Met Ser Thr Tyr Gln	5
1	

gac gat cgt ttc cca ggc cca gac ccc tac gca ccg ctt ggt gaa aag	163
Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala Pro Leu Gly Glu Lys	20
10	15

cca agc ttt acc ctc acc tcc acc gac ttg gaa aac ggt gca aag ctg	211
Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu Asn Gly Ala Lys Leu	35
25	30

gcc gaa gcc caa ctc ggt ggc acc gat att tcc cca cag ctg tcc tgg	259
Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser Pro Gln Leu Ser Trp	50
40	45

tca gat ctt cca gaa ggc acc aaa tcc ctc gcg atc acc tgc ctc gac	307
Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala Ile Thr Cys Leu Asp	65
55	60

cca gat gcc cca acc ggc gct ggt ttc tgg cac tgg gca gtg ttt aac	355
Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His Trp Ala Val Phe Asn	85
70	75

atc ccc aca act gtc acg gag atc ccc acc ggt gct ggc gat gaa acc	403
Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly Ala Gly Asp Glu Thr	100
90	95

ctc ggc ggc atc gaa ggc gta gtt tcc ctc aag ggt gat tcc ggc aag	451
Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys Gly Asp Ser Gly Lys	

105	110	115	
cgt ggc ttc tac gga gcg caa cct cca gct ggc cac gca ccg cac cgt			499
Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly His Ala Pro His Arg			
120	125	130	
tac ctc ttc gca gtt cat gca ctt gat gtg gaa aaa ctc gac atc gcc			547
Tyr Leu Phe Ala Val His Ala Leu Asp Val Glu Lys Leu Asp Ile Ala			
135	140	145	
ccc gac gct acc ccc act ggt cta ggc ttc aac ctg tat ttc cac act			595
Pro Asp Ala Thr Pro Thr Gly Leu Gly Phe Asn Leu Tyr Phe His Thr			
150	155	160	165
ctt ggc			601
Leu Gly			

<210> 1044
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1044
 Met Ser Thr Tyr Gln Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala
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 Pro Leu Gly Glu Lys Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu
 20 25 30
 Asn Gly Ala Lys Leu Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser
 35 40 45
 Pro Gln Leu Ser Trp Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala
 50 55 60
 Ile Thr Cys Leu Asp Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His
 65 70 75 80
 Trp Ala Val Phe Asn Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly
 85 90 95
 Ala Gly Asp Glu Thr Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys
 100 105 110
 Gly Asp Ser Gly Lys Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly
 115 120 125
 His Ala Pro His Arg Tyr Leu Phe Ala Val His Ala Leu Asp Val Glu
 130 135 140
 Lys Leu Asp Ile Ala Pro Asp Ala Thr Pro Thr Gly Leu Gly Phe Asn
 145 150 155 160
 Leu Tyr Phe His Thr Leu Gly
 165

<210> 1045
 <211> 520

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> FRXA02223

<400> 1045

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tccaccacaa actctagaga tttggggtag aaacgaagac atg agc acc tac caa 115
                                         Met Ser Thr Tyr Gln
                                         1                               5

gac gat cgt ttc cca ggc cca gac ccc tac gca ccg ctt ggt gaa aag 163
Asp Asp Arg Phe Pro Gly Pro Asp Pro Tyr Ala Pro Leu Gly Glu Lys
                        10                        15                        20

cca agc ttt acc ctc acc tcc acc gac ttg gaa aac ggt gca aag ctg 211
Pro Ser Phe Thr Leu Thr Ser Thr Asp Leu Glu Asn Gly Ala Lys Leu
                        25                        30                        35

gcc gaa gcc caa ctc ggt ggc acc gat att tcc cca cag ctg tcc tgg 259
Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser Pro Gln Leu Ser Trp
                        40                        45                        50

tca gat ctt cca gaa ggc acc aaa tcc ctc gcg atc acc tgc ctc gac 307
Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala Ile Thr Cys Leu Asp
                        55                        60                        65

cca gat gcc cca acc ggc gct ggt ttc tgg cac tgg gca gtg ttt aac 355
Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His Trp Ala Val Phe Asn
                        70                        75                        80                        85

atc ccc aca act gtc acg gag atc ccc acc ggt gct ggc gat gaa acc 403
Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly Ala Gly Asp Glu Thr
                        90                        95                        100

ctc ggc ggc atc gaa ggc gta gtt tcc ctc aag ggt gat tcc ggc aag 451
Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys Gly Asp Ser Gly Lys
                        105                        110                        115

cgt ggc ttc tac gga gcg caa cct cca gct ggc cac gca ccg cac cgt 499
Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly His Ala Pro His Arg
                        120                        125                        130

tac ctc ttc gca gtt cat gca 520
Tyr Leu Phe Ala Val His Ala
                        135                        140

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<210> 1046

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 1046

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  1                               5                        10                        15

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 20 25 30
 Asn Gly Ala Lys Leu Ala Glu Ala Gln Leu Gly Gly Thr Asp Ile Ser
 35 40 45
 Pro Gln Leu Ser Trp Ser Asp Leu Pro Glu Gly Thr Lys Ser Leu Ala
 50 55 60
 Ile Thr Cys Leu Asp Pro Asp Ala Pro Thr Gly Ala Gly Phe Trp His
 65 70 75 80
 Trp Ala Val Phe Asn Ile Pro Thr Thr Val Thr Glu Ile Pro Thr Gly
 85 90 95
 Ala Gly Asp Glu Thr Leu Gly Gly Ile Glu Gly Val Val Ser Leu Lys
 100 105 110
 Gly Asp Ser Gly Lys Arg Gly Phe Tyr Gly Ala Gln Pro Pro Ala Gly
 115 120 125
 His Ala Pro His Arg Tyr Leu Phe Ala Val His Ala
 130 135 140

<210> 1047

<211> 1156

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1156)

<223> RXN02226

<400> 1047

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 gtcgcgcggc caggacgacc ctagctttta aggaccacc atg act gag aac cag 115
 Met Thr Glu Asn Gln
 1 5
 act ccc agc tcc acc tct gca ccg aag ccg gga cct cgc ccg ggc cca 163
 Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly Pro Arg Pro Gly Pro
 10 15 20
 cgg cca gga ccc cga cct ggg gct cag gtt gct gca aag aaa gct gcg 211
 Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala Ala Lys Lys Ala Ala
 25 30 35
 gtt gct aca cct gcg ccg atc gcc aaa act tct aac gat cct gca aag 259
 Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser Asn Asp Pro Ala Lys
 40 45 50
 ttt ggt cgc gtt gag gca gac gga tct gca tat gtc acc acc tct gct 307
 Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr Val Thr Thr Ser Ala
 55 60 65
 ggc gag cgt ctg att ggt tct tgg cag gcc ggc acc cct gag gaa ggt 355
 Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly Thr Pro Glu Glu Gly
 70 75 80 85

ctt gct cac tac ggc gcc cgt ttt gat gat ctg gcc acc gaa gtt gag	403
Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu Ala Thr Glu Val Glu	
90 95 100	
ctc atg gaa cag cgc cta atc tcc cac cct gat gat gcg acc tcc atc	451
Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp Asp Ala Thr Ser Ile	
105 110 115	
cgc acg aag gct gaa gaa ctc aag gca acc ctg ccc acc atc gct gcg	499
Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu Pro Thr Ile Ala Ala	
120 125 130	
atc ggt gac ctt gat ggc gtt gaa gct cgc ctg tcc aag atc atc aac	547
Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu Ser Lys Ile Ile Asn	
135 140 145	
aac tcc gag gaa gcc aac gag cgc gcc aag gaa caa aag gct aaa aac	595
Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu Gln Lys Ala Lys Asn	
150 155 160 165	
cgt gag cgc gca gta gct cgc aag gaa gag ctc gct gtt gag gct gaa	643
Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu Ala Val Glu Ala Glu	
170 175 180	
acc ttg gca gaa aac tcc tcc gac tgg aag gtt gct ggc gac cgc atc	691
Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val Ala Gly Asp Arg Ile	
185 190 195	
cgc gcc atc ctg gat gag tgg aag tcc atc cac ggc atc gac cgc aag	739
Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His Gly Ile Asp Arg Lys	
200 205 210	
acc gat gat gaa ctg tgg aaa cgc tac tcc cgt gcg cgt gac tcc ttc	787
Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg Ala Arg Asp Ser Phe	
215 220 225	
aac cgt cgc cgc ggc gca cac ttc gca gag ctg gat cgc acc cgc gca	835
Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu Asp Arg Thr Arg Ala	
230 235 240 245	
tct gca cgc aaa ctc aag gaa gaa ctc gtt gag cgc gcc aat gct ctc	883
Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu Arg Ala Asn Ala Leu	
250 255 260	
aag gaa tcc act gag tgg aac gac acc gcc cgc gca ttc cgc gat ctc	931
Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg Ala Phe Arg Asp Leu	
265 270 275	
atg acc gaa tgg aaa gcc gcc ggc cgc gca cca cgc gaa atc gac gac	979
Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro Arg Glu Ile Asp Asp	
280 285 290	
aag ctg tgg gca gca ttc aag ggc gcc cag gac tac ttc ttt gat aag	1027
Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp Tyr Phe Phe Asp Lys	
295 300 305	
cgc aac gcc gta gcc aag gaa cgc gac cag gaa ttc gaa gcc aac gca	1075
Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu Phe Glu Ala Asn Ala	
310 315 320 325	

acc gca aag cag cag ctc atc gac gaa tac gac gca cag atc aac ccc 1123
 Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp Ala Gln Ile Asn Pro
 330 335 340

gag cag ggc ctc gat gga gcg cgc agc aag ctc 1156
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 345 350

<210> 1048

<211> 352

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

Met Thr Glu Asn Gln Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly
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Pro Arg Pro Gly Pro Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala
 20 25 30

Ala Lys Lys Ala Ala Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser
 35 40 45

Asn Asp Pro Ala Lys Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr
 50 55 60

Val Thr Thr Ser Ala Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly
 65 70 75 80

Thr Pro Glu Glu Gly Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu
 85 90 95

Ala Thr Glu Val Glu Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp
 100 105 110

Asp Ala Thr Ser Ile Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu
 115 120 125

Pro Thr Ile Ala Ala Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu
 130 135 140

Ser Lys Ile Ile Asn Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu
 145 150 155 160

Gln Lys Ala Lys Asn Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu
 165 170 175

Ala Val Glu Ala Glu Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val
 180 185 190

Ala Gly Asp Arg Ile Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His
 195 200 205

Gly Ile Asp Arg Lys Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg
 210 215 220

Ala Arg Asp Ser Phe Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu
 225 230 235 240

Asp Arg Thr Arg Ala Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu

245	250	255
Arg Ala Asn Ala Leu Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg		
260	265	270
Ala Phe Arg Asp Leu Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro		
275	280	285
Arg Glu Ile Asp Asp Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp		
290	295	300
Tyr Phe Phe Asp Lys Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu		
305	310	315
Phe Glu Ala Asn Ala Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp		
325	330	335
Ala Gln Ile Asn Pro Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu		
340	345	350

<210> 1049

<211> 1156

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1156)

<223> FRXA02226

<400> 1049

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gtcgcgcggc caggacgacc ctagctttta aggacccacc atg act gag aac cag	115
Met Thr Glu Asn Gln	
1 5	

act ccc agc tcc acc tct gca ccg aag ccg gga cct cgc ccg ggc cca	163
Thr Pro Ser Ser Thr Ser Ala Pro Lys Pro Gly Pro Arg Pro Gly Pro	
10 15 20	

cgg cca gga ccc cga cct ggg gct cag gtt gct gca aag aaa gct gcg	211
Arg Pro Gly Pro Arg Pro Gly Ala Gln Val Ala Ala Lys Lys Ala Ala	
25 30 35	

gtt gct aca cct gcg ccg atc gcc aaa act tct aac gat cct gca aag	259
Val Ala Thr Pro Ala Pro Ile Ala Lys Thr Ser Asn Asp Pro Ala Lys	
40 45 50	

ttt ggt cgc gtt gag gca gac gga tct gca tat gtc acc acc tct gct	307
Phe Gly Arg Val Glu Ala Asp Gly Ser Ala Tyr Val Thr Thr Ser Ala	
55 60 65	

ggc gag cgt ctg att ggt tct tgg cag gcc ggc acc cct gag gaa ggt	355
Gly Glu Arg Leu Ile Gly Ser Trp Gln Ala Gly Thr Pro Glu Glu Gly	
70 75 80 85	

ctt gct cac tac ggc gcc cgt ttt gat gat ctg gcc acc gaa gtt gag	403
Leu Ala His Tyr Gly Ala Arg Phe Asp Asp Leu Ala Thr Glu Val Glu	
90 95 100	

ctc atg gaa cag cgc cta atc tcc cac cct gat gat gcg acc tcc atc	451
Leu Met Glu Gln Arg Leu Ile Ser His Pro Asp Asp Ala Thr Ser Ile	
105 110 115	
cgc acg aag gct gaa gaa ctc aag gca acc ctg ccc acc atc gct gcg	499
Arg Thr Lys Ala Glu Glu Leu Lys Ala Thr Leu Pro Thr Ile Ala Ala	
120 125 130	
atc ggt gac ctt gat ggc gtt gaa gct cgc ctg tcc aag atc atc aac	547
Ile Gly Asp Leu Asp Gly Val Glu Ala Arg Leu Ser Lys Ile Ile Asn	
135 140 145	
aac tcc gag gaa gcc aac gag cgc gcc aag gaa caa aag gct aaa aac	595
Asn Ser Glu Glu Ala Asn Glu Arg Ala Lys Glu Gln Lys Ala Lys Asn	
150 155 160 165	
cgt gag cgc gca gta gct cgc aag gaa gag ctc gct gtt gag gct gaa	643
Arg Glu Arg Ala Val Ala Arg Lys Glu Glu Leu Ala Val Glu Ala Glu	
170 175 180	
acc ttg gca gaa aac tcc tcc gac tgg aag gtt gct ggc gac cgc atc	691
Thr Leu Ala Glu Asn Ser Ser Asp Trp Lys Val Ala Gly Asp Arg Ile	
185 190 195	
cgc gcc atc ctg gat gag tgg aag tcc atc cac ggc atc gac cgc aag	739
Arg Ala Ile Leu Asp Glu Trp Lys Ser Ile His Gly Ile Asp Arg Lys	
200 205 210	
acc gat gat gaa ctg tgg aaa cgc tac tcc cgt gcg cgt gac tcc ttc	787
Thr Asp Asp Glu Leu Trp Lys Arg Tyr Ser Arg Ala Arg Asp Ser Phe	
215 220 225	
aac cgt cgc cgc ggc gca cac ttc gca gag ctg gat cgc acc cgc gca	835
Asn Arg Arg Arg Gly Ala His Phe Ala Glu Leu Asp Arg Thr Arg Ala	
230 235 240 245	
tct gca cgc aaa ctc aag gaa gaa ctc gtt gag cgc gcc aat gct ctc	883
Ser Ala Arg Lys Leu Lys Glu Glu Leu Val Glu Arg Ala Asn Ala Leu	
250 255 260	
aag gaa tcc act gag tgg aac gac acc gcc cgc gca ttc cgc gat ctc	931
Lys Glu Ser Thr Glu Trp Asn Asp Thr Ala Arg Ala Phe Arg Asp Leu	
265 270 275	
atg acc gaa tgg aaa gcc gcc ggc cgc gca cca cgc gaa atc gac gac	979
Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro Arg Glu Ile Asp Asp	
280 285 290	
aag ctg tgg gca gca ttc aag ggc gcc cag gac tac ttc ttt gat aag	1027
Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp Tyr Phe Phe Asp Lys	
295 300 305	
cgc aac gcc gta gcc aag gaa cgc gac cag gaa ttc gaa gcc aac gca	1075
Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu Phe Glu Ala Asn Ala	
310 315 320 325	
acc gca aag cag cag ctc atc gac gaa tac gac gca cag atc aac ccc	1123
Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp Ala Gln Ile Asn Pro	
330 335 340	

Ala Phe Arg Asp Leu Met Thr Glu Trp Lys Ala Ala Gly Arg Ala Pro
 275 280 285

Arg Glu Ile Asp Asp Lys Leu Trp Ala Ala Phe Lys Gly Ala Gln Asp
 290 295 300

Tyr Phe Phe Asp Lys Arg Asn Ala Val Ala Lys Glu Arg Asp Gln Glu
 305 310 315 320

Phe Glu Ala Asn Ala Thr Ala Lys Gln Gln Leu Ile Asp Glu Tyr Asp
 325 330 335

Ala Gln Ile Asn Pro Glu Gln Gly Leu Asp Gly Ala Arg Ser Lys Leu
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<210> 1051

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXN02238

<400> 1051

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ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

gcc ctg gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 90 95

cac 408

<210> 1052

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1052

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
 1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
 20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 85 90 95

<210> 1053

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(385)

<223> FRXA02238

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ctcttaacac tactgtccat atacttttga aaagggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
90 95

cac 408

<210> 1054

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
85 90 95

<210> 1055

<211> 800

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(777)

<223> RXN02254

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Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
1 5 10 15

cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc 96
Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
20 25 30

gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt 144
Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
35 40 45

gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta 192
Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
50 55 60

tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct 240

Cys	Ala	Glu	Pro	Leu	Asp	Leu	Glu	Ala	Glu	Val	Ser	Gly	Leu	Asp	Ser		
65					70					75					80		
gat	gct	cga	gtc	atg	cgt	caa	gtt	cgt	ggc	caa	gtg	gcg	gta	gct	gca		288
Asp	Ala	Arg	Val	Met	Arg	Gln	Val	Arg	Gly	Gln	Val	Ala	Val	Ala	Ala		
				85					90					95			
acc	ccc	ggg	cag	gtg	cga	cgc	gtt	cga	atc	att	ccg	gac	aat	cca	gaa		336
Thr	Pro	Gly	Gln	Val	Arg	Arg	Val	Arg	Ile	Ile	Pro	Asp	Asn	Pro	Glu		
			100					105					110				
ccg	aac	ccc	gct	gcc	atc	gag	gcc	att	ctc	gat	gca	gat	ttg	gtc	acc		384
Pro	Asn	Pro	Ala	Ala	Ile	Glu	Ala	Ile	Leu	Asp	Ala	Asp	Leu	Val	Thr		
		115					120					125					
ctt	ggc	cca	ggc	tcc	tgg	ttc	tcc	tct	gtg	att	cca	cac	att	ttg	gtc		432
Leu	Gly	Pro	Gly	Ser	Trp	Phe	Ser	Ser	Val	Ile	Pro	His	Ile	Leu	Val		
	130					135					140						
cca	ggg	atc	gtt	gat	gcc	ttg	gcg	cag	aca	aaa	gca	acc	aaa	acc	gtg		480
Pro	Gly	Ile	Val	Asp	Ala	Leu	Ala	Gln	Thr	Lys	Ala	Thr	Lys	Thr	Val		
145					150					155					160		
gtg	tta	aac	ctg	acg	tcc	gag	cca	ggg	gag	acc	gcg	gga	ttc	tct	gca		528
Val	Leu	Asn	Leu	Thr	Ser	Glu	Pro	Gly	Glu	Thr	Ala	Gly	Phe	Ser	Ala		
				165					170					175			
gaa	cga	cac	atc	cat	gtg	ctc	cgc	cag	cat	gct	cga	aac	ctt	cag	gtt		576
Glu	Arg	His	Ile	His	Val	Leu	Arg	Gln	His	Ala	Arg	Asn	Leu	Gln	Val		
			180					185					190				
gac	caa	gtc	att	gtc	gat	gcc	aag	aca	ctg	tcc	tca	caa	acc	gaa	cgc		624
Asp	Gln	Val	Ile	Val	Asp	Ala	Lys	Thr	Leu	Ser	Ser	Gln	Thr	Glu	Arg		
		195					200					205					
aat	cat	gta	gaa	cga	gct	gct	cgc	acc	ctt	ggc	gca	gaa	gtc	tcc	ttc		672
Asn	His	Val	Glu	Arg	Ala	Ala	Arg	Thr	Leu	Gly	Ala	Glu	Val	Ser	Phe		
		210				215					220						
cat	gat	gtc	cag	gct	gaa	gat	ggc	cgt	ggc	cga	ttc	acc	agt	att	cac		720
His	Asp	Val	Gln	Ala	Glu	Asp	Gly	Arg	Gly	Arg	Phe	Thr	Ser	Ile	His		
225					230					235					240		
gat	cca	gca	aag	ctg	tgt	gca	gcg	ttg	ctg	gca	agt	ttt	gct	gga	gca		768
Asp	Pro	Ala	Lys	Leu	Cys	Ala	Ala	Leu	Leu	Ala	Ser	Phe	Ala	Gly	Ala		
			245					250						255			
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Arg	Lys	Arg															

<210> 1056

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 1056

Ile	Ala	Val	Ala	Glu	Glu	Gly	Gly	Leu	Trp	Glu	Asn	Leu	Leu	Gln	His	
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Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
20 25 30
Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
35 40 45
Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
50 55 60
Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
65 70 75 80
Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
85 90 95
Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
100 105 110
Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
115 120 125
Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
130 135 140
Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145 150 155 160
Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
165 170 175
Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
180 185 190
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
195 200 205
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
210 215 220
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225 230 235 240
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
245 250 255

Arg Lys Arg

<210> 1057

<211> 804

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(781)

<223> FRXA02254

<400> 1057

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												Val	Ile	Ala	Ala	Leu	
												1				5	
acc	gac	att	ttg	ggc	acc	tcc	cag	cat	gcg	ctt	gat	caa	atc	gct	caa	163	
Thr	Asp	Ile	Leu	Gly	Thr	Ser	Gln	His	Ala	Leu	Asp	Gln	Ile	Ala	Gln		
				10					15					20			
ctc	gct	gga	gcc	aaa	gga	cgc	atc	atc	ccg	gta	tgt	gct	gaa	cct	ttg	211	
Leu	Ala	Gly	Ala	Lys	Gly	Arg	Ile	Ile	Pro	Val	Cys	Ala	Glu	Pro	Leu		
				25				30					35				
gat	ctt	gaa	gcg	gaa	gta	tca	ggt	cta	gac	tct	gat	gct	cga	gtc	atg	259	
Asp	Leu	Glu	Ala	Glu	Val	Ser	Gly	Leu	Asp	Ser	Asp	Ala	Arg	Val	Met		
		40					45					50					
cgt	caa	gtt	cgt	ggt	caa	gtg	gcg	gta	gct	gca	acc	ccc	ggg	cag	gtg	307	
Arg	Gln	Val	Arg	Gly	Gln	Val	Ala	Val	Ala	Ala	Thr	Pro	Gly	Gln	Val		
	55					60					65						
cga	cgc	gtt	cga	atc	att	ccg	gac	aat	cca	gaa	ccg	aac	ccc	gct	gcc	355	
Arg	Arg	Val	Arg	Ile	Ile	Pro	Asp	Asn	Pro	Glu	Pro	Asn	Pro	Ala	Ala		
	70				75					80					85		
atc	gag	gcc	att	ctc	gat	gca	gat	ttg	gtc	acc	ctt	ggc	cca	ggt	tcc	403	
Ile	Glu	Ala	Ile	Leu	Asp	Ala	Asp	Leu	Val	Thr	Leu	Gly	Pro	Gly	Ser		
				90					95					100			
tg	g	ttc	tcc	tct	gtg	att	cca	cac	att	ttg	gtc	cca	ggg	atc	gtt	gat	451
Trp	Phe	Ser	Ser	Val	Ile	Pro	His	Ile	Leu	Val	Pro	Gly	Ile	Val	Asp		
			105					110					115				
gcc	ttg	gcg	cag	aca	aaa	gca	acc	aaa	acc	gtg	gtg	tta	aac	ctg	acg	499	
Ala	Leu	Ala	Gln	Thr	Lys	Ala	Thr	Lys	Thr	Val	Val	Leu	Asn	Leu	Thr		
			120				125					130					
tcc	gag	cca	ggg	gag	acc	gcg	gga	ttc	tct	gca	gaa	cga	cac	atc	cat	547	
Ser	Glu	Pro	Gly	Glu	Thr	Ala	Gly	Phe	Ser	Ala	Glu	Arg	His	Ile	His		
	135					140					145						
gtg	ctc	cgc	cag	cat	gct	cga	aac	ctt	cag	gtt	gac	caa	gtc	att	gtc	595	
Val	Leu	Arg	Gln	His	Ala	Arg	Asn	Leu	Gln	Val	Asp	Gln	Val	Ile	Val		
	150				155				160						165		
gat	gcc	aag	aca	ctg	tcc	tca	caa	acc	gaa	cgc	aat	cat	gta	gaa	cga	643	
Asp	Ala	Lys	Thr	Leu	Ser	Ser	Gln	Thr	Glu	Arg	Asn	His	Val	Glu	Arg		
				170					175					180			
gct	gct	cgc	acc	ctt	ggt	gca	gaa	gtc	tcc	ttc	cat	gat	gtc	cag	gct	691	
Ala	Ala	Arg	Thr	Leu	Gly	Ala	Glu	Val	Ser	Phe	His	Asp	Val	Gln	Ala		
			185					190					195				
gaa	gat	ggc	cgt	ggt	cga	ttc	acc	agt	att	cac	gat	cca	gca	aag	ctg	739	
Glu	Asp	Gly	Arg	Gly	Arg	Phe	Thr	Ser	Ile	His	Asp	Pro	Ala	Lys	Leu		
		200					205					210					
tgt	gca	gcg	ttg	ctg	gca	agt	ttt	gct	gga	gca	cga	aag	cgt			781	
Cys	Ala	Ala	Leu	Leu	Ala	Ser	Phe	Ala	Gly	Ala	Arg	Lys	Arg				
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804

<210> 1058

<211> 227

<212> PRT

<213> Corynebacterium glutamicum

<400> 1058

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20 25 30

Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
35 40 45

Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
50 55 60

Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
65 70 75 80

Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
85 90 95

Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
100 105 110

Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
115 120 125

Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
130 135 140

Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
145 150 155 160

Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
165 170 175

Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
180 185 190

His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
195 200 205

Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
210 215 220

Arg Lys Arg
225

<210> 1059

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(658)
 <223> RXN02271

<400> 1059

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               Met Ser Phe Leu Asn
               1               5

tct gca aaa acc aag acc gta gcc ctc acc gca acc ttc gtt ggt gca 163
Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala Thr Phe Val Gly Ala
               10               15               20

gca acc ctt gca act cct gca atc gca tcc gct gac atc gtc gac aac 211
Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala Asp Ile Val Asp Asn
               25               30               35

gcc ctc gca gcc ctc cca tcc ggt gag atc agc tgc tcc cag gct gaa 259
Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser Cys Ser Gln Ala Glu
               40               45               50

aag tac tgg acc acc gaa gct gat tac aac agc aag gtt gca cag gcc 307
Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser Lys Val Ala Gln Ala
               55               60               65

aac gcc ttg gca atg ttt gac tcc cgc ggc cca cag atc cag gca gct 355
Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro Gln Ile Gln Ala Ala
               70               75               80               85

ctc gca cgc gtt gac gaa gca gca aac cgc tgc gga ctc aag ggc ggc 403
Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys Gly Leu Lys Gly Gly
               90               95               100

acc gta gct gcg cag gct gag gca act gag gct gcg cct gcc gct cca 451
Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala Ala Pro Ala Ala Pro
               105               110               115

gca cct gca ccg cag gat aac acc ggc act tct cag act gcc cct gcc 499
Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser Gln Thr Ala Pro Ala
               120               125               130

cca gca gca cca gca gca cca gca gct acc cct gtg gtt aac ctt gca 547
Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro Val Val Asn Leu Ala
               135               140               145

cct gca gga tca cca act ttc acc att gaa gtt cca gga gtt ggc ggg 595
Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val Pro Gly Val Gly Gly
               150               155               160               165

gtt cag ctg cca gat cta tac caa atc gtc caa cag ttc ttg gca cag 643
Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln Gln Phe Leu Ala Gln
               170               175               180

ttc gga atc aag atc taaatctatt cacatccctt aac 681
Phe Gly Ile Lys Ile
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<210> 1060

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 1060

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Thr Phe Val Gly Ala Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala
 20 25 30

Asp Ile Val Asp Asn Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser
 35 40 45

Cys Ser Gln Ala Glu Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser
 50 55 60

Lys Val Ala Gln Ala Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro
 65 70 75 80

Gln Ile Gln Ala Ala Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys
 85 90 95

Gly Leu Lys Gly Gly Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala
 100 105 110

Ala Pro Ala Ala Pro Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser
 115 120 125

Gln Thr Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro
 130 135 140

Val Val Asn Leu Ala Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val
 145 150 155 160

Pro Gly Val Gly Gly Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln
 165 170 175

Gln Phe Leu Ala Gln Phe Gly Ile Lys Ile
 180 185

<210> 1061

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(658)

<223> FRXA02271

<400> 1061

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acactgggtgt atttcagtta catccgtatg gttattgggt atg agc ttt ctt aac 115
 Met Ser Phe Leu Asn
 1 5

tct gca aaa acc aag acc gta gcc ctc acc gca acc ttc gtt ggt gca 163
 Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala Thr Phe Val Gly Ala

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gca acc ott gca act cct gca atc gca tcc gct gac atc gtc gac aac Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala Asp Ile Val Asp Asn 25 30 35	211		
gcc ctc gca gcc ctc cca tcc ggt gag atc agc tgc tcc cag gct gaa Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser Cys Ser Gln Ala Glu 40 45 50	259		
aag tac tgg acc acc gaa gct gat tac aac agc aag gtt gca cag gcc Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser Lys Val Ala Gln Ala 55 60 65	307		
aac gcc ttg gca atg ttt gac tcc cgc ggc cca cag atc cag gca gct Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro Gln Ile Gln Ala Ala 70 75 80 85	355		
ctc gca cgc gtt gac gaa gca gca aac cgc tgc gga ctc aag ggc ggc Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys Gly Leu Lys Gly Gly 90 95 100	403		
acc gta gct gcg cag gct gag gca act gag gct gcg cct gcc gct cca Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala Ala Pro Ala Ala Pro 105 110 115	451		
gca cct gca ccg cag gat aac acc ggc act tct cag act gcc cct gcc Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser Gln Thr Ala Pro Ala 120 125 130	499		
cca gca gca cca gca gca cca gca gct acc cct gtg gtt aac ctt gca Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro Val Val Asn Leu Ala 135 140 145	547		
cct gca gga tca cca act ttc acc att gaa gtt cca gga gtt ggc ggg Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val Pro Gly Val Gly Gly 150 155 160 165	595		
gtt cag ctg cca gat cta tac caa atc gtc caa cag ttc ttg gca cag Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln Gln Phe Leu Ala Gln 170 175 180	643		
ttc gga atc aag atc taaatctatt cacatccctt aac Phe Gly Ile Lys Ile 185	681		

<210> 1062

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 1062

Met Ser Phe Leu Asn Ser Ala Lys Thr Lys Thr Val Ala Leu Thr Ala
1 5 10 15

Thr Phe Val Gly Ala Ala Thr Leu Ala Thr Pro Ala Ile Ala Ser Ala
20 25 30

Asp Ile Val Asp Asn Ala Leu Ala Ala Leu Pro Ser Gly Glu Ile Ser
35 40 45

Cys Ser Gln Ala Glu Lys Tyr Trp Thr Thr Glu Ala Asp Tyr Asn Ser
 50 55 60
 Lys Val Ala Gln Ala Asn Ala Leu Ala Met Phe Asp Ser Arg Gly Pro
 65 70 75 80
 Gln Ile Gln Ala Ala Leu Ala Arg Val Asp Glu Ala Ala Asn Arg Cys
 85 90 95
 Gly Leu Lys Gly Gly Thr Val Ala Ala Gln Ala Glu Ala Thr Glu Ala
 100 105 110
 Ala Pro Ala Ala Pro Ala Pro Ala Pro Gln Asp Asn Thr Gly Thr Ser
 115 120 125
 Gln Thr Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Ala Thr Pro
 130 135 140
 Val Val Asn Leu Ala Pro Ala Gly Ser Pro Thr Phe Thr Ile Glu Val
 145 150 155 160
 Pro Gly Val Gly Gly Val Gln Leu Pro Asp Leu Tyr Gln Ile Val Gln
 165 170 175
 Gln Phe Leu Ala Gln Phe Gly Ile Lys Ile
 180 185

<210> 1063

<211> 1581

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1558)

<223> RXN02279

<400> 1063

ggtaagaggg cattttccga tgcgcagcga ttcttgctca acgccgacga gctcgcggag 60

ctttctgatt atgagcgtct ggcttatgcc atcaccttgc ttg atc agc ctg gaa 115
 Leu Ile Ser Leu Glu
 1 5

aag aag cag aag gac gcg aac ttt ttc ctt tcg gag ctt cgc cgc cag 163
 Lys Lys Gln Lys Asp Ala Asn Phe Phe Leu Ser Glu Leu Arg Arg Gln
 10 15 20

ggc tac cgc gct gtc gat ttc ttg gaa tcc cag act gtt gac cag ctg 211
 Gly Tyr Arg Ala Val Asp Phe Leu Glu Ser Gln Thr Val Asp Gln Leu
 25 30 35

aat aac ccc gat gtc cag act tac ctc acc gaa gcg gaa ctg att cgc 259
 Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu Leu Ile Arg
 40 45 50

gat gac ttg agg tct tgg gca gtc atc aat caa atg gca ttg gac aac 307
 Asp Asp Leu Arg Ser Trp Ala Val Ile Asn Gln Met Ala Leu Asp Asn
 55 60 65

atc gat ctt gtt cca tac ggc gag gaa aac gac gag cca ctt gca atc Ile Asp Leu Val Pro Tyr Gly Glu Glu Asn Asp Glu Pro Leu Ala Ile 70 75 80 85	355
gcc cgc aag atc atc gag gaa acc gct tcc cat cct gag ctg aga ttc Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu Leu Arg Phe 90 95 100	403
gaa aac ctc gag gcc cag ttc tcc gag ttc acc atc ttg ctt gct caa Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu Leu Ala Gln 105 110 115	451
agc ccg gag aac ctc gac gta gcc cgc tac cag gag ctt cgt aca cag Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu Arg Thr Gln 120 125 130	499
gga aac ttt gtt caa gaa ctc gcc ttg gac agc att ttc ggc caa cat Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe Gly Gln His 135 140 145	547
gcc gtt gtt caa gac acc gga aac ggc gaa gcc atc cta gat gaa act Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu Asp Glu Thr 150 155 160 165	595
atc ggg tac atg atc ggc gcc ggc atg cgt gaa acc act gcc cgc acc Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr Ala Arg Thr 170 175 180	643
gcc agc cag ttc gcg cag ctt tac tca ttt gtg ggc agg cag gaa cgc Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg Gln Glu Arg 185 190 195	691
tcc att gaa atg gca cga ctc gct ttc gag gaa ctt caa gcg gca gga Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln Ala Ala Gly 200 205 210	739
ctt ccc cac cgt gag gaa gaa ctg cga ttg ggc atg caa ctc gcc cag Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln Leu Ala Gln 215 220 225	787
gtt gaa cca att gaa gcc cgc gaa atc ctg gaa aag ctg ctg ctg cct Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu Leu Leu Pro 230 235 240 245	835
aaa ttc gag cag aat ctg aca ctt gat gaa ctt gaa act gaa gca ctc Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr Glu Ala Leu 250 255 260	883
ctt cct ttg ggt gct acc gtt gct atc cac gac ccc cag gct gcc gca Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln Ala Ala Ala 265 270 275	931
gca att ttg cgc cac gct cgc gaa aac gcc gca ggg ttc ggc aac ttc Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe Gly Asn Phe 280 285 290	979
gaa ctc gca gtc caa gcg atg acc atg atc acg gat gtc ctc tac acc Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val Leu Tyr Thr 295 300 305	1027

caa aac atg cac gag caa ctg ctg gag gag ctc aac cac tct ctc ccc 1075
 Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His Ser Leu Pro
 310 315 320 325

tat gct caa atg ctt gat gat caa cac caa gct gaa ctg aaa ctg ctg 1123
 Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu Lys Leu Leu
 330 335 340

gag agc atc gcc atc gtc cag gca gag ctc ggt tcc acc gaa gcg ctg 1171
 Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr Glu Ala Leu
 345 350 355

gaa acc ctg gcc acc gca atg gga ctc gca gaa acc aca gct cag aag 1219
 Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr Ala Gln Lys
 360 365 370

cta tac gtg cag gaa tcc ctc aac cgc gca tac ttc act ttt gcc cgc 1267
 Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr Phe Ala Arg
 375 380 385

cct gaa gat tgc atc agc gga gca gcc gag gct tct gcc ctg gcc atg 1315
 Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala Leu Ala Met
 390 395 400 405

caa aac gat gag cct tcc aat gca gct gcc cag ttg gag cag tgt gca 1363
 Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu Gln Cys Ala
 410 415 420

cag tac ttg ttc caa ttg ggc cac gaa act gag ggc gca agc ctg ctg 1411
 Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala Ser Leu Leu
 425 430 435

gaa tct gca ttc agg gtt gaa ggc atc ccc act gag cag gca ctg tac 1459
 Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln Ala Leu Tyr
 440 445 450

tac gca aat gca ctg tct tcc atc tat gaa gat ttc ggc gat tcc gcg 1507
 Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly Asp Ser Ala
 455 460 465

aag tcg cag tac tgg gag cag cag gcg cag gaa aag cag cag ctt ctg 1555
 Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln Gln Leu Leu
 470 475 480 485

gag taacggccgt ttaaagagtc gaa 1581
 Glu

<210> 1064

<211> 486

<212> PRT

<213> Corynebacterium glutamicum

<400> 1064

Leu Ile Ser Leu Glu Lys Lys Gln Lys Asp Ala Asn Phe Phe Leu Ser
 1 5 10 15

Glu Leu Arg Arg Gln Gly Tyr Arg Ala Val Asp Phe Leu Glu Ser Gln
 20 25 30

Thr Val Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu
35 40 45

Ala Glu Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Asn Gln
50 55 60

Met Ala Leu Asp Asn Ile Asp Leu Val Pro Tyr Gly Glu Glu Asn Asp
65 70 75 80

Glu Pro Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His
85 90 95

Pro Glu Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr
100 105 110

Ile Leu Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln
115 120 125

Glu Leu Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser
130 135 140

Ile Phe Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala
145 150 155 160

Ile Leu Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu
165 170 175

Thr Thr Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val
180 185 190

Gly Arg Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu
195 200 205

Leu Gln Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly
210 215 220

Met Gln Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu
225 230 235 240

Lys Leu Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu
245 250 255

Glu Thr Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp
260 265 270

Pro Gln Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala
275 280 285

Gly Phe Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr
290 295 300

Asp Val Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu
305 310 315 320

Asn His Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala
325 330 335

Glu Leu Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly
340 345 350

Ser Thr Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu

355	360	365
Thr Thr Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr		
370	375	380
Phe Thr Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala		
385	390	395
Ser Ala Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln		
405	410	415
Leu Glu Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp		
420	425	430
Gly Ala Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr		
435	440	445
Glu Gln Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp		
450	455	460
Phe Gly Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu		
465	470	475
Lys Gln Gln Leu Leu Glu		
485		

<210> 1065
 <211> 1427
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1404)
 <223> FRXA02279

<220>
 <221> misc_feature
 <222> (1, 3)
 <223> n = a, t, c, or g

<220>
 <221> VARIANT
 <222> (1)
 <223> Xaa = Ala, Pro, Ser, or Thr

<400> 1065	
ncn gcc agg gct acc gcg ctt gtc gat ttc ttg gaa tcc cag act gtt	48
Xaa Ala Arg Ala Thr Ala Leu Val Asp Phe Leu Glu Ser Gln Thr Val	
1 5 10 15	
gac cag ctg aat aac ccc gat gtc cag act tac ctc acc gaa gcg gaa	96
Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu	
20 25 30	
ctg att cgc gat gac ttg agg tct tgg gca gtc atc aaa tca aat ggc	144
Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Lys Ser Asn Gly	
35 40 45	
att gga caa cat cga tct tgt tcc ata cgg cga gga aac gac gag cca	192

Ile	Gly	Gln	His	Arg	Ser	Cys	Ser	Ile	Arg	Arg	Gly	Asn	Asp	Glu	Pro		
	50					55					60						
ctt	gca	atc	gcc	cgc	aag	atc	atc	gag	gaa	acc	gct	tcc	cat	cct	gag	240	
Leu	Ala	Ile	Ala	Arg	Lys	Ile	Ile	Glu	Glu	Thr	Ala	Ser	His	Pro	Glu		
	65				70				75						80		
ctg	aga	ttc	gaa	aac	ctc	gag	gcc	cag	ttc	tcc	gag	ttc	acc	atc	ttg	288	
Leu	Arg	Phe	Glu	Asn	Leu	Glu	Ala	Gln	Phe	Ser	Glu	Phe	Thr	Ile	Leu		
				85					90					95			
ctt	gct	caa	agc	ccg	gag	aac	ctc	gac	gta	gcc	cgc	tac	cag	gag	ctt	336	
Leu	Ala	Gln	Ser	Pro	Glu	Asn	Leu	Asp	Val	Ala	Arg	Tyr	Gln	Glu	Leu		
			100					105					110				
cgt	aca	cag	gga	aac	ttt	gtt	caa	gaa	ctc	gcc	ttg	gac	agc	att	ttc	384	
Arg	Thr	Gln	Gly	Asn	Phe	Val	Gln	Glu	Leu	Ala	Leu	Asp	Ser	Ile	Phe		
		115					120					125					
ggc	caa	cat	gcc	gtt	gtt	caa	gac	acc	gga	aac	ggc	gaa	gcc	atc	cta	432	
Gly	Gln	His	Ala	Val	Val	Gln	Asp	Thr	Gly	Asn	Gly	Glu	Ala	Ile	Leu		
	130					135					140						
gat	gaa	act	atc	ggg	tac	atg	atc	ggc	gcc	ggc	atg	cgt	gaa	acc	act	480	
Asp	Glu	Thr	Ile	Gly	Tyr	Met	Ile	Gly	Ala	Gly	Met	Arg	Glu	Thr	Thr		
	145				150					155					160		
gcc	cgc	acc	gcc	agc	cag	ttc	gcg	cag	ctt	tac	tca	ttt	gtg	ggc	agg	528	
Ala	Arg	Thr	Ala	Ser	Gln	Phe	Ala	Gln	Leu	Tyr	Ser	Phe	Val	Gly	Arg		
				165					170					175			
cag	gaa	cgc	tcc	att	gaa	atg	gca	cga	ctc	gct	ttc	gag	gaa	ctt	caa	576	
Gln	Glu	Arg	Ser	Ile	Glu	Met	Ala	Arg	Leu	Ala	Phe	Glu	Glu	Leu	Gln		
			180					185					190				
gcg	gca	gga	ctt	ccc	cac	cgt	gag	gaa	gaa	ctg	cga	ttg	ggc	atg	caa	624	
Ala	Ala	Gly	Leu	Pro	His	Arg	Glu	Glu	Glu	Leu	Arg	Leu	Gly	Met	Gln		
		195					200					205					
ctc	gcc	cag	gtt	gaa	cca	att	gaa	gcc	cgc	gaa	atc	ctg	gaa	aag	ctg	672	
Leu	Ala	Gln	Val	Glu	Pro	Ile	Glu	Ala	Arg	Glu	Ile	Leu	Glu	Lys	Leu		
	210					215					220						
ctg	ctg	cct	aaa	ttc	gag	cag	aat	ctg	aca	ctt	gat	gaa	ctt	gaa	act	720	
Leu	Leu	Pro	Lys	Phe	Glu	Gln	Asn	Leu	Thr	Leu	Asp	Glu	Leu	Glu	Thr		
	225				230					235					240		
gaa	gca	ctc	ctt	cct	ttg	ggt	gct	acc	gtt	gct	atc	cac	gac	ccc	cag	768	
Glu	Ala	Leu	Leu	Pro	Leu	Gly	Ala	Thr	Val	Ala	Ile	His	Asp	Pro	Gln		
				245					250					255			
gct	gcc	gca	gca	att	ttg	cgc	cac	gct	cgc	gaa	aac	gcc	gca	ggg	ttc	816	
Ala	Ala	Ala	Ala	Ile	Leu	Arg	His	Ala	Arg	Glu	Asn	Ala	Ala	Gly	Phe		
			260					265					270				
ggc	aac	ttc	gaa	ctc	gca	gtc	caa	gcg	atg	acc	atg	atc	acg	gat	gtc	864	
Gly	Asn	Phe	Glu	Leu	Ala	Val	Gln	Ala	Met	Thr	Met	Ile	Thr	Asp	Val		
		275					280					285					
ctc	tac	acc	caa	aac	atg	cac	gag	caa	ctg	ctg	gag	gag	ctc	aac	cac	912	
Leu	Tyr	Thr	Gln	Asn	Met	His	Glu	Gln	Leu	Leu	Glu	Glu	Leu	Asn	His		

290	295	300	
tct ctc ccc tat gct caa atg ctt gat gat caa cac caa gct gaa ctg			960
Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu			
305	310	315	320
aaa ctg ctg gac agc atc gcc atc gtc cag gca gac ctc ggt tcc acc			1008
Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr			
	325	330	335
gaa gcg ctg gaa acc ctg ggc acc gca atg gga ctc gca gaa acc aca			1056
Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr			
	340	345	350
gct cag aag cta tac gtg cag gaa tcc ctc aac cgc gca tac ttc act			1104
Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr			
	355	360	365
ttt gcc cgc cct gaa gat tgc atc agc gga gca gcc gac gct tct gcc			1152
Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala			
	370	375	380
ctg gcc atg caa aac gat gac cct tcc aat gca gct gcc cag ttg gag			1200
Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu			
	385	390	400
cag tgt gca cag tac ttg ttc caa ttg ggc cac gaa act gac ggc gca			1248
Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala			
	405	410	415
agc ctg ctg gaa tct gca ttc agg gtt gaa ggc atc ccc act gag cag			1296
Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln			
	420	425	430
gca ctg tac tac gca aat gca ctg tct tcc atc tat gaa gat ttc ggc			1344
Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly			
	435	440	445
gat tcc gcg aag tcg cag tac tgg gag cag cag gcg cag gaa aag cag			1392
Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln			
	450	455	460
cag ctt ctg gag taacggccgt ttaaagagtc gaa			1427
Gln Leu Leu Glu			
465			

<210> 1066

<211> 468

<212> PRT

<213> Corynebacterium glutamicum

<220>

<221> VARIANT

<222> (1)

<223> Xaa = Ala, Pro, Ser, or Thr

<400> 1066

Xaa Ala Arg Ala Thr Ala Leu Val Asp Phe Leu Glu Ser Gln Thr Val

1

5

10

15

Asp Gln Leu Asn Asn Pro Asp Val Gln Thr Tyr Leu Thr Glu Ala Glu
 20 25 30
 Leu Ile Arg Asp Asp Leu Arg Ser Trp Ala Val Ile Lys Ser Asn Gly
 35 40 45
 Ile Gly Gln His Arg Ser Cys Ser Ile Arg Arg Gly Asn Asp Glu Pro
 50 55 60
 Leu Ala Ile Ala Arg Lys Ile Ile Glu Glu Thr Ala Ser His Pro Glu
 65 70 75 80
 Leu Arg Phe Glu Asn Leu Glu Ala Gln Phe Ser Glu Phe Thr Ile Leu
 85 90 95
 Leu Ala Gln Ser Pro Glu Asn Leu Asp Val Ala Arg Tyr Gln Glu Leu
 100 105 110
 Arg Thr Gln Gly Asn Phe Val Gln Glu Leu Ala Leu Asp Ser Ile Phe
 115 120 125
 Gly Gln His Ala Val Val Gln Asp Thr Gly Asn Gly Glu Ala Ile Leu
 130 135 140
 Asp Glu Thr Ile Gly Tyr Met Ile Gly Ala Gly Met Arg Glu Thr Thr
 145 150 155 160
 Ala Arg Thr Ala Ser Gln Phe Ala Gln Leu Tyr Ser Phe Val Gly Arg
 165 170 175
 Gln Glu Arg Ser Ile Glu Met Ala Arg Leu Ala Phe Glu Glu Leu Gln
 180 185 190
 Ala Ala Gly Leu Pro His Arg Glu Glu Glu Leu Arg Leu Gly Met Gln
 195 200 205
 Leu Ala Gln Val Glu Pro Ile Glu Ala Arg Glu Ile Leu Glu Lys Leu
 210 215 220
 Leu Leu Pro Lys Phe Glu Gln Asn Leu Thr Leu Asp Glu Leu Glu Thr
 225 230 235 240
 Glu Ala Leu Leu Pro Leu Gly Ala Thr Val Ala Ile His Asp Pro Gln
 245 250 255
 Ala Ala Ala Ala Ile Leu Arg His Ala Arg Glu Asn Ala Ala Gly Phe
 260 265 270
 Gly Asn Phe Glu Leu Ala Val Gln Ala Met Thr Met Ile Thr Asp Val
 275 280 285
 Leu Tyr Thr Gln Asn Met His Glu Gln Leu Leu Glu Glu Leu Asn His
 290 295 300
 Ser Leu Pro Tyr Ala Gln Met Leu Asp Asp Gln His Gln Ala Glu Leu
 305 310 315 320
 Lys Leu Leu Asp Ser Ile Ala Ile Val Gln Ala Asp Leu Gly Ser Thr
 325 330 335
 Glu Ala Leu Glu Thr Leu Gly Thr Ala Met Gly Leu Ala Glu Thr Thr

340	345	350
Ala Gln Lys Leu Tyr Val Gln Glu Ser Leu Asn Arg Ala Tyr Phe Thr 355	360	365
Phe Ala Arg Pro Glu Asp Cys Ile Ser Gly Ala Ala Asp Ala Ser Ala 370	375	380
Leu Ala Met Gln Asn Asp Asp Pro Ser Asn Ala Ala Ala Gln Leu Glu 385	390	395
Gln Cys Ala Gln Tyr Leu Phe Gln Leu Gly His Glu Thr Asp Gly Ala 405	410	415
Ser Leu Leu Glu Ser Ala Phe Arg Val Glu Gly Ile Pro Thr Glu Gln 420	425	430
Ala Leu Tyr Tyr Ala Asn Ala Leu Ser Ser Ile Tyr Glu Asp Phe Gly 435	440	445
Asp Ser Ala Lys Ser Gln Tyr Trp Glu Gln Gln Ala Gln Glu Lys Gln 450	455	460
Gln Leu Leu Glu 465		

<210> 1067

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXN02296

<400> 1067

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gggaatcacc agtatattctg gacggttaag gatgattcat	atg cgt aat caa aca	115
	Met Arg Asn Gln Thr	
	1	5

atc gct gcg gtc gca gct ttg gtc ctg ctc acc gcc gcc acg ccc gcg	163
Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr Ala Ala Thr Pro Ala	
10	15
20	

atc gct gcc acc ccg gcg aca gct gga aac gga ctc tat tcc att gac	211
Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly Leu Tyr Ser Ile Asp	
25	30
35	

atg ggc gac gag caa aag ctt acc tgc gtg ctt ttc gat gag ccc tcc	259
Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu Phe Asp Glu Pro Ser	
40	45
50	

acc gaa gcg cac gtc gtc gcc agc tgt gct gcg act ttc ccg gtg acc	307
Thr Glu Ala His Val Val Ala Ser Cys Ala Ala Thr Phe Pro Val Thr	
55	60
65	

tgg aag ctt ctc gac ggc gct cac gaa caa gcc gcg aaa ctt gaa atc	355
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Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala Ala Lys Leu Glu Ile
 70 75 80 85
 acc cag gct caa gac ggt gaa ctc tcg gtg aca gcc agc aag cag ccg 403
 Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr Ala Ser Lys Gln Pro
 90 95 100
 ttg atc acc acg atg att gcg ccc acc agc atc act aag ccc atc act 451
 Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile Thr Lys Pro Ile Thr
 105 110 115
 gtc aat agg ctt gtg gtt gtt cct ggt gag aat gag gtt cgc ttt tat 499
 Val Asn Arg Leu Val Val Val Pro Gly Glu Asn Glu Val Arg Phe Tyr
 120 125 130
 gct acc gat cct gat gtt tta cca gtg ctg atc acg cct gac tcc tat 547
 Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile Thr Pro Asp Ser Tyr
 135 140 145
 gaa gtg ttg acc gat tcc gct gct aaa gtg aaa gcg aca tta 589
 Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys Ala Thr Leu
 150 155 160
 tgaaataaac gtggatcaag gag 612

<210> 1068

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 1068

Met Arg Asn Gln Thr Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr
 1 5 10 15
 Ala Ala Thr Pro Ala Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly
 20 25 30
 Leu Tyr Ser Ile Asp Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu
 35 40 45
 Phe Asp Glu Pro Ser Thr Glu Ala His Val Val Ala Ser Cys Ala Ala
 50 55 60
 Thr Phe Pro Val Thr Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala
 65 70 75 80
 Ala Lys Leu Glu Ile Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr
 85 90 95
 Ala Ser Lys Gln Pro Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile
 100 105 110
 Thr Lys Pro Ile Thr Val Asn Arg Leu Val Val Val Pro Gly Glu Asn
 115 120 125
 Glu Val Arg Phe Tyr Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile
 130 135 140
 Thr Pro Asp Ser Tyr Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys
 145 150 155 160

Ala Thr Leu

<210> 1069

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> FRXA02296

<400> 1069

gcatcatttg tgttgtttaa agtatatggc tgttgaagtg ccattttcgc ggattagcat 60

gggaatcacc	agtatattctg	gacgggtaag	gatgattcat	atg	cgt	aat	caa	aca	115
				Met	Arg	Asn	Gln	Thr	
				1				5	

atc	gct	gcg	gtc	gca	gct	ttg	gtc	ctg	ctc	acc	gcc	gcc	acg	ccc	gcg	163
Ile	Ala	Ala	Val	Ala	Ala	Leu	Val	Leu	Leu	Thr	Ala	Ala	Thr	Pro	Ala	
			10					15						20		

atc	gct	gcc	acc	ccg	gcg	aca	gct	gga	aac	gga	ctc	tat	tcc	att	gac	211
Ile	Ala	Ala	Thr	Pro	Ala	Thr	Ala	Gly	Asn	Gly	Leu	Tyr	Ser	Ile	Asp	
			25					30					35			

atg	ggc	gac	gag	caa	aag	ctt	acc	tgc	gtg	ctt	ttc	gat	gag	ccc	tcc	259
Met	Gly	Asp	Glu	Gln	Lys	Leu	Thr	Cys	Val	Leu	Phe	Asp	Glu	Pro	Ser	
		40					45					50				

acc	gaa	gcg	cac	gtc	gtc	gcc	agc	tgt	gct	gcg	act	ttc	ccg	gtg	acc	307
Thr	Glu	Ala	His	Val	Val	Ala	Ser	Cys	Ala	Ala	Thr	Phe	Pro	Val	Thr	
	55					60					65					

tgg	aag	ctt	ctc	gac	ggc	gct	cac	gaa	caa	gcc	gcg	aaa	ctt	gaa	atc	355
Trp	Lys	Leu	Leu	Asp	Gly	Ala	His	Glu	Gln	Ala	Ala	Lys	Leu	Glu	Ile	
	70				75					80				85		

acc	cag	gct	caa	gac	ggt	gaa	ctc	tgc	gtg	aca	gcc	agc	aag	cag	ccg	403
Thr	Gln	Ala	Gln	Asp	Gly	Glu	Leu	Ser	Val	Thr	Ala	Ser	Lys	Gln	Pro	
			90					95						100		

ttg	atc	acc	acg	atg	att	gcg	ccc	acc	agc	atc	act	aag	ccc	atc	act	451
Leu	Ile	Thr	Thr	Met	Ile	Ala	Pro	Thr	Ser	Ile	Thr	Lys	Pro	Ile	Thr	
			105					110					115			

gtc	aat	agg	ctt	gtg	gtt	gtt	cct	ggt	gag	aat	gag	gtt	cgc	ttt	tat	499
Val	Asn	Arg	Leu	Val	Val	Val	Pro	Gly	Glu	Asn	Glu	Val	Arg	Phe	Tyr	
		120					125					130				

gct	acc	gat	cct	gat	gtt	tta	cca	gtg	ctg	atc	acg	cct	gac	tcc	tat	547
Ala	Thr	Asp	Pro	Asp	Val	Leu	Pro	Val	Leu	Ile	Thr	Pro	Asp	Ser	Tyr	
	135					140					145					

gaa	gtg	ttg	acc	gat	tcc	gct	gct	aaa	gtg	aaa	gcg	aca	tta			589
Glu	Val	Leu	Thr	Asp	Ser	Ala	Ala	Lys	Val	Lys	Ala	Thr	Leu			
150					155				160							

tgaaataaac gtggatcaag gag

612

<210> 1070

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 1070

Met Arg Asn Gln Thr Ile Ala Ala Val Ala Ala Leu Val Leu Leu Thr
 1 5 10 15

Ala Ala Thr Pro Ala Ile Ala Ala Thr Pro Ala Thr Ala Gly Asn Gly
 20 25 30

Leu Tyr Ser Ile Asp Met Gly Asp Glu Gln Lys Leu Thr Cys Val Leu
 35 40 45

Phe Asp Glu Pro Ser Thr Glu Ala His Val Val Ala Ser Cys Ala Ala
 50 55 60

Thr Phe Pro Val Thr Trp Lys Leu Leu Asp Gly Ala His Glu Gln Ala
 65 70 75 80

Ala Lys Leu Glu Ile Thr Gln Ala Gln Asp Gly Glu Leu Ser Val Thr
 85 90 95

Ala Ser Lys Gln Pro Leu Ile Thr Thr Met Ile Ala Pro Thr Ser Ile
 100 105 110

Thr Lys Pro Ile Thr Val Asn Arg Leu Val Val Val Pro Gly Glu Asn
 115 120 125

Glu Val Arg Phe Tyr Ala Thr Asp Pro Asp Val Leu Pro Val Leu Ile
 130 135 140

Thr Pro Asp Ser Tyr Glu Val Leu Thr Asp Ser Ala Ala Lys Val Lys
 145 150 155 160

Ala Thr Leu

<210> 1071

<211> 456

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(433)

<223> RXN02300

<400> 1071

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caatgctgtc caaagcggag cgtaaagata aggatcagaa atg aaa act tat gca 115
 Met Lys Thr Tyr Ala
 1 5

gta cta att gcg gtg gca ggg ttg gca ctt gct ggg tgt agc tgc tgc 163
 Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala Gly Cys Ser Ser Ser
 10 15 20

 gct cct gga atc tgg cgt gcc act gaa ccc gca gat gcc tac ctt gaa 211
 Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala Asp Ala Tyr Leu Glu
 25 30 35

 ata gcc gat gac ggc acg ctg tcc gga acc gac ggc tgc aac aga ctt 259
 Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp Gly Cys Asn Arg Leu
 40 45 50

 ttt ggt ggc tgg gaa aaa gac ggc tct acc atc act ttc ggc gcc atc 307
 Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile Thr Phe Gly Ala Ile
 55 60 65

 ggt atg aca gaa atg tac tgc gaa ggc gtc aac gat tgg ctg tcc cag 355
 Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn Asp Trp Leu Ser Gln
 70 75 80 85

 atg cac acc gcc acc gtc acc gat gcc acc atg acc att ttc aac gag 403
 Met His Thr Ala Thr Val Thr Asp Ala Thr Met Thr Ile Phe Asn Glu
 90 95 100

 gcc ggc agc aat att ggc gag cta aaa cgc taaatgcttc tcgacgtcaa 453
 Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
 105 110

 aag 456

<210> 1072

<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 1072

Met Lys Thr Tyr Ala Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala
 1 5 10 15

 Gly Cys Ser Ser Ser Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala
 20 25 30

 Asp Ala Tyr Leu Glu Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp
 35 40 45

 Gly Cys Asn Arg Leu Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile
 50 55 60

 Thr Phe Gly Ala Ile Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn
 65 70 75 80

 Asp Trp Leu Ser Gln Met His Thr Ala Thr Val Thr Asp Ala Thr Met
 85 90 95

 Thr Ile Phe Asn Glu Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
 100 105 110

<210> 1073

<211> 456

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(433)

<223> FRXA02300

<400> 1073

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gggtcattcc ggtgaacacg gatttcgcgc cgggtgaatct gacgggtcagc caattgcggg 60
caatgctgtc caaagcggag cgtaaagata aggatcagaa atg aaa act tat gca 115
                                         Met Lys Thr Tyr Ala
                                         1                               5

gta cta att gcg gtg gca ggg ttg gca ctt gct ggg tgt agc tcg tcg 163
Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala Gly Cys Ser Ser Ser
                10                15                20

gct cct gga atc tgg cgt gcc act gaa ccc gca gat gcc tac ctt gaa 211
Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala Asp Ala Tyr Leu Glu
                25                30                35

ata gcc gat gac ggc acg ctg tcc gga acc gac ggc tgc aac aga ctt 259
Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp Gly Cys Asn Arg Leu
                40                45                50

ttt ggt ggc tgg gaa aaa gac ggc tct acc atc act ttc ggc gcc atc 307
Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile Thr Phe Gly Ala Ile
                55                60                65

ggt atg aca gaa atg tac tgc gaa ggc gtc aac gat tgg ctg tcc cag 355
Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn Asp Trp Leu Ser Gln
                70                75                80                85

atg cac acc gcc acc gtc acc gat gcc acc atg acc att ttc aac gag 403
Met His Thr Ala Thr Val Thr Asp Ala Thr Met Thr Ile Phe Asn Glu
                90                95                100

gcc ggc agc aat att ggc gag cta aaa cgc taaatgcttc tcgacgtcaa 453
Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
                105                110

aag - 456

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<210> 1074

<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 1074

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Met Lys Thr Tyr Ala Val Leu Ile Ala Val Ala Gly Leu Ala Leu Ala
  1                5                10                15

Gly Cys Ser Ser Ser Ala Pro Gly Ile Trp Arg Ala Thr Glu Pro Ala
                20                25                30

Asp Ala Tyr Leu Glu Ile Ala Asp Asp Gly Thr Leu Ser Gly Thr Asp
                35                40                45

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Gly Cys Asn Arg Leu Phe Gly Gly Trp Glu Lys Asp Gly Ser Thr Ile
 50 55 60
 Thr Phe Gly Ala Ile Gly Met Thr Glu Met Tyr Cys Glu Gly Val Asn
 65 70 75 80
 Asp Trp Leu Ser Gln Met His Thr Ala Thr Val Thr Asp Ala Thr Met
 85 90 95
 Thr Ile Phe Asn Glu Ala Gly Ser Asn Ile Gly Glu Leu Lys Arg
 100 105 110

<210> 1075

<211> 840

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> RXN02301

<400> 1075

gcttcgcata tgtctggatc ttattggatg tatgagtcag agatcagga gatcgcgcac 60

taaccgaacc tggccagtgc aacaggatta tgtttaaagc atg gat ctt gca ctg 115
 Met Asp Leu Ala Leu
 1 5

gct cag gtt gat tcc acc gtt tcc ggg ctt tat gac gcc ctc gat ctc 163
 Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr Asp Ala Leu Asp Leu
 10 15 20

atc ggc gtg ctg ctg aac gga ata atc ggt gga acg atc gcc agg caa 211
 Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly Thr Ile Ala Arg Gln
 25 30 35

cga ggc tat gac atc att ggc ttt ctg ttc ctg gcg tta ttt tct gcg 259
 Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu Ala Leu Phe Ser Ala
 40 45 50

ctg ggt ggc gga atg atc cgt gac atg ctg att cag cag ggg act gtc 307
 Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile Gln Gln Gly Thr Val
 55 60 65

gcg gcg atc gat aat cag atc tac ctt gcg ctc gcg ttt tct ggc gcg 355
 Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu Ala Phe Ser Gly Ala
 70 75 80 85

ctg att gcc atg gcg gtg aac ttt aaa ggc agg gtg tgg gag ctg ttt 403
 Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg Val Trp Glu Leu Phe
 90 95 100

aaa gtt cac ggc gat gcc att gtg ttg ggc gtc tgg gcg gtg acg ggt 451
 Lys Val His Gly Asp Ala Ile Val Leu Gly Val Trp Ala Val Thr Gly
 105 110 115

tcc gtg aag gcg atg aat gcg ggg gtg gct ccg ctg ccg agt att ttc 499
 Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro Leu Pro Ser Ile Phe
 120 125 130

atg ggc gtg ctc acc gcg gtg ggt ggt ggc atg gtg cgt gat gtg gct 547
 Met Gly Val Leu Thr Ala Val Gly Gly Gly Met Val Arg Asp Val Ala
 135 140 145
 act ggc cag acg ccg acg att ttt ggt ggc gga act ctt tac gct gtg 595
 Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly Thr Leu Tyr Ala Val
 150 155 160 165
 cct gcg acg ctt tct gcc acg tca atg gtt att ttt cat agc ttt gac 643
 Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile Phe His Ser Phe Asp
 170 175 180
 cag gta att ctg ggt atg att att tca ccg ttc ttg ggt atc gcg ttg 691
 Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe Leu Gly Ile Ala Leu
 185 190 195
 gcg gtt act gcg tat tgg tgc ggt tgg gtc att ccg gtg aac acg gat 739
 Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile Pro Val Asn Thr Asp
 200 205 210
 ttc gcg ccg gtg aat ctg acg gtc agc caa ttg ccg gca atg ctg tcc 787
 Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu Arg Ala Met Leu Ser
 215 220 225
 aaa gcg gag cgt aaa gat aag gat cag aaa tgaaaactta tgcagtacta 837
 Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
 230 235
 att 840

<210> 1076

<211> 239

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1076

Met Asp Leu Ala Leu Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr
 1 5 10 15
 Asp Ala Leu Asp Leu Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly
 20 25 30
 Thr Ile Ala Arg Gln Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu
 35 40 45
 Ala Leu Phe Ser Ala Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile
 50 55 60
 Gln Gln Gly Thr Val Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu
 65 70 75 80
 Ala Phe Ser Gly Ala Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg
 85 90 95
 Val Trp Glu Leu Phe Lys Val His Gly Asp Ala Ile Val Leu Gly Val
 100 105 110
 Trp Ala Val Thr Gly Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro
 115 120 125

Leu Pro Ser Ile Phe Met Gly Val Leu Thr Ala Val Gly Gly Gly Met
 130 135 140
 Val Arg Asp Val Ala Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly
 145 150 155 160
 Thr Leu Tyr Ala Val Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile
 165 170 175
 Phe His Ser Phe Asp Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe
 180 185 190
 Leu Gly Ile Ala Leu Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile
 195 200 205
 Pro Val Asn Thr Asp Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu
 210 215 220
 Arg Ala Met Leu Ser Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
 225 230 235

<210> 1077

<211> 840

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> FRXA02301

<400> 1077

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 taaccgaacc tggccagtgc aacaggatta tgtttaaagc atg gat ctt gca ctg 115
 Met Asp Leu Ala Leu 5
 1
 gct cag gtt gat tcc acc gtt tcg ggg ctt tat gac gcc ctc gat ctc 163
 Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr Asp Ala Leu Asp Leu 20
 10 15
 atc ggc gtg ctg ctg aac gga ata atc ggt gga acg atc gcc agg caa 211
 Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly Thr Ile Ala Arg Gln 35
 25 30
 cga ggc tat gac atc att ggc ttt ctg ttc ctg gcg tta ttt tct gcg 259
 Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu Ala Leu Phe Ser Ala 50
 40 45
 ctg ggt ggc gga atg atc cgt gac atg ctg att cag cag ggg act gtc 307
 Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile Gln Gln Gly Thr Val 65
 55 60
 gcg gcg atc gat aat cag atc tac ctt gcg ctc gcg ttt tct ggc gcg 355
 Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu Ala Phe Ser Gly Ala 85
 70 75 80
 ctg att gcc atg gcg gtg aac ttt aaa ggc agg gtg tgg gag ctg ttt 403

Leu Ile Ala Met Ala Val Asn Phe Lys Gly Arg Val Trp Glu Leu Phe
 90 95 100
 aaa gtt cac ggc gat gcc att gtg ttg ggc gtc tgg gcg gtg acg ggt 451
 Lys Val His Gly Asp Ala Ile Val Leu Gly Val Trp Ala Val Thr Gly
 105 110 115
 tcc gtg aag gcg atg aat gcg ggg gtg gct ccg ctg ccg agt att ttc 499
 Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro Leu Pro Ser Ile Phe
 120 125 130
 atg ggc gtg ctc acc gcg gtg ggt ggt ggc atg gtg cgt gat gtg gct 547
 Met Gly Val Leu Thr Ala Val Gly Gly Gly Met Val Arg Asp Val Ala
 135 140 145
 act ggc cag acg ccg acg att ttt ggt ggc gga act ctt tac gct gtg 595
 Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly Thr Leu Tyr Ala Val
 150 155 160 165
 cct gcg acg ctt tct gcc acg tca atg gtt att ttt cat agc ttt gac 643
 Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile Phe His Ser Phe Asp
 170 175 180
 cag gta att ctg ggt atg att att tca ccg ttc ttg ggt atc gcg ttg 691
 Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe Leu Gly Ile Ala Leu
 185 190 195
 gcg gtt act gcg tat tgg tgc ggt tgg gtc att ccg gtg aac acg gat 739
 Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile Pro Val Asn Thr Asp
 200 205 210
 ttc gcg ccg gtg aat ctg acg gtc agc caa ttg cgg gca atg ctg tcc 787
 Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu Arg Ala Met Leu Ser
 215 220 225
 aaa gcg gag cgt aaa gat aag gat cag aaa tgaaaactta tgcagtacta 837
 Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys
 230 235
 att 840

<210> 1078

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

Met Asp Leu Ala Leu Ala Gln Val Asp Ser Thr Val Ser Gly Leu Tyr
 1 5 10 15

Asp Ala Leu Asp Leu Ile Gly Val Leu Leu Asn Gly Ile Ile Gly Gly
 20 25 30

Thr Ile Ala Arg Gln Arg Gly Tyr Asp Ile Ile Gly Phe Leu Phe Leu
 35 40 45

Ala Leu Phe Ser Ala Leu Gly Gly Gly Met Ile Arg Asp Met Leu Ile
 50 55 60

Gln Gln Gly Thr Val Ala Ala Ile Asp Asn Gln Ile Tyr Leu Ala Leu

65	70	75	80
Ala Phe Ser Gly	Ala Leu Ile Ala Met	Ala Val Asn Phe Lys Gly Arg	
	85	90	95
Val Trp Glu Leu Phe Lys Val His Gly Asp Ala Ile Val Leu Gly Val			
	100	105	110
Trp Ala Val Thr Gly Ser Val Lys Ala Met Asn Ala Gly Val Ala Pro			
	115	120	125
Leu Pro Ser Ile Phe Met Gly Val Leu Thr Ala Val Gly Gly Gly Met			
	130	135	140
Val Arg Asp Val Ala Thr Gly Gln Thr Pro Thr Ile Phe Gly Gly Gly			
145	150	155	160
Thr Leu Tyr Ala Val Pro Ala Thr Leu Ser Ala Thr Ser Met Val Ile			
	165	170	175
Phe His Ser Phe Asp Gln Val Ile Leu Gly Met Ile Ile Ser Pro Phe			
	180	185	190
Leu Gly Ile Ala Leu Ala Val Thr Ala Tyr Trp Cys Gly Trp Val Ile			
	195	200	205
Pro Val Asn Thr Asp Phe Ala Pro Val Asn Leu Thr Val Ser Gln Leu			
	210	215	220
Arg Ala Met Leu Ser Lys Ala Glu Arg Lys Asp Lys Asp Gln Lys			
225	230	235	

<210> 1079

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXN02302

<400> 1079

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agacatatgc gaagctaatag aaggaaacga ggagctgata	gtg gca aca aat cgt	115
	Val Ala Thr Asn Arg	
	1	5

aca tct tcc gct ggt gtc atc acg tct gtt ctc gca tcc gct ttg ttc	163
Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu Ala Ser Ala Leu Phe	
	10
	15
	20

gga gcg atc ttt ttc atc tct ggg gcg att gag gca aag gcg gaa aca	211
Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu Ala Lys Ala Glu Thr	
	25
	30
	35

ctt gtt gct tgg cgt gtc ctt cta aca gcg gca tgc tat ttg ctt gcc	259
Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala Cys Tyr Leu Leu Ala	
	40
	45
	50

ctt ctg cac cct gct ggt cgg aag gtg ttt aag gaa ttt tgg gac aca	307
Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys Glu Phe Trp Asp Thr	
55 60 65	
cta agg tcc caa cct cgt caa att ctg tac ttt atc ttc ctc gtt gta	355
Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe Ile Phe Leu Val Val	
70 75 80 85	
ctc atc acg ctt cag ctg tgg ctg ttt tct tgg tcg cct aag agt cat	403
Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp Ser Pro Lys Ser His	
90 95 100	
gct tta gat gcc tca ctt ggt tac ctg tta ctg ccc att ttc cta gta	451
Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu Pro Ile Phe Leu Val	
105 110 115	
att gtg ggg cgg ttt ttc ttc gct gat tac atc acc agg ctg cag tgg	499
Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile Thr Arg Leu Gln Trp	
120 125 130	
att gcg gtg gga atc gcg ctg atc gca gta acc ttg aaa ttt gtc att	547
Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr Leu Lys Phe Val Ile	
135 140 145	
agt gcg caa tta tcg tgg gta act ttt gcc atc gct gcg ggt tat gca	595
Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile Ala Ala Gly Tyr Ala	
150 155 160 165	
ctg tat ttt gcg ctt cgt aaa tac tcg ggg ctg aac aac gct ttt gct	643
Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu Asn Asn Ala Phe Ala	
170 175 180	
tac ggc gca gaa gtt tta gcg tta agt ccc ctg gca ttt ttc atg ctc	691
Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu Ala Phe Phe Met Leu	
185 190 195	
gcc act gtc gag gat ccg ctg tct aac gcc atg ttg tca atg gtt att	739
Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met Leu Ser Met Val Ile	
200 205 210	
ctg gcg ggc ctc gct ggc gca tta gct atg gcg ttg tat cta gcc gcc	787
Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala Leu Tyr Leu Ala Ala	
215 220 225	
tca act ctg ctt agt atg ccg atg ttt ggc ctg ctc agt tat ggt gaa	835
Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu Leu Ser Tyr Gly Glu	
230 235 240 245	
cca atc ttg ctg ttt gtt gca gca cta tta ctt ggt gaa acg ttg aat	883
Pro Ile Leu Leu Phe Val Ala Ala Leu Leu Leu Gly Glu Thr Leu Asn	
250 255 260	
ctc agc gac gcc att gtc tac tca cta ctg gcg tgc gcc ctg gcg tta	931
Leu Ser Asp Ala Ile Val Tyr Ser Leu Leu Ala Cys Ala Leu Ala Leu	
265 270 275	
ctg gga ttt gat ggg ata cga agg tct cga aaa aac ctc gag acc gat	979
Leu Gly Phe Asp Gly Ile Arg Arg Ser Arg Lys Asn Leu Glu Thr Asp	
280 285 290	

taactttctgc tcaacttccc acc

1002

<210> 1080

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1080

Val Ala Thr Asn Arg Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu
1 5 10 15

Ala Ser Ala Leu Phe Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu
20 25 30

Ala Lys Ala Glu Thr Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala
35 40 45

Cys Tyr Leu Leu Ala Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys
50 55 60

Glu Phe Trp Asp Thr Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe
65 70 75 80

Ile Phe Leu Val Val Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp
85 90 95

Ser Pro Lys Ser His Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu
100 105 110

Pro Ile Phe Leu Val Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile
115 120 125

Thr Arg Leu Gln Trp Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr
130 135 140

Leu Lys Phe Val Ile Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile
145 150 155 160

Ala Ala Gly Tyr Ala Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu
165 170 175

Asn Asn Ala Phe Ala Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu
180 185 190

Ala Phe Phe Met Leu Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met
195 200 205

Leu Ser Met Val Ile Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala
210 215 220

Leu Tyr Leu Ala Ala Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu
225 230 235 240

Leu Ser Tyr Gly Glu Pro Ile Leu Leu Phe Val Ala Ala Leu Leu Leu
245 250 255

Gly Glu Thr Leu Asn Leu Ser Asp Ala Ile Val Tyr Ser Leu Leu Ala
260 265 270

Cys Ala Leu Ala Leu Leu Gly Phe Asp Gly Ile Arg Arg Ser Arg Lys

275

280

285

Asn Leu Glu Thr Asp
290

<210> 1081

<211> 865

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> FRXA02302

<400> 1081

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Val Ala Thr Asn Arg
1 5

aca tct tcc gct ggt gtc atc acg tct gtt ctc gca tcc gct ttg ttc 163
Thr Ser Ser Ala Gly Val Ile Thr Ser Val Leu Ala Ser Ala Leu Phe
10 15 20

gga gcg atc ttt ttc atc tct ggg gcg att gag gca aag gcg gaa aca 211
Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu Ala Lys Ala Glu Thr
25 30 35

ctt gtt gct tgg cgt gtc ctt cta aca gcg gca tgc tat ttg ctt gcc 259
Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala Cys Tyr Leu Leu Ala
40 45 50

ctt ctg cac cct gct ggt cgg aag gtg ttt aag gaa ttt tgg gac aca 307
Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys Glu Phe Trp Asp Thr
55 60 65

cta agg tcc caa cct cgt caa att ctg tac ttt atc ttc ctc gtt gta 355
Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe Ile Phe Leu Val Val
70 75 80 85

ctc atc acg ctt cag ctg tgg ctg ttt tct tgg tcg cct aag agt cat 403
Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp Ser Pro Lys Ser His
90 95 100

gct tta gat gcc tca ctt ggt tac ctg tta ctg ccc att ttc cta gta 451
Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu Pro Ile Phe Leu Val
105 110 115

att gtg ggg cgg ttt ttc ttc gct gat tac atc acc agg ctg cag tgg 499
Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile Thr Arg Leu Gln Trp
120 125 130

att gcg gtg gga atc gcg ctg atc gca gta acc ttg aaa ttt gtc att 547
Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr Leu Lys Phe Val Ile
135 140 145

agt gcg caa tta tcg tgg gta act ttt gcc atc gct gcg ggt tat gca 595
Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile Ala Ala Gly Tyr Ala

150 155 160 165
 ctg tat ttt gcg ctt cgt aaa tac tcg ggg ctg aac aac gct ttt gct 643
 Leu Tyr Phe Ala Leu Arg Lys Tyr Ser Gly Leu Asn Asn Ala Phe Ala
 170 175 180
 tac ggc gca gaa gtt tta gcg tta agt ccc ctg gca ttt ttc atg ctc 691
 Tyr Gly Ala Glu Val Leu Ala Leu Ser Pro Leu Ala Phe Phe Met Leu
 185 190 195
 gcc act gtc gag gat ccg ctg tct aac gcc atg ttg tca atg gtt att 739
 Ala Thr Val Glu Asp Pro Leu Ser Asn Ala Met Leu Ser Met Val Ile
 200 205 210
 ctg gcg ggc ctc gct ggc gca tta gct atg gcg ttg tat cta gcc gcc 787
 Leu Ala Gly Leu Ala Gly Ala Leu Ala Met Ala Leu Tyr Leu Ala Ala
 215 220 225
 tca act ctg ctt agt atg ccg atg ttt ggc ctg ctc agt tat ggt gaa 835
 Ser Thr Leu Leu Ser Met Pro Met Phe Gly Leu Leu Ser Tyr Gly Glu
 230 235 240 245
 cca atc ttg ctg ttt gtt gca gca cta tta 865
 Pro Ile Leu Leu Phe Val Ala Ala Leu Leu
 250 255

 <210> 1082
 <211> 255
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 1082
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 Ala Ser Ala Leu Phe Gly Ala Ile Phe Phe Ile Ser Gly Ala Ile Glu
 20 25 30
 Ala Lys Ala Glu Thr Leu Val Ala Trp Arg Val Leu Leu Thr Ala Ala
 35 40 45
 Cys Tyr Leu Leu Ala Leu Leu His Pro Ala Gly Arg Lys Val Phe Lys
 50 55 60
 Glu Phe Trp Asp Thr Leu Arg Ser Gln Pro Arg Gln Ile Leu Tyr Phe
 65 70 75 80
 Ile Phe Leu Val Val Leu Ile Thr Leu Gln Leu Trp Leu Phe Ser Trp
 85 90 95
 Ser Pro Lys Ser His Ala Leu Asp Ala Ser Leu Gly Tyr Leu Leu Leu
 100 105 110
 Pro Ile Phe Leu Val Ile Val Gly Arg Phe Phe Phe Ala Asp Tyr Ile
 115 120 125
 Thr Arg Leu Gln Trp Ile Ala Val Gly Ile Ala Leu Ile Ala Val Thr
 130 135 140
 Leu Lys Phe Val Ile Ser Ala Gln Leu Ser Trp Val Thr Phe Ala Ile

ggt gtg agc gtc gat gac gtc ccg gag gtc gga ggc gcg att ttc cac 451
 Gly Val Ser Val Asp Asp Val Pro Glu Val Gly Gly Ala Ile Phe His
 105 110 115

ccg tcg aat ccg acg ggc cgc tgg gct gta tcg ttc cac agc ggt ggt 499
 Pro Ser Asn Pro Thr Gly Arg Trp Ala Val Ser Phe His Ser Gly Gly
 120 125 130

tgg tgg cgc ggt tcc ggt gat gcg ttg gag ttc cag tgg cgt cca gag 547
 Trp Trp Arg Gly Ser Gly Asp Ala Leu Glu Phe Gln Trp Arg Pro Glu
 135 140 145

gtc gcg gca gct gcg gaa ttg tcc ggc aca acc atc ctt gac ctg gac 595
 Val Ala Ala Ala Ala Glu Leu Ser Gly Thr Thr Ile Leu Asp Leu Asp
 150 155 160 165

tat ccg ctg gcc cca ggc cat aac ctc cac gat atg aat gag gtt gtg 643
 Tyr Pro Leu Ala Pro Gly His Asn Leu His Asp Met Asn Glu Val Val
 170 175 180

ggc aag gcg gtc ggt tac gcc cgc cac cat aat ccg gtg tcg atc acg 691
 Gly Lys Ala Val Gly Tyr Ala Arg His His Asn Pro Val Ser Ile Thr
 185 190 195

ggt tgg ggt tat tcc tcg ggc gcg gcg tta gcc gcg att aat gca tcg 739
 Gly Trp Gly Tyr Ser Ser Gly Ala Ala Leu Ala Ala Ile Asn Ala Ser
 200 205 210

ctt ttc gac gcc ctg gtc ctc acc ttt ccg gac ctg ggt agc gtc gag 787
 Leu Phe Asp Ala Leu Val Leu Thr Phe Pro Asp Leu Gly Ser Val Glu
 215 220 225

aag ctc cct gcc gaa att cgt gga gac gct gta gtg ccc gcg gcg gct 835
 Lys Leu Pro Ala Glu Ile Arg Gly Asp Ala Val Val Pro Ala Ala Ala
 230 235 240 245

gcg tgg ccg acg acc ttt gtg cag atc gcg gcg cag gat gag atc gcg 883
 Ala Trp Pro Thr Thr Phe Val Gln Ile Ala Ala Gln Asp Glu Ile Ala
 250 255 260

gag cgg cca gga gag ctt ggc gac gcg acc gtg aag gaa tac gtt tcc 931
 Glu Arg Pro Gly Glu Leu Gly Asp Ala Thr Val Lys Glu Tyr Val Ser
 265 270 275

cgc cac cgt att tcc aca ccg aag gtc gcg cgc gaa aaa atc acc gac 979
 Arg His Arg Ile Ser Thr Pro Lys Val Ala Arg Glu Lys Ile Thr Asp
 280 285 290

gtg gcg gag ttc ctt aaa act gtt tgc taatgtgccg gcaggttgta 1026
 Val Ala Glu Phe Leu Lys Thr Val Cys
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aat 1029

<210> 1084

<211> 302

<212> PRT

<213> Corynebacterium glutamicum

<400> 1084

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Arg Phe Arg Glu Glu Phe Glu Val Gly Gly Lys Asp Arg Gln Leu Ser
20 25 30
Glu Glu Glu Gln Leu Glu Gln Leu Gly Ser Tyr Ile Asp Ala His Tyr
35 40 45
Pro Val Pro Asp Phe Thr Pro Pro Trp Ala Gly Gly Ala Gly Asp Pro
50 55 60
Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr Thr His
65 70 75 80
Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met Pro Gly
85 90 95
Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu Val Gly
100 105 110
Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala Val Ser
115 120 125
Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu Glu Phe
130 135 140
Gln Trp Arg Pro Glu Val Ala Ala Ala Ala Glu Leu Ser Gly Thr Thr
145 150 155 160
Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu His Asp
165 170 175
Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His His Asn
180 185 190
Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala Leu Ala
195 200 205
Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe Pro Asp
210 215 220
Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp Ala Val
225 230 235 240
Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile Ala Ala
245 250 255
Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala Thr Val
260 265 270
Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val Ala Arg
275 280 285
Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
290 295 300

<210> 1085

<211> 743

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(720)

<223> FRXA02303

<400> 1085

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Asp Pro Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr	
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acg cat act gcg atg atc atg ttg ggt tct ggc ctt gat cat tcc atg	96
Thr His Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met	
20 25 30	
ccg ggt gtc gca ttt atc ggt ggt gtg agc gtc gat gac gtc ccg gag	144
Pro Gly Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu	
35 40 45	
gtc gga ggc gcg att ttc cac ccg tcg aat ccg acg ggc cgc tgg gct	192
Val Gly Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala	
50 55 60	
gta tcg ttc cac agc ggt ggt tgg tgg cgc ggt tcc ggt gat gcg ttg	240
Val Ser Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu	
65 70 75 80	
gag ttc cag tgg cgt cca gag gtc gcg gca gct gcg gaa ttg tcc ggc	288
Glu Phe Gln Trp Arg Pro Glu Val Ala Ala Ala Glu Leu Ser Gly	
85 90 95	
aca acc atc ctt gac ctg gac tat ccg ctg gcc cca ggc cat aac ctc	336
Thr Thr Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu	
100 105 110	
cac gat atg aat gag gtt gtg ggc aag gcg gtc ggt tac gcc cgc cac	384
His Asp Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His	
115 120 125	
cat aat ccg gtg tcg atc acg ggt tgg ggt tat tcc tcg ggc gcg gcg	432
His Asn Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala	
130 135 140	
tta gcc gcg att aat gca tcg ctt ttc gac gcc ctg gtc ctc acc ttt	480
Leu Ala Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe	
145 150 155 160	
ccg gac ctg ggt agc gtc gag aag ctc cct gcc gaa att cgt gga gac	528
Pro Asp Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp	
165 170 175	
gct gta gtg ccc gcg gcg gct gcg tgg ccg acg acc ttt gtg cag atc	576
Ala Val Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile	
180 185 190	
gcg gcg cag gat gag atc gcg gag cgg cca gga gag ctt ggc gac gcg	624
Ala Ala Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala	
195 200 205	

acc gtg aag gaa tac gtt tcc cgc cac cgt att tcc aca ccg aag gtc 672
 Thr Val Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val
 210 215 220

gcg cgc gaa aaa atc acc gac gtg gcg gag ttc ctt aaa act gtt tgc 720
 Ala Arg Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
 225 230 235 240

taatgtgccca gcaggttgta aat 743

<210> 1086

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 1086

Asp Pro Asp Pro Ala Asp Arg Tyr Ile Ala His Leu Pro Asp Arg Thr
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Thr His Thr Ala Met Ile Met Leu Gly Ser Gly Leu Asp His Ser Met
 20 25 30

Pro Gly Val Ala Phe Ile Gly Gly Val Ser Val Asp Asp Val Pro Glu
 35 40 45

Val Gly Gly Ala Ile Phe His Pro Ser Asn Pro Thr Gly Arg Trp Ala
 50 55 60

Val Ser Phe His Ser Gly Gly Trp Trp Arg Gly Ser Gly Asp Ala Leu
 65 70 75 80

Glu Phe Gln Trp Arg Pro Glu Val Ala Ala Ala Glu Leu Ser Gly
 85 90 95

Thr Thr Ile Leu Asp Leu Asp Tyr Pro Leu Ala Pro Gly His Asn Leu
 100 105 110

His Asp Met Asn Glu Val Val Gly Lys Ala Val Gly Tyr Ala Arg His
 115 120 125

His Asn Pro Val Ser Ile Thr Gly Trp Gly Tyr Ser Ser Gly Ala Ala
 130 135 140

Leu Ala Ala Ile Asn Ala Ser Leu Phe Asp Ala Leu Val Leu Thr Phe
 145 150 155 160

Pro Asp Leu Gly Ser Val Glu Lys Leu Pro Ala Glu Ile Arg Gly Asp
 165 170 175

Ala Val Val Pro Ala Ala Ala Ala Trp Pro Thr Thr Phe Val Gln Ile
 180 185 190

Ala Ala Gln Asp Glu Ile Ala Glu Arg Pro Gly Glu Leu Gly Asp Ala
 195 200 205

Thr Val Lys Glu Tyr Val Ser Arg His Arg Ile Ser Thr Pro Lys Val
 210 215 220

Ala Arg Glu Lys Ile Thr Asp Val Ala Glu Phe Leu Lys Thr Val Cys
 225 230 235 240

<210> 1087
 <211> 744
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(721)
 <223> RXN02307

<400> 1087

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                                         Met Ser Gly Thr Ala
                                         1 5

atc atg tac gac acg aca gtt gtt cca tcg aag aaa gaa atc gcg cag 163
Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys Lys Glu Ile Ala Gln
          10          15          20

gct tgg act ggt tat gtg gat ctt cag gga agc tac cgc ctg gta gat 211
Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser Tyr Arg Leu Val Asp
          25          30          35

acg gtg gat ggg gaa gtt ggc gtt gag gtg ctg att tcc aag gat cgg 259
Thr Val Asp Gly Glu Val Gly Val Glu Val Leu Ile Ser Lys Asp Arg
          40          45          50

gag ggg cgt tta ctc cag att ccg ttt agt tat cgt tcg gca gag att 307
Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr Arg Ser Ala Glu Ile
          55          60          65

aac cca gag cag aca ctt tcc aca ttg gag cat ggt gtg ttg ggc aag 355
Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His Gly Val Leu Gly Lys
          70          75          80          85

cgt tgg gtg act aat gcg ttg ggt gac ccg gtg gca gtg cgg gag ttt 403
Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val Ala Val Arg Glu Phe
          90          95          100

att cgc act att ttg acg ggc gat gat ggt gca gct cgt agc gat ggc 451
Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala Ala Arg Ser Asp Gly
          105          110          115

gtg aag ggc tat ctg gat att aaa ggt tcc ggc gat gct gag tcg gtg 499
Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly Asp Ala Glu Ser Val
          120          125          130

gat tta cag gat gta aag ctt act gag gtt aca agg cag cgt gcg att 547
Asp Leu Gln Asp Val Lys Leu Thr Glu Val Thr Arg Gln Arg Ala Ile
          135          140          145

ggt tcg gta acc atc aac ggt gag cga aag caa ttc tcg ctg cgg ttg 595
Gly Ser Val Thr Ile Asn Gly Glu Arg Lys Gln Phe Ser Leu Arg Leu
          150          155          160          165

cct cag ttg ctg aag aat ttc agg gag aca gcc gcg ggc cat aca gct 643
Pro Gln Leu Leu Lys Asn Phe Arg Glu Thr Ala Ala Gly His Thr Ala

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170	175	180	
acg act ctt cgt att gtg gcg act cat ccg gaa aag gac gat gtt gag			691
Thr Thr Leu Arg Ile Val Ala Thr His Pro Glu Lys Asp Asp Val Glu			
185	190	195	
ctg ctg gtc gct gag ttc aac tgg atg gaa taatccgaga cagctcctga			741
Leu Leu Val Ala Glu Phe Asn Trp Met Glu			
200	205		
aag			744
<210> 1088			
<211> 207			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1088			
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Lys Glu Ile Ala Gln Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser			
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Tyr Arg Leu Val Asp Thr Val Asp Gly Glu Val Gly Val Glu Val Leu			
35	40	45	
Ile Ser Lys Asp Arg Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr			
50	55	60	
Arg Ser Ala Glu Ile Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His			
65	70	75	80
Gly Val Leu Gly Lys Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val			
85	90	95	
Ala Val Arg Glu Phe Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala			
100	105	110	
Ala Arg Ser Asp Gly Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly			
115	120	125	
Asp Ala Glu Ser Val Asp Leu Gln Asp Val Lys Leu Thr Glu Val Thr			
130	135	140	
Arg Gln Arg Ala Ile Gly Ser Val Thr Ile Asn Gly Glu Arg Lys Gln			
145	150	155	160
Phe Ser Leu Arg Leu Pro Gln Leu Leu Lys Asn Phe Arg Glu Thr Ala			
165	170	175	
Ala Gly His Thr Ala Thr Thr Leu Arg Ile Val Ala Thr His Pro Glu			
180	185	190	
Lys Asp Asp Val Glu Leu Leu Val Ala Glu Phe Asn Trp Met Glu			
195	200	205	

<210> 1089

<211> 490

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(490)

<223> FRXA02307

<400> 1089

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                                         Met Ser Gly Thr Ala
                                         1           5

atc atg tac gac acg aca gtt gtt cca tcg aag aaa gaa atc gcg cag 163
Ile Met Tyr Asp Thr Thr Val Val Pro Ser Lys Lys Glu Ile Ala Gln
              10              15              20

gct tgg act ggt tat gtg gat ctt cag gga agc tac cgc ctg gta gat 211
Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser Tyr Arg Leu Val Asp
              25              30              35

acg gtg gat ggg gaa gtt ggc gtt gag gtg ctg att tcc aag gat cgg 259
Thr Val Asp Gly Glu Val Gly Val Glu Val Leu Ile Ser Lys Asp Arg
              40              45              50

gag ggg cgt tta ctc cag att ccg ttt agt tat cgt tcg gca gag att 307
Glu Gly Arg Leu Leu Gln Ile Pro Phe Ser Tyr Arg Ser Ala Glu Ile
              55              60              65

aac cca gag cag aca ctt tcc aca ttg gag cat ggt gtg ttg ggc aag 355
Asn Pro Glu Gln Thr Leu Ser Thr Leu Glu His Gly Val Leu Gly Lys
              70              75              80              85

cgt tgg gtg act aat gcg ttg ggt gac ccg gtg gca gtg cgg gag ttt 403
Arg Trp Val Thr Asn Ala Leu Gly Asp Pro Val Ala Val Arg Glu Phe
              90              95              100

att cgc act att ttg acg ggc gat gat ggt gca gct cgt agc gat ggc 451
Ile Arg Thr Ile Leu Thr Gly Asp Asp Gly Ala Ala Arg Ser Asp Gly
              105              110              115

gtg aag ggc tat ctg gat att aaa ggt tcc ggc gat gct 490
Val Lys Gly Tyr Leu Asp Ile Lys Gly Ser Gly Asp Ala
              120              125              130

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<210> 1090

<211> 130

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1090

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Lys Glu Ile Ala Gln Ala Trp Thr Gly Tyr Val Asp Leu Gln Gly Ser
 20           25           30

Tyr Arg Leu Val Asp Thr Val Asp Gly Glu Val Gly Val Glu Val Leu

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gta gaa ggc cgc aag tgg aca ctg tcc atc atc cca gcg ctt agt gtc 451
 Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile Pro Ala Leu Ser Val
 105 110 115

gca gct gtc gcc acc gct acc tgg tca gta cta tgg ctg gga gtg ggc 499
 Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu Trp Leu Gly Val Gly
 120 125 130

aga ttc gga aga cga tcc gac gac gcc aac gaa acc aca gtg 541
 Arg Phe Gly Arg Arg Ser Asp Ala Asn Glu Thr Thr Val
 135 140 145

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<210> 1092
 <211> 147
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1092
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 35 40 45
 Gln Val Thr Asn Val Gly Ser Tyr Arg Thr Thr Val Asp Phe Gln Asp
 50 55 60
 Glu Asn Gly Ile Tyr His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr
 65 70 75 80
 Gly Leu Gly Glu Gly Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp
 85 90 95
 Pro Asp Leu Val Lys Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile
 100 105 110
 Pro Ala Leu Ser Val Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu
 115 120 125
 Trp Leu Gly Val Gly Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu
 130 135 140
 Thr Thr Val
 145

<210> 1093
 <211> 564
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(541)

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 Glu Asn Gly Ile Tyr His Ser Pro Ala Thr Gly Leu Leu Phe Pro Thr
 65 70 75 80
 Gly Leu Gly Glu Gly Gln Arg Val Trp Val Asn Tyr Ala Lys Ser Asp
 85 90 95
 Pro Asp Leu Val Lys Val Glu Gly Arg Lys Trp Thr Leu Ser Ile Ile
 100 105 110
 Pro Ala Leu Ser Val Ala Ala Val Ala Thr Ala Thr Trp Ser Val Leu
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 Trp Leu Gly Val Gly Arg Phe Gly Arg Arg Ser Asp Asp Ala Asn Glu
 130 135 140
 Thr Thr Val
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 <210> 1095
 <211> 1446
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1423)
 <223> RXN02337

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 Met Ser Lys Leu Tyr
 1 5
 gcg ggg gca agg atc aat gca ctg cgc cga acc cat cag ctc acc caa 163
 Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr His Gln Leu Thr Gln
 10 15 20
 tca gca ttg gcc gac aag ctt gat ctc tcc acc agc tat ctc aac cag 211
 Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr Ser Tyr Leu Asn Gln
 25 30 35
 ttg gaa aat gac gga cgg cca ctc act gcc acg gtg ctt ctg cag ctg 259
 Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr Val Leu Leu Gln Leu
 40 45 50
 atg aaa gtg ttc gat gtt gag gcc agt tac ttc tcc cct gac cgg ggt 307
 Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe Ser Pro Asp Arg Gly
 55 60 65
 acg gcc act gct acc cga ctg gct gaa acc ttg gcg atg aat cag ggt 355
 Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu Ala Met Asn Gln Gly
 70 75 80 85

ccg acg atg tcg atg gat gat ctt tta gat ttc gcg gat cgt ttc cct 403
 Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe Ala Asp Arg Phe Pro
 90 95 100

cag tta gcg cag cat att atc cag cct gct gag gtt gat ccc acg cat 451
 Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu Val Asp Pro Thr His
 105 110 115

agt tct gcg cat gat ttt gtt cgg gat tat ttt gcc acc cac aaa aac 499
 Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe Ala Thr His Lys Asn
 120 125 130

tac att gat tcg ctc gat cgc ctt gga gag gag ttg gca act gcc att 547
 Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu Leu Ala Thr Ala Ile
 135 140 145

ggt cag ccg gga ctt cgg gtt act agg ctc gcg cag ttg ctt gat gcg 595
 Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala Gln Leu Leu Asp Ala
 150 155 160 165

gag tac aac atc acg gtg cgt ttc cgg gcg ccg gat att act ggc cgg 643
 Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro Asp Ile Thr Gly Arg
 170 175 180

agg cac ttt gat ccc caa tcg cgt cag att ctg ctg cgg caa gat ctc 691
 Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu Leu Arg Gln Asp Leu
 185 190 195

agc gag gcg cag cag tgt ttc cag ttg gcg gag gaa ttg acg ttt ctt 739
 Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu Glu Leu Thr Phe Leu
 200 205 210

gct cat gca gag ctc ttg gat acc ctg acc aca gat caa ccg gat ctc 787
 Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr Asp Gln Pro Asp Leu
 215 220 225

cct tct gag gca gct atc cgc ctg gct aag gtg ggt ctc tcc caa tat 835
 Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val Gly Leu Ser Gln Tyr
 230 235 240 245

ttc gcg gct gct gtt gtc atg ccg tac acc cgc ttt ttg gaa ttc gcc 883
 Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg Phe Leu Glu Phe Ala
 250 255 260

cag gat aag cac tat gac atc gag ttg atc tct gag gcg ttt gga gtg 931
 Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser Glu Ala Phe Gly Val
 265 270 275

tct ttc gag tct gca tgc cac cgc ctg tct act ctg cag cgt tcg ggg 979
 Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr Leu Gln Arg Ser Gly
 280 285 290

gcg tca ggg gtg ccg ttt ttc ttt gtg cgc tcg gat cgt gca gga aat 1027
 Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser Asp Arg Ala Gly Asn
 295 300 305

atc tcc aag cgg caa tct gca gct acg ttc cac ttc tcg cga aca gac 1075
 Ile Ser Lys Arg Gln Ser Ala Ala Thr Phe His Phe Ser Arg Thr Asp
 310 315 320 325

ggc act tgt cct ttg tgg gcg ctg cat cgt gct ttt gaa cgt cag gga 1123

Gly Thr Cys Pro Leu Trp Ala Leu His Arg Ala Phe Glu Arg Gln Gly
 330 335 340
 aac atc acc cgc cag gtt gct cgc atg ccg gat ggc cgg acc tat ttg 1171
 Asn Ile Thr Arg Gln Val Ala Arg Met Pro Asp Gly Arg Thr Tyr Leu
 345 350 355
 tgg ctc gca cgc gcg gtg aaa ggt cga act cat ggt ttc ggg tat cct 1219
 Trp Leu Ala Arg Ala Val Lys Gly Arg Thr His Gly Phe Gly Tyr Pro
 360 365 370
 gct gcg gaa ttc gcc atc ggc ctg ggc tgc gat atc agc gag gca cca 1267
 Ala Ala Glu Phe Ala Ile Gly Leu Gly Cys Asp Ile Ser Glu Ala Pro
 375 380 385
 ggc ttg gtg tat tcc caa ggc ctt aat ttg gat ccc gag tcc gcc gca 1315
 Gly Leu Val Tyr Ser Gln Gly Leu Asn Leu Asp Pro Glu Ser Ala Ala
 390 395 400 405
 gag atc ggc cct ggt tgt cgg atc tgt cct cgg gag aac tgt gtg cag 1363
 Glu Ile Gly Pro Gly Cys Arg Ile Cys Pro Arg Glu Asn Cys Val Gln
 410 415 420
 cgt gca ttc cca cca tcg ggt caa gaa tct atc cgc cca gcc cct gtc 1411
 Arg Ala Phe Pro Pro Ser Gly Gln Glu Ser Ile Arg Pro Ala Pro Val
 425 430 435
 caa ctc ctc aac taaaaaggca gcacttaaaa aac 1446
 Gln Leu Leu Asn
 440

<210> 1096

<211> 441

<212> PRT

<213> Corynebacterium glutamicum

<400> 1096

Met Ser Lys Leu Tyr Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr
 1 5 10 15
 His Gln Leu Thr Gln Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr
 20 25 30
 Ser Tyr Leu Asn Gln Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr
 35 40 45
 Val Leu Leu Gln Leu Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe
 50 55 60
 Ser Pro Asp Arg Gly Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu
 65 70 75 80
 Ala Met Asn Gln Gly Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe
 85 90 95
 Ala Asp Arg Phe Pro Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu
 100 105 110
 Val Asp Pro Thr His Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe
 115 120 125

Ala Thr His Lys Asn Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu
130 135 140

Leu Ala Thr Ala Ile Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala
145 150 155 160

Gln Leu Leu Asp Ala Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro
165 170 175

Asp Ile Thr Gly Arg Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu
180 185 190

Leu Arg Gln Asp Leu Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu
195 200 205

Glu Leu Thr Phe Leu Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr
210 215 220

Asp Gln Pro Asp Leu Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val
225 230 235 240

Gly Leu Ser Gln Tyr Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg
245 250 255

Phe Leu Glu Phe Ala Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser
260 265 270

Glu Ala Phe Gly Val Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr
275 280 285

Leu Gln Arg Ser Gly Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser
290 295 300

Asp Arg Ala Gly Asn Ile Ser Lys Arg Gln Ser Ala Ala Thr Phe His
305 310 315 320

Phe Ser Arg Thr Asp Gly Thr Cys Pro Leu Trp Ala Leu His Arg Ala
325 330 335

Phe Glu Arg Gln Gly Asn Ile Thr Arg Gln Val Ala Arg Met Pro Asp
340 345 350

Gly Arg Thr Tyr Leu Trp Leu Ala Arg Ala Val Lys Gly Arg Thr His
355 360 365

Gly Phe Gly Tyr Pro Ala Ala Glu Phe Ala Ile Gly Leu Gly Cys Asp
370 375 380

Ile Ser Glu Ala Pro Gly Leu Val Tyr Ser Gln Gly Leu Asn Leu Asp
385 390 395 400

Pro Glu Ser Ala Ala Glu Ile Gly Pro Gly Cys Arg Ile Cys Pro Arg
405 410 415

Glu Asn Cys Val Gln Arg Ala Phe Pro Pro Ser Gly Gln Glu Ser Ile
420 425 430

Arg Pro Ala Pro Val Gln Leu Leu Asn
435 440

<210> 1097
<211> 1024
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1024)
<223> FRXA02337

<400> 1097
cacaaggtaa aatttgtgta attgtgtcgt gtggatttga aggtttttgt aaatctagtt 60
aaatcatgag gtcataagct tttcgggagg ttgtcaaagg atg tcg aag ctt tac 115
Met Ser Lys Leu Tyr
1 5
gcg ggg gca agg atc aat gca ctg cgc cga acc cat cag ctc acc caa 163
Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr His Gln Leu Thr Gln
10 15 20
tca gca ttg gcc gac aag ctt gat ctc tcc acc agc tat ctc aac cag 211
Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr Ser Tyr Leu Asn Gln
25 30 35
ttg gaa aat gac gga cgg cca ctc act gcc acg gtg ctt ctg cag ctg 259
Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr Val Leu Leu Gln Leu
40 45 50
atg aaa gtg ttc gat gtt gag gcc agt tac ttc tcc cct gac cgg ggt 307
Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe Ser Pro Asp Arg Gly
55 60 65
acg gcc act gct acc cga ctg gct gaa acc ttg gcg atg aat cag ggt 355
Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu Ala Met Asn Gln Gly
70 75 80 85
ccg acg atg tcg atg gat gat ctt tta gat ttc gcg gat cgt ttc cct 403
Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe Ala Asp Arg Phe Pro
90 95 100
cag tta gcg cag cat att atc cag cct gct gag gtt gat ccc acg cat 451
Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu Val Asp Pro Thr His
105 110 115
agt tct gcg cat gat ttt gtt cgg gat tat ttt gcc acc cac aaa aac 499
Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe Ala Thr His Lys Asn
120 125 130
tac att gat tcg ctc gat cgc ctt gga gag gag ttg gca act gcc att 547
Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu Leu Ala Thr Ala Ile
135 140 145
ggt cag ccg gga ctt cgg gtt act agg ctc gcg cag ttg ctt gat gcg 595
Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala Gln Leu Leu Asp Ala
150 155 160 165
gag tac aac atc acg gtg cgt ttc cgg gcg ccg gat att act ggc cgg 643
Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro Asp Ile Thr Gly Arg
170 175 180

agg cac ttt gat ccc caa tcg cgt cag att ctg ctg cgg caa gat ctc 691
 Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu Leu Arg Gln Asp Leu
 185 190 195
 agc gag gcg cag cag tgt ttc cag ttg gcg gag gaa ttg acg ttt ctt 739
 Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu Glu Leu Thr Phe Leu
 200 205 210
 gct cat gca gag ctc ttg gat acc ctg acc aca gat caa ccg gat ctc 787
 Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr Asp Gln Pro Asp Leu
 215 220 225
 cct tct gag gca gct atc cgc ctg gct aag gtg ggt ctc tcc caa tat 835
 Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val Gly Leu Ser Gln Tyr
 230 235 240 245
 ttc gcg gct gct gtt gtc atg ccg tac acc cgc ttt ttg gaa ttc gcc 883
 Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg Phe Leu Glu Phe Ala
 250 255 260
 cag gat aag cac tat gac atc gag ttg atc tct gag gcg ttt gga gtg 931
 Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser Glu Ala Phe Gly Val
 265 270 275
 tct ttc gag tct gca tgc cac cgc ctg tct act ctg cag cgt tcg ggg 979
 Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr Leu Gln Arg Ser Gly
 280 285 290
 gcg tca ggg gtg ccg ttt ttc ttt gtg cgc tcg gat cgt gca gga 1024
 Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser Asp Arg Ala Gly
 295 300 305

<210> 1098

<211> 308

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1098

Met Ser Lys Leu Tyr Ala Gly Ala Arg Ile Asn Ala Leu Arg Arg Thr
 1 5 10 15
 His Gln Leu Thr Gln Ser Ala Leu Ala Asp Lys Leu Asp Leu Ser Thr
 20 25 30
 Ser Tyr Leu Asn Gln Leu Glu Asn Asp Gly Arg Pro Leu Thr Ala Thr
 35 40 45
 Val Leu Leu Gln Leu Met Lys Val Phe Asp Val Glu Ala Ser Tyr Phe
 50 55 60
 Ser Pro Asp Arg Gly Thr Ala Thr Ala Thr Arg Leu Ala Glu Thr Leu
 65 70 75 80
 Ala Met Asn Gln Gly Pro Thr Met Ser Met Asp Asp Leu Leu Asp Phe
 85 90 95
 Ala Asp Arg Phe Pro Gln Leu Ala Gln His Ile Ile Gln Pro Ala Glu
 100 105 110

Val Asp Pro Thr His Ser Ser Ala His Asp Phe Val Arg Asp Tyr Phe
 115 120 125
 Ala Thr His Lys Asn Tyr Ile Asp Ser Leu Asp Arg Leu Gly Glu Glu
 130 135 140
 Leu Ala Thr Ala Ile Gly Gln Pro Gly Leu Arg Val Thr Arg Leu Ala
 145 150 155 160
 Gln Leu Leu Asp Ala Glu Tyr Asn Ile Thr Val Arg Phe Arg Ala Pro
 165 170 175
 Asp Ile Thr Gly Arg Arg His Phe Asp Pro Gln Ser Arg Gln Ile Leu
 180 185 190
 Leu Arg Gln Asp Leu Ser Glu Ala Gln Gln Cys Phe Gln Leu Ala Glu
 195 200 205
 Glu Leu Thr Phe Leu Ala His Ala Glu Leu Leu Asp Thr Leu Thr Thr
 210 215 220
 Asp Gln Pro Asp Leu Pro Ser Glu Ala Ala Ile Arg Leu Ala Lys Val
 225 230 235 240
 Gly Leu Ser Gln Tyr Phe Ala Ala Ala Val Val Met Pro Tyr Thr Arg
 245 250 255
 Phe Leu Glu Phe Ala Gln Asp Lys His Tyr Asp Ile Glu Leu Ile Ser
 260 265 270
 Glu Ala Phe Gly Val Ser Phe Glu Ser Ala Cys His Arg Leu Ser Thr
 275 280 285
 Leu Gln Arg Ser Gly Ala Ser Gly Val Pro Phe Phe Phe Val Arg Ser
 290 295 300
 Asp Arg Ala Gly
 305

<210> 1099

<211> 515

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(492)

<223> RXN02339

<400> 1099

ccc acc gac aac ctc ttt tca tat cct gca caa cgc tat gat ctt ctc 48
 Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
 1 5 10 15

aca ctt gcc ttt gaa gtt agg att ggg gac atg gtt caa att aat gac 96
 Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
 20 25 30

atg ctt gcc cct cct cca gta aaa ctt ccg gaa gat cct gcc ctc ggc 144
 Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly

35	40	45	
gcc gat cca act ttg acc tcg aca gcg att gcg cat cct gac agc cca			192
Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro			
50	55	60	
ttg gtg tgg gcg tac cga gct gaa aat ctt atc aaa tct gca tca aat			240
Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn			
65	70	75	80
gat gaa gag aag att cag gcc tac gct ttt gcg cgc acg ggt tac cac			288
Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His			
85	90	95	
cgc agt ctc gat cgt ctg cgt gcc aat ggt tgg aag ggt tgg ggt cct			336
Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro			
100	105	110	
gtc ccc ttc tct cat gag cca aac cag gga gtg ttg cgg gct atc gct			384
Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala			
115	120	125	
tcc cta gct ctt gct gcg aag ctg att ggt gag gac aac gaa tac gat			432
Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp			
130	135	140	
cgt tgc cgc cag atg ctc tct gat gcg gat cca gag tcc gtc gca gtc			480
Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val			
145	150	155	160
cta ctc gac aaa taaaccacca aaaataaaac aat			515
Leu Leu Asp Lys			

<210> 1100

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1100

Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
1 5 10 15

Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
20 25 30

Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
35 40 45

Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
50 55 60

Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
65 70 75 80

Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
85 90 95

Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
100 105 110

Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
 115 120 125

Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
 130 135 140

Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
 145 150 155 160

Leu Leu Asp Lys

<210> 1101
 <211> 515
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(492)
 <223> FRXA02339

<400> 1101

ccc acc gac aac ctc ttt tca tat cct gca caa cgc tat gat ctt ctc	48
Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu	
1 5 10 15	
aca ctt gcc ttt gaa gtt agg att ggg gac atg gtt caa att aat gac	96
Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp	
20 25 30	
atg ctt gcc cct cct cca gta aaa ctt ccg gaa gat cct gcc ctc ggc	144
Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly	
35 40 45	
gcc gat cca act ttg acc tcg aca gcg att gcg cat cct gac agc cca	192
Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro	
50 55 60	
ttg gtg tgg gcg tac cga gct gaa aat ctt atc aaa tct gca tca aat	240
Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn	
65 70 75 80	
gat gaa gag aag att cag gcc tac gct ttt gcg cgc acg ggt tac cac	288
Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His	
85 90 95	
cgc agt ctc gat cgt ctg cgt gcc aat ggt tgg aag ggt tgg ggt cct	336
Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro	
100 105 110	
gtc ccc ttc tct cat gag cca aac cag gga gtg ttg cgg gct atc gct	384
Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala	
115 120 125	
tcc cta gct ctt gct gcg aag ctg att ggt gag gac aac gaa tac gat	432
Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp	
130 135 140	

cgt tgc cgc cag atg ctc tct gat gcg gat cca gag tcc gtc gca gtc 480
 Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
 145 150 155 160

cta ctc gac aaa taaaccacca aaaataaaac aat 515
 Leu Leu Asp Lys

<210> 1102

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

Pro Thr Asp Asn Leu Phe Ser Tyr Pro Ala Gln Arg Tyr Asp Leu Leu
 1 5 10 15

Thr Leu Ala Phe Glu Val Arg Ile Gly Asp Met Val Gln Ile Asn Asp
 20 25 30

Met Leu Ala Pro Pro Pro Val Lys Leu Pro Glu Asp Pro Ala Leu Gly
 35 40 45

Ala Asp Pro Thr Leu Thr Ser Thr Ala Ile Ala His Pro Asp Ser Pro
 50 55 60

Leu Val Trp Ala Tyr Arg Ala Glu Asn Leu Ile Lys Ser Ala Ser Asn
 65 70 75 80

Asp Glu Glu Lys Ile Gln Ala Tyr Ala Phe Ala Arg Thr Gly Tyr His
 85 90 95

Arg Ser Leu Asp Arg Leu Arg Ala Asn Gly Trp Lys Gly Trp Gly Pro
 100 105 110

Val Pro Phe Ser His Glu Pro Asn Gln Gly Val Leu Arg Ala Ile Ala
 115 120 125

Ser Leu Ala Leu Ala Ala Lys Leu Ile Gly Glu Asp Asn Glu Tyr Asp
 130 135 140

Arg Cys Arg Gln Met Leu Ser Asp Ala Asp Pro Glu Ser Val Ala Val
 145 150 155 160

Leu Leu Asp Lys

<210> 1103

<211> 1188

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1165)

<223> RXN02340

<400> 1103

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aaaagtgcctt caagttatga gaaagtgaaa tccaacacccc	atg aaa aag agc atc	115
	Met Lys Lys Ser Ile	
	1 5	
gtt gta ttt gaa gtc gaa ggc ggc tcc gac aag cac ttc gac ggt cac	163	
Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys His Phe Asp Gly His		
10 15 20		
cgt aaa gac acc atg cct atc gtc aac tcc ata aat gat gct ggc tgg	211	
Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile Asn Asp Ala Gly Trp		
25 30 35		
cag gca gag gtt gtg tac tac cgc cca gag tgg acc gaa ggt ctc ttt	259	
Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp Thr Glu Gly Leu Phe		
40 45 50		
gag tac gta tct gaa aac ttc gac ggc tac atc tca cgt gtc aac cca	307	
Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile Ser Arg Val Asn Pro		
55 60 65		
ggc aac atc cca ggc ggc gag cgc ggc tac ttt gac ctg ctc acc cgc	355	
Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe Asp Leu Leu Thr Arg		
70 75 80 85		
ctg tcc gaa gca ggg ctc gtg ggc atg tcc acc cct gag gaa atg atg	403	
Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr Pro Glu Glu Met Met		
90 95 100		
gca tac ggc gcg aaa gat gcg ctg gtc aag cta tcc caa acc gac ctg	451	
Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu Ser Gln Thr Asp Leu		
105 110 115		
gtg cca tcc gac acc gag gcg tac tac gac gtg gag acc ttc cac aag	499	
Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val Glu Thr Phe His Lys		
120 125 130		
gtt ttc cca acc tcc ctg tcc ttc ggt gag cgc gtg ctc aag caa aac	547	
Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Arg Val Leu Lys Gln Asn		
135 140 145		
cgt ggc tcc acc ggc tcc ggc att tgg cgc gtc cag ttg gta gac aag	595	
Arg Gly Ser Thr Gly Ser Gly Ile Trp Arg Val Gln Leu Val Asp Lys		
150 155 160 165		
gaa ctg gct gca tcc atc gag cca ggc acc gca ctg cca ttg gac act	643	
Glu Leu Ala Ala Ser Ile Glu Pro Gly Thr Ala Leu Pro Leu Asp Thr		
170 175 180		
gaa atc aag tgc acc gaa gca gtc gac aac cac act gaa gtc cgc aag	691	
Glu Ile Lys Cys Thr Glu Ala Val Asp Asn His Thr Glu Val Arg Lys		
185 190 195		
ctc ggc gag ttc atg gat ttc tgt gac cag tac atc atc ggc gac aac	739	
Leu Gly Glu Phe Met Asp Phe Cys Asp Gln Tyr Ile Ile Gly Asp Asn		
200 205 210		
ggc atg ctc gtt gat atg cgt ttc atg cca cgc atc gtc gaa ggc gaa	787	
Gly Met Leu Val Asp Met Arg Phe Met Pro Arg Ile Val Glu Gly Glu		
215 220 225		

atc cgc atc ctt ctc gtc gga cca cac cca gtg ttc gtc gtg cac aag 835
 Ile Arg Ile Leu Leu Val Gly Pro His Pro Val Phe Val Val His Lys
 230 235 240 245
 aag cca gca gaa ggc ggc gac aac ttc tcc gca acc ctg ttc tcc ggc 883
 Lys Pro Ala Glu Gly Gly Asp Asn Phe Ser Ala Thr Leu Phe Ser Gly
 250 255 260
 gcg aag tac acc tac gac aag cca gag cag tgg cag gaa ctg att gac 931
 Ala Lys Tyr Thr Tyr Asp Lys Pro Glu Gln Trp Gln Glu Leu Ile Asp
 265 270 275
 ctc ttc gca gac gct cgc cca gtc atc gca gaa aag ctc ggc ggc gac 979
 Leu Phe Ala Asp Ala Arg Pro Val Ile Ala Glu Lys Leu Gly Gly Asp
 280 285 290
 aac atc cca ttg atc tgg acc gca gac ttc atg ctc ggc gat gtc gtt 1027
 Asn Ile Pro Leu Ile Trp Thr Ala Asp Phe Met Leu Gly Asp Val Val
 295 300 305
 gac ggc aag gac acc tac gtg ctc ggt gaa atc aac tgc tcc tgc gtc 1075
 Asp Gly Lys Asp Thr Tyr Val Leu Gly Glu Ile Asn Cys Ser Cys Val
 310 315 320 325
 ggc ttc acc tcc gag ctg gac atg ggc atc cag cag ctt gtg gca tca 1123
 Gly Phe Thr Ser Glu Leu Asp Met Gly Ile Gln Gln Leu Val Ala Ser
 330 335 340
 gag gcc atc aag cgc atc gag gaa ttc gcg cag ctt act gtt 1165
 Glu Ala Ile Lys Arg Ile Glu Glu Phe Ala Gln Leu Thr Val
 345 350 355
 taaaactttg cttctcgacg tct 1188

<210> 1104

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 1104

Met Lys Lys Ser Ile Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys
 1 5 10 15

His Phe Asp Gly His Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile
 20 25 30

Asn Asp Ala Gly Trp Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp
 35 40 45

Thr Glu Gly Leu Phe Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile
 50 55 60

Ser Arg Val Asn Pro Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe
 65 70 75 80

Asp Leu Leu Thr Arg Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr
 85 90 95

Pro Glu Glu Met Met Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu
 100 105 110

Ser Gln Thr Asp Leu Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val
115 120 125

Glu Thr Phe His Lys Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Arg
130 135 140

Val Leu Lys Gln Asn Arg Gly Ser Thr Gly Ser Gly Ile Trp Arg Val
145 150 155 160

Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly Thr Ala
165 170 175

Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp Asn His
180 185 190

Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp Gln Tyr
195 200 205

Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met Pro Arg
210 215 220

Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His Pro Val
225 230 235 240

Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe Ser Ala
245 250 255

Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu Gln Trp
260 265 270

Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile Ala Glu
275 280 285

Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp Phe Met
290 295 300

Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly Glu Ile
305 310 315 320

Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly Ile Gln
325 330 335

Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe Ala Gln
340 345 350

Leu Thr Val
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<210> 1105

<211> 580

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02338

<400> 1105

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aaaagtgcctt caagttatga gaaagtgaag tccaacaccc atg aaa aag agc atc 115
                                     Met Lys Lys Ser Ile
                                     1 5

ggt gta ttt gaa gtc gaa ggc ggc tcc gac aag cac ttc gac ggt cac 163
Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys His Phe Asp Gly His
          10          15          20

cgt aaa gac acc atg cct atc gtc aac tcc ata aat gat gct ggc tgg 211
Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile Asn Asp Ala Gly Trp
          25          30          35

cag gca gag gtt gtg tac tac cgc cca gag tgg acc gaa ggt ctc ttt 259
Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp Thr Glu Gly Leu Phe
          40          45          50

gag tac gta tct gaa aac ttc gac ggc tac atc tca cgt gtc aac cca 307
Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile Ser Arg Val Asn Pro
          55          60          65

ggc aac atc cca ggc ggc gag cgc ggc tac ttt gac ctg ctc acc cgc 355
Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe Asp Leu Leu Thr Arg
          70          75          80          85

ctg tcc gaa gca ggg ctc gtg ggc atg tcc acc cct gag gaa atg atg 403
Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr Pro Glu Glu Met Met
          90          95          100

gca tac ggc gcg aaa gat gcg ctg gtc aag cta tcc caa acc gac ctg 451
Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu Ser Gln Thr Asp Leu
          105          110          115

gtg cca tcc gac acc gag gcg tac tac gac gtg gag acc ttc cac aag 499
Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val Glu Thr Phe His Lys
          120          125          130

gtt ttc cca acc tcc ctg tcc ttc ggt gaa gcg cgt gct caa gca aaa 547
Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Ala Arg Ala Gln Ala Lys
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acc tgg ctt cac cgg ctt ccg cat ttg gcg cgt 580
Thr Trp Leu His Arg Leu Pro His Leu Ala Arg
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<210> 1106

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1106

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Met Lys Lys Ser Ile Val Val Phe Glu Val Glu Gly Gly Ser Asp Lys
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His Phe Asp Gly His Arg Lys Asp Thr Met Pro Ile Val Asn Ser Ile
  20          25          30

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Asn Asp Ala Gly Trp Gln Ala Glu Val Val Tyr Tyr Arg Pro Glu Trp
  35          40          45

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Thr Glu Gly Leu Phe Glu Tyr Val Ser Glu Asn Phe Asp Gly Tyr Ile
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 Ser Arg Val Asn Pro Gly Asn Ile Pro Gly Gly Glu Arg Gly Tyr Phe
 65 70 75 80
 Asp Leu Leu Thr Arg Leu Ser Glu Ala Gly Leu Val Gly Met Ser Thr
 85 90 95
 Pro Glu Glu Met Met Ala Tyr Gly Ala Lys Asp Ala Leu Val Lys Leu
 100 105 110
 Ser Gln Thr Asp Leu Val Pro Ser Asp Thr Glu Ala Tyr Tyr Asp Val
 115 120 125
 Glu Thr Phe His Lys Val Phe Pro Thr Ser Leu Ser Phe Gly Glu Ala
 130 135 140
 Arg Ala Gln Ala Lys Thr Trp Leu His Arg Leu Pro His Leu Ala Arg
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<211> 662

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<223> FRXA02340

<400> 1107

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cgc gtc cag ttg gta gac aag gaa ctg gct gca tcc atc gag cca ggc 96
 Arg Val Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly
 20 25 30

acc gca ctg cca ttg gac act gaa atc aag tgc acc gaa gca gtc gac 144
 Thr Ala Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp
 35 40 45

aac cac act gaa gtc cgc aag ctc ggc gag ttc atg gat ttc tgt gac 192
 Asn His Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp
 50 55 60

cag tac atc atc ggc gac aac ggc atg ctc gtt gat atg cgt ttc atg 240
 Gln Tyr Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met
 65 70 75 80

cca cgc atc gtc gaa ggc gaa atc cgc atc ctt ctc gtc gga cca cac 288
 Pro Arg Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His
 85 90 95

cca gtg ttc gtc gtg cac aag aag cca gca gaa ggc ggc gac aac ttc 336
 Pro Val Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe
 100 105 110

tcc gca acc ctg ttc tcc ggc gcg aag tac acc tac gac aag cca gag 384
 Ser Ala Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu
 115 120 125
 cag tgg cag gaa ctg att gac ctc ttc gca gac gct cgc cca gtc atc 432
 Gln Trp Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile
 130 135 140
 gca gaa aag ctc ggc ggc gac aac atc cca ttg atc tgg acc gca gac 480
 Ala Glu Lys Leu Gly Gly Asp Asn Ile Pro Leu Ile Trp Thr Ala Asp
 145 150 155 160
 ttc atg ctc ggc gat gtc gtt gac ggc aag gac acc tac gtg ctc ggt 528
 Phe Met Leu Gly Asp Val Val Asp Gly Lys Asp Thr Tyr Val Leu Gly
 165 170 175
 gaa atc aac tgc tcc tgc gtc ggc ttc acc tcc gag ctg gac atg ggc 576
 Glu Ile Asn Cys Ser Cys Val Gly Phe Thr Ser Glu Leu Asp Met Gly
 180 185 190
 atc cag cag ctt gtg gca tca gag gcc atc aag cgc atc gag gaa ttc 624
 Ile Gln Gln Leu Val Ala Ser Glu Ala Ile Lys Arg Ile Glu Glu Phe
 195 200 205
 gcg cag ctt act gtt taaaactttg cttctcgacg tct 662
 Ala Gln Leu Thr Val
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<210> 1108

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 1108

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 Arg Val Gln Leu Val Asp Lys Glu Leu Ala Ala Ser Ile Glu Pro Gly
 20 25 30
 Thr Ala Leu Pro Leu Asp Thr Glu Ile Lys Cys Thr Glu Ala Val Asp
 35 40 45
 Asn His Thr Glu Val Arg Lys Leu Gly Glu Phe Met Asp Phe Cys Asp
 50 55 60
 Gln Tyr Ile Ile Gly Asp Asn Gly Met Leu Val Asp Met Arg Phe Met
 65 70 75 80
 Pro Arg Ile Val Glu Gly Glu Ile Arg Ile Leu Leu Val Gly Pro His
 85 90 95
 Pro Val Phe Val Val His Lys Lys Pro Ala Glu Gly Gly Asp Asn Phe
 100 105 110
 Ser Ala Thr Leu Phe Ser Gly Ala Lys Tyr Thr Tyr Asp Lys Pro Glu
 115 120 125
 Gln Trp Gln Glu Leu Ile Asp Leu Phe Ala Asp Ala Arg Pro Val Ile

105	110	115	
agc tac att cag cga gtc caa cgt cgg cga aac acc ctg gtc tta ggt			499
Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn Thr Leu Val Leu Gly			
120	125	130	
ggt ggt gga cac cac cga ccc tat gta atc aac cag gtt ccc aag gct			547
Val Gly Gly His His Arg Pro Tyr Val Ile Asn Gln Val Pro Lys Ala			
135	140	145	
cga aaa gtg gaa gcg ctg ctc aaa gat ctt aca ttt tgg tgaaggcggt			596
Arg Lys Val Glu Ala Leu Leu Lys Asp Leu Thr Phe Trp			
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<210> 1110

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 1110

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Leu Ile Val Ile Thr Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp
35 40 45

Gln Leu Pro Gly Ile Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu
50 55 60

Gly Thr Arg Asn Leu Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp
65 70 75 80

Arg Phe Gly Leu Pro Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu
85 90 95

Ser Asp Arg Lys Leu Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe
100 105 110

Asp Ser Ile Pro Leu Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn
115 120 125

Thr Leu Val Leu Gly Val Gly Gly His His Arg Pro Tyr Val Ile Asn
130 135 140

Gln Val Pro Lys Ala Arg Lys Val Glu Ala Leu Leu Lys Asp Leu Thr
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Phe Trp

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<211> 511

<212> DNA

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<223> FRXA02341

<400> 1111

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                                         Met Gly Asn Ser Leu
                                         1      5

gag aaa cat att gca gag gga gac cgg atc cac gtc gat ctg aca tct 163
Glu Lys His Ile Ala Glu Gly Asp Arg Ile His Val Asp Leu Thr Ser
                        10                        15                        20

cct tta tcc gca atg ttg ttc ccc att ttt gaa ctc att gtg att act 211
Pro Leu Ser Ala Met Leu Phe Pro Ile Phe Glu Leu Ile Val Ile Thr
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gga atc tgt tgg atg ggc atc ggc ttt ttg gat cag ctt cca gga atc 259
Gly Ile Cys Trp Met Gly Ile Gly Phe Leu Asp Gln Leu Pro Gly Ile
                        40                        45                        50

gat ggc acc aac ccc gcc gat agc ttc ccc gaa ggc acc cgc aat ctt 307
Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu Gly Thr Arg Asn Leu
                        55                        60                        65

cta gtg ggt gtg tgg gca gta ctt gct gca tgg cgt ttc ggt ctt cct 355
Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp Arg Phe Gly Leu Pro
                        70                        75                        80                        85

tta ata agg caa cgt cga ctc cgc gtg atc ttg agc gac cgc aaa ctg 403
Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu Ser Asp Arg Lys Leu
                        90                        95                        100

ctg gtc cga cgc gcg ggt ctg cgc acc ggg ttc gat tcc att cca ctg 451
Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe Asp Ser Ile Pro Leu
                        105                        110                        115

agc tac att cag cga gtc caa cgt cgg cga aac acc ctg gtc tta ggt 499
Ser Tyr Ile Gln Arg Val Gln Arg Arg Arg Asn Thr Leu Val Leu Gly
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<210> 1112

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 1112

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  20      25      30

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 Gln Leu Pro Gly Ile Asp Gly Thr Asn Pro Ala Asp Ser Phe Pro Glu
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 Gly Thr Arg Asn Leu Leu Val Gly Val Trp Ala Val Leu Ala Ala Trp
 65 70 75 80
 Arg Phe Gly Leu Pro Leu Ile Arg Gln Arg Arg Leu Arg Val Ile Leu
 85 90 95
 Ser Asp Arg Lys Leu Leu Val Arg Arg Ala Gly Leu Arg Thr Gly Phe
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 <223> RXN02360

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 Met Arg Gly Asp Val
 1 5
 caa aaa ata acc aag gtt tat gac ggc aag cac cga acc ttg gaa atc 163
 Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His Arg Thr Leu Glu Ile
 10 15 20
 ccg gtt tat caa cgc aat tac gac tgg act gaa aag caa tgt tca cgc 211
 Pro Val Tyr Gln Arg Asn Tyr Asp Trp Thr Glu Lys Gln Cys Ser Arg
 25 30 35
 ctc ttt gat gac ctc agc gaa gtg gtc aaa gaa aac cac cgt caa cat 259
 Leu Phe Asp Asp Leu Ser Glu Val Val Lys Glu Asn His Arg Gln His
 40 45 50
 ttt ttt gga gct gtg gtt ggt aag cct caa ggc agc tgg acc tgg gtt 307
 Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly Ser Trp Thr Trp Val
 55 60 65
 gtc atc gat gga cag cag cgt ctt aca aca atc agc ttg ttc atg ctt 355
 Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile Ser Leu Phe Met Leu
 70 75 80 85
 gcg ctg gta cat tcc ttg cgc gca tct gaa gtt gaa gaa ggt gag ttt 403

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Asn	Ala	Gly	Tyr	Asn	Ile	Asp	Leu	Ala	Thr	Leu	Ile	Glu	Asp	Asp	Tyr		
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ctc	cga	tcc	ggc	aat	gag	gga	aac	ctc	aag	ttc	aag	ctc	aag	cca	gtt	499	
Leu	Arg	Ser	Gly	Asn	Glu	Gly	Asn	Leu	Lys	Phe	Lys	Leu	Lys	Pro	Val		
			120				125						130				
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Lys	Asn	Asp	Asn	Glu	Ala	Tyr	Gln	Lys	Leu	Phe	Gly	Pro	Glu	Ser	Glu		
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ttc	ata	gag	tcc	tca	aac	ctc	act	gct	aat	tat	cgc	tac	ttc	cgc	aat	595	
Phe	Ile	Glu	Ser	Ser	Asn	Leu	Thr	Ala	Asn	Tyr	Arg	Tyr	Phe	Arg	Asn		
					155					160					165		
gtc	ctt	aag	gca	acc	gat	ctc	acc	gca	gct	caa	cta	tgg	gaa	gct	atc	643	
Val	Leu	Lys	Ala	Thr	Asp	Leu	Thr	Ala	Ala	Gln	Leu	Trp	Glu	Ala	Ile		
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gag	aaa	ctc	agg	gtc	atg	tat	ctt	gac	ctt	gag	gaa	ttt	gat	gat	ccg	691	
Glu	Lys	Leu	Arg	Val	Met	Tyr	Leu	Asp	Leu	Glu	Glu	Phe	Asp	Asp	Pro		
			185					190					195				
cag	cga	atc	ttt	gaa	agt	ctc	aac	tcc	acg	gga	tta	gag	ctc	agt	gaa	739	
Gln	Arg	Ile	Phe	Glu	Ser	Leu	Asn	Ser	Thr	Gly	Leu	Glu	Leu	Ser	Glu		
			200				205					210					
gct	gat	aag	gta	cgc	aac	ttg	gtt	ctt	atg	gat	cag	gag	ctc	aaa	acc	787	
Ala	Asp	Lys	Val	Arg	Asn	Leu	Val	Leu	Met	Asp	Gln	Glu	Leu	Lys	Thr		
			215			220					225						
caa	gaa	aag	ctc	tat	gag	cag	cgt	tgg	aat	ccc	att	gaa	gtc	tgc	gtg	835	
Gln	Glu	Lys	Leu	Tyr	Glu	Gln	Arg	Trp	Asn	Pro	Ile	Glu	Val	Cys	Val		
					235					240					245		
aaa	ttt	gat	acc	gac	aat	ttc	att	cgc	tgg	tac	tta	act	ctc	aaa	acc	883	
Lys	Phe	Asp	Thr	Asp	Asn	Phe	Ile	Arg	Trp	Tyr	Leu	Thr	Leu	Lys	Thr		
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Ile	Arg	Asn	Ser	Lys	Leu	Pro	Val	Glu	Phe	Ile	Leu	Asp	Asp	Met	Tyr		
			280				285					290					
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Glu	Tyr	Ala	Lys	Leu	Tyr	Arg	Asp	Leu	Leu	Gly	Ala	Thr	Thr	Gly	Phe		
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Ile	Ala	Ala	Asp	Arg	Cys	Leu	Lys	Arg	Phe	Val	Pro	Val	Met	Gly	Asp		
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gtg	gtt	ttg	cct	ttt	ctg	ctg	cct	gtt	ctc	aaa	gat	gct	aaa	gac	ggc	1123	
Val	Val	Leu	Pro	Phe	Leu	Leu	Pro	Val	Leu	Lys	Asp	Ala	Lys	Asp	Gly		

330										335					340					
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345 350 355																				
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Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala Ser Asn Ala Leu Ser																				
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Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn Arg Arg Tyr Leu Phe																				
425 430 435																				
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Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val Arg Asp Ile Gln Thr																				
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agt ctg gat gaa gga tct ctc tcc att gaa cac atc atg cca cgt agc	1507																			
Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His Ile Met Pro Arg Ser																				
455 460 465																				
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470 475 480 485																				
cat gag act tgg att aat aga att ggt aac ctc acc atc acc ggc tac	1603																			
His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu Thr Ile Thr Gly Tyr																				
490 495 500																				
aac tcc gcc tat tca aat tct tcc tat gag cgc aag cgg acg atg gaa	1651																			
Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg Lys Arg Thr Met Glu																				
505 510 515																				
aat gga ttt ttg gta tcc ccc tat cgc atc aat aat ttc atc aaa aag	1699																			
Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn Asn Phe Ile Lys Lys																				
520 525 530																				
cag aag cat tgg tct gaa gaa cag cta att gag cga acc gag ctg ctc	1747																			
Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu Arg Thr Glu Leu Leu																				
535 540 545																				
act caa gca gcg ctg gac tac tgg ccc ctt cca aaa gaa acc ttc cag	1795																			
Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro Lys Glu Thr Phe Gln																				
550 555 560 565																				
cca cca caa gct gtg ctt cct aca gaa tcc tta gat agt gat ctt tct	1843																			
Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu Asp Ser Asp Leu Ser																				
570 575 580																				

ttc cgc gga cgc gaa att gtc gcc ttt gaa tat gag gac tac aag gaa	1891
Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr Glu Asp Tyr Lys Glu	
585 590 595	
acg gta acg tcc tgg gca gac atg ctc cag agc gtt cta aaa gtc ttg	1939
Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser Val Leu Lys Val Leu	
600 605 610	
aac caa tcc ttc cgc cag gaa ctc ata gct ttg acc aat gaa gaa atc	1987
Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu Thr Asn Glu Glu Ile	
615 620 625	
tgc ctg gca act tca aac aac agt aac agc agt ctc cgt gaa att gac	2035
Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser Leu Arg Glu Ile Asp	
630 635 640 645	
cac ggg ctt ttt gta gac act ggc tct agt acg agt gta aag att ggc	2083
His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr Ser Val Lys Ile Gly	
650 655 660	
ttc ctc cgc aga gtt ttt act caa ctg ggg cta gag cag gaa gca ttg	2131
Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu Glu Gln Glu Ala Leu	
665 670 675	
gtt ttc acc ctt cga cca ctg gca aat gat gta gaa ccc cga gat gat	2179
Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val Glu Pro Arg Asp Asp	
680 685 690	
gaa ctc gag gta gag gta gaa aag aaa tat tcc gat ttg act aaa ttc	2227
Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser Asp Leu Thr Lys Phe	
695 700 705	
atc cca cag tta gaa gaa gct gag aat ctc gag ggg gcg gat aca gag	2275
Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu Gly Ala Asp Thr Glu	
710 715 720 725	
gtt att cct ctc ctc tca aag ctc aag gaa caa ctg aca gcc ttt agc	2323
Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln Leu Thr Ala Phe Ser	
730 735 740	
ccg gag aat cct caa gca gcc cta ggg ggc cta cct gtt cca gaa ttc	2371
Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu Pro Val Pro Glu Phe	
745 750 755	
ctc aaa caa aat gtg att gaa caa cta agc gca gag cac atc ctt gct	2419
Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala Glu His Ile Leu Ala	
760 765 770	
gta ctc act caa cac ttt aat atc gca tcc atg atg ggt gat gac tat	2467
Val Leu Thr Gln His Phe Asn Ile Ala Ser Met Met Gly Asp Asp Tyr	
775 780 785	
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Leu Leu Glu Glu Leu Arg Ser Gly Arg Leu Arg Glu Leu Leu Gln Arg	
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<213> Corynebacterium glutamicum

<400> 1114

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35 40 45

Asn His Arg Gln His Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly
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Ser Trp Thr Trp Val Val Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile
65 70 75 80

Ser Leu Phe Met Leu Ala Leu Val His Ser Leu Arg Ala Ser Glu Val
85 90 95

Glu Glu Gly Glu Phe Asn Ala Gly Tyr Asn Ile Asp Leu Ala Thr Leu
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Ile Glu Asp Asp Tyr Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe
115 120 125

Lys Leu Lys Pro Val Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe
130 135 140

Gly Pro Glu Ser Glu Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr
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Arg Tyr Phe Arg Asn Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln
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Leu Trp Glu Ala Ile Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu
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Glu Phe Asp Asp Pro Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly
195 200 205

Leu Glu Leu Ser Glu Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp
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Gln Glu Leu Lys Thr Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro
225 230 235 240

Ile Glu Val Cys Val Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr
245 250 255

Leu Thr Leu Lys Thr Ala Arg Thr Pro Arg Lys Gln Asp Val Tyr Glu
260 265 270

Glu Phe Lys Lys Phe Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile
275 280 285

Leu Asp Asp Met Tyr Glu Tyr Ala Lys Leu Tyr Arg Asp Leu Leu Gly
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Ala Thr Thr Gly Phe Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val
305 310 315 320

Pro Val Met Gly Asp Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys
325 330 335

Asp Ala Lys Asp Gly Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu
340 345 350

Lys Val Leu Glu Ser Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala
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Ser Asn Ala Leu Ser Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys
370 375 380

Lys Phe Trp Thr Pro Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile
385 390 395 400

Leu Lys Arg Arg Asp Gly Ser Gly Arg Phe Pro Ser Asp Ser Glu Phe
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Arg Glu Asn Phe Ala Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn
420 425 430

Arg Arg Tyr Leu Phe Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val
435 440 445

Arg Asp Ile Gln Thr Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His
450 455 460

Ile Met Pro Arg Ser Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro
465 470 475 480

Glu Tyr Ala Arg Ile His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu
485 490 495

Thr Ile Thr Gly Tyr Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg
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Lys Arg Thr Met Glu Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn
515 520 525

Asn Phe Ile Lys Lys Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu
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Arg Thr Glu Leu Leu Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro
545 550 555 560

Lys Glu Thr Phe Gln Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu
565 570 575

Asp Ser Asp Leu Ser Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr
580 585 590

Glu Asp Tyr Lys Glu Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser
595 600 605

Val Leu Lys Val Leu Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu

610	615	620
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Ser Val Lys Ile Gly Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu 660 665 670		
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Glu Pro Arg Asp Asp Glu Leu Glu Val Glu Val Glu Lys Lys Tyr Ser 690 695 700		
Asp Leu Thr Lys Phe Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu 705 710 715 720		
Gly Ala Asp Thr Glu Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln 725 730 735		
Leu Thr Ala Phe Ser Pro Glu Asn Pro Gln Ala Ala Leu Gly Gly Leu 740 745 750		
Pro Val Pro Glu Phe Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala 755 760 765		
Glu His Ile Leu Ala Val Leu Thr Gln His Phe Asn Ile Ala Ser Met 770 775 780		
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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2533)

<223> FRXA02360

<400> 1115

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Met Arg Gly Asp Val	
1 5	

caa aaa ata acc aag gtt tat gac ggc aag cac cga acc ttg gaa atc	163
Gln Lys Ile Thr Lys Val Tyr Asp Gly Lys His Arg Thr Leu Glu Ile	
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ccg gtt tat caa cgc aat tac gac tgg act gaa aag caa tgt tca cgc 211

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Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu Arg Thr Glu Leu Leu	
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Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr Glu Asp Tyr Lys Glu	
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Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser Val Leu Lys Val Leu	
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Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser Leu Arg Glu Ile Asp	
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His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr Ser Val Lys Ile Gly	
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Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val Glu Pro Arg Asp Asp	
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Asn His Arg Gln His Phe Phe Gly Ala Val Val Gly Lys Pro Gln Gly
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Ser Leu Phe Met Leu Ala Leu Val His Ser Leu Arg Ala Ser Glu Val
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Ile Glu Asp Asp Tyr Leu Arg Ser Gly Asn Glu Gly Asn Leu Lys Phe
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Lys Leu Lys Pro Val Lys Asn Asp Asn Glu Ala Tyr Gln Lys Leu Phe
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Gly Pro Glu Ser Glu Phe Ile Glu Ser Ser Asn Leu Thr Ala Asn Tyr
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Arg Tyr Phe Arg Asn Val Leu Lys Ala Thr Asp Leu Thr Ala Ala Gln
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Leu Trp Glu Ala Ile Glu Lys Leu Arg Val Met Tyr Leu Asp Leu Glu
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Glu Phe Asp Asp Pro Gln Arg Ile Phe Glu Ser Leu Asn Ser Thr Gly
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Leu Glu Leu Ser Glu Ala Asp Lys Val Arg Asn Leu Val Leu Met Asp
210 215 220

Gln Glu Leu Lys Thr Gln Glu Lys Leu Tyr Glu Gln Arg Trp Asn Pro
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Ile Glu Val Cys Val Lys Phe Asp Thr Asp Asn Phe Ile Arg Trp Tyr
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Glu Phe Lys Lys Phe Ile Arg Asn Ser Lys Leu Pro Val Glu Phe Ile
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Ala Thr Thr Gly Phe Ile Ala Ala Asp Arg Cys Leu Lys Arg Phe Val
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Pro Val Met Gly Asp Val Val Leu Pro Phe Leu Leu Pro Val Leu Lys
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Asp Ala Lys Asp Gly Ile Ile Thr Glu Ser Asp Phe Leu Gly Val Leu
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Lys Val Leu Glu Ser Tyr Leu Phe Arg Arg Phe Ala Val Gly Val Ala
355 360 365

Ser Asn Ala Leu Ser Lys Ile Phe Ser Thr Ala Tyr Ser Asp Ile Lys
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Lys Phe Trp Thr Pro Gly Gln Ser Tyr Ser Ser Leu Leu Ala Tyr Ile
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405 410 415

Arg Glu Asn Phe Ala Thr Lys Asn Phe Trp Asn Ile His Asn Glu Asn
420 425 430

Arg Arg Tyr Leu Phe Asp Cys Leu Glu Asn Ala Asp Ser Asn Asp Val
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Arg Asp Ile Gln Thr Ser Leu Asp Glu Gly Ser Leu Ser Ile Glu His
450 455 460

Ile Met Pro Arg Ser Leu Asn Asp Gln Trp Arg Ala Glu Leu Gly Pro
465 470 475 480

Glu Tyr Ala Arg Ile His Glu Thr Trp Ile Asn Arg Ile Gly Asn Leu
485 490 495

Thr Ile Thr Gly Tyr Asn Ser Ala Tyr Ser Asn Ser Ser Tyr Glu Arg
500 505 510

Lys Arg Thr Met Glu Asn Gly Phe Leu Val Ser Pro Tyr Arg Ile Asn
515 520 525

Asn Phe Ile Lys Lys Gln Lys His Trp Ser Glu Glu Gln Leu Ile Glu
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 Arg Thr Glu Leu Leu Thr Gln Ala Ala Leu Asp Tyr Trp Pro Leu Pro
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 Lys Glu Thr Phe Gln Pro Pro Gln Ala Val Leu Pro Thr Glu Ser Leu
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 Asp Ser Asp Leu Ser Phe Arg Gly Arg Glu Ile Val Ala Phe Glu Tyr
 580 585 590
 Glu Asp Tyr Lys Glu Thr Val Thr Ser Trp Ala Asp Met Leu Gln Ser
 595 600 605
 Val Leu Lys Val Leu Asn Gln Ser Phe Arg Gln Glu Leu Ile Ala Leu
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 Thr Asn Glu Glu Ile Cys Leu Ala Thr Ser Asn Asn Ser Asn Ser Ser
 625 630 635 640
 Leu Arg Glu Ile Asp His Gly Leu Phe Val Asp Thr Gly Ser Ser Thr
 645 650 655
 Ser Val Lys Ile Gly Phe Leu Arg Arg Val Phe Thr Gln Leu Gly Leu
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 Glu Gln Glu Ala Leu Val Phe Thr Leu Arg Pro Leu Ala Asn Asp Val
 675 680 685
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 690 695 700
 Asp Leu Thr Lys Phe Ile Pro Gln Leu Glu Glu Ala Glu Asn Leu Glu
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 Gly Ala Asp Thr Glu Val Ile Pro Leu Leu Ser Lys Leu Lys Glu Gln
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 Pro Val Pro Glu Phe Leu Lys Gln Asn Val Ile Glu Gln Leu Ser Ala
 755 760 765
 Glu His Ile Leu Ala Val Leu Thr Gln His Phe Asn Ile Ala Ser Met
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<213> Corynebacterium glutamicum

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 <222> (101)..(751)
 <223> RXN02361

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His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg Leu Thr Val Tyr Asn
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Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala Ile Thr Leu Asp Asn
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tgg gcg tcc aag gtt ggc aat atg ctc ctt gag gaa ttg gat ctg gag 259
Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu Glu Leu Asp Leu Glu
                        40                               45                               50

gaa ggc tcg ctc atc act att gat ttg ccg gtg agc tgg cag gcc gca 307
Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val Ser Trp Gln Ala Ala
                        55                               60                               65

atg att atg ctc ggc gct tta gca act agt gtt gag gtc tct ttt gat 355
Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val Glu Val Ser Phe Asp
                        70                               75                               80                               85

gat ccc gag gca gat gcc atc ttt acc tcc ctc gat aga ttt tcc cac 403
Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu Asp Arg Phe Ser His
                        90                               95                               100

tac aag ggc cat agt gat gtg ctg att gtc agc gag gat cct ttt ggt 451
Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser Glu Asp Pro Phe Gly
                        105                               110                               115

cgt gga gtt gtt gaa ggt ggc ggt gaa ctg cct aat ggt gcc atc gat 499
Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro Asn Gly Ala Ile Asp
                        120                               125                               130

ttt ggc ccc aca gtg cgt ttt tat ggc gat caa ttc ttc cag cct acc 547
Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln Phe Phe Gln Pro Thr
                        135                               140                               145

cgc aca ttg ccg gaa atc atc cag cat tct gat gtt ccg gtt ggc gcc 595
Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp Val Pro Val Gly Ala
                        150                               155                               160                               165

aga gtt ctt gca act ggt tgg tca gat atc gag tcc ttc aat cac cag 643
Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu Ser Phe Asn His Gln
                        170                               175                               180

gtt tta gaa cca ctc gca gtg ggt ggc tct gca gta att gtg acc gga 691
Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala Val Ile Val Thr Gly
                        185                               190                               195

ctg gct gat att gag cgt tta aac cag att gca acc aat gag aag aca 739
Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala Thr Asn Glu Lys Thr

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200

205

210

acc cac cgt atc taggcaaatt tcggttacta cta
Thr His Arg Ile
215

774

<210> 1118

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 1118

Met Glu Leu Leu Ser His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg
1 5 10 15

Leu Thr Val Tyr Asn Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala
20 25 30

Ile Thr Leu Asp Asn Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu
35 40 45

Glu Leu Asp Leu Glu Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val
50 55 60

Ser Trp Gln Ala Ala Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val
65 70 75 80

Glu Val Ser Phe Asp Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu
85 90 95

Asp Arg Phe Ser His Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser
100 105 110

Glu Asp Pro Phe Gly Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro
115 120 125

Asn Gly Ala Ile Asp Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln
130 135 140

Phe Phe Gln Pro Thr Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp
145 150 155 160

Val Pro Val Gly Ala Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu
165 170 175

Ser Phe Asn His Gln Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala
180 185 190

Val Ile Val Thr Gly Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala
195 200 205

Thr Asn Glu Lys Thr Thr His Arg Ile
210 215

<210> 1119

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> FRXA02361

<400> 1119

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ctttaagcac aatctctagc ttttatttag gcttggagtt atg gaa ctt ctc tcc 115
                                         Met Glu Leu Leu Ser
                                         1 5

cac ttg ctt gct ctt gat cct gcc tcc cct cgt ttg act gtt tat aac 163
His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg Leu Thr Val Tyr Asn
          10          15          20

gag tcc acg ggt gcg cgt ttg gat ttc tcc gcc atc act ctt gat aac 211
Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala Ile Thr Leu Asp Asn
          25          30          35

tgg gcg tcc aag gtt ggc aat atg ctc ctt gag gaa ttg gat ctg gag 259
Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu Glu Leu Asp Leu Glu
          40          45          50

gaa ggc tcg ctc atc act att gat ttg ccg gtg agc tgg cag gcc gca 307
Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val Ser Trp Gln Ala Ala
          55          60          65

atg att atg ctc ggc gct tta gca act agt gtt gag gtc tct ttt gat 355
Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val Glu Val Ser Phe Asp
          70          75          80          85

gat ccc gag gca gat gcc atc ttt acc tcc ctc gat aga ttt tcc cac 403
Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu Asp Arg Phe Ser His
          90          95          100

tac aag ggc cat agt gat gtg ctg att gtc agc gag gat cct ttt ggt 451
Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser Glu Asp Pro Phe Gly
          105          110          115

cgt gga gtt gtt gaa ggt ggc ggt gaa ctg cct aat ggt gcc atc gat 499
Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro Asn Gly Ala Ile Asp
          120          125          130

ttt ggc ccc aca gtg cgt ttt tat ggc gat caa ttc ttc cag cct acc 547
Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln Phe Phe Gln Pro Thr
          135          140          145

cgc aca ttg ccg gaa atc atc cag cat tct gat gtt ccg gtt ggc gcc 595
Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp Val Pro Val Gly Ala
          150          155          160          165

aga gtt ctt gca act ggt tgg tca gat atc gag tcc ttc aat cac cag 643
Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu Ser Phe Asn His Gln
          170          175          180

gtt tta gaa cca ctc gca gtg ggt ggc tct gca gta att gtg acc gga 691
Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala Val Ile Val Thr Gly
          185          190          195

ctg gct gat att gag cgt tta aac cag att gca acc aat gag aag aca 739

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Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala Thr Asn Glu Lys Thr
200 205 210

acc cac cgt atc taggcaaatt tcggttacta cta
Thr His Arg Ile
215

774

<210> 1120

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 1120

Met Glu Leu Leu Ser His Leu Leu Ala Leu Asp Pro Ala Ser Pro Arg
1 5 10 15

Leu Thr Val Tyr Asn Glu Ser Thr Gly Ala Arg Leu Asp Phe Ser Ala
20 25 30

Ile Thr Leu Asp Asn Trp Ala Ser Lys Val Gly Asn Met Leu Leu Glu
35 40 45

Glu Leu Asp Leu Glu Glu Gly Ser Leu Ile Thr Ile Asp Leu Pro Val
50 55 60

Ser Trp Gln Ala Ala Met Ile Met Leu Gly Ala Leu Ala Thr Ser Val
65 70 75 80

Glu Val Ser Phe Asp Asp Pro Glu Ala Asp Ala Ile Phe Thr Ser Leu
85 90 95

Asp Arg Phe Ser His Tyr Lys Gly His Ser Asp Val Leu Ile Val Ser
100 105 110

Glu Asp Pro Phe Gly Arg Gly Val Val Glu Gly Gly Gly Glu Leu Pro
115 120 125

Asn Gly Ala Ile Asp Phe Gly Pro Thr Val Arg Phe Tyr Gly Asp Gln
130 135 140

Phe Phe Gln Pro Thr Arg Thr Leu Pro Glu Ile Ile Gln His Ser Asp
145 150 155 160

Val Pro Val Gly Ala Arg Val Leu Ala Thr Gly Trp Ser Asp Ile Glu
165 170 175

Ser Phe Asn His Gln Val Leu Glu Pro Leu Ala Val Gly Gly Ser Ala
180 185 190

Val Ile Val Thr Gly Leu Ala Asp Ile Glu Arg Leu Asn Gln Ile Ala
195 200 205

Thr Asn Glu Lys Thr Thr His Arg Ile
210 215

<210> 1121

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXN02367

<400> 1121

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ggtcacgttt cctcagctca ggagaagttc ggagaagtcc atg tca aac gca gaa 115
 Met Ser Asn Ala Glu
 1 5

att aat ccc gtt gaa tat gaa atc aac aac cac gcc cct ggt acc gcg 163
 Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His Ala Pro Gly Thr Ala
 10 15 20

cta aac cca cag tgc gaa gac ggc gcc aac gta gaa atc atc acc tcc 211
 Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val Glu Ile Ile Thr Ser
 25 30 35

cgt gaa gtc ccc ctc ggc gga cca cgc gcc atg acc gtg cac cgc aca 259
 Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met Thr Val His Arg Thr
 40 45 50

ctc ccc caa cgc cag cgc tcc ctc atc ggt gcc tgg tgt ttt gtg gat 307
 Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala Trp Cys Phe Val Asp
 55 60 65

cat tac ggc ccc gat gat gtc tca cta acc ggt ggc atg gat atg gcc 355
 His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly Gly Met Asp Met Ala
 70 75 80 85

tcc cac ccg cac acc gga ttg caa aca gtc acg tgg ctt ttt gaa ggc 403
 Ser His Pro His Thr Gly Leu Gln Thr Val Thr Trp Leu Phe Glu Gly
 90 95 100

gaa gtc acc cac cat gat tcc ggc gga aat cac gca gtc gtg ctt cct 451
 Glu Val Thr His His Asp Ser Gly Gly Asn His Ala Val Val Leu Pro
 105 110 115

ggc gaa gtc aac ctc atg acc gcc ggc gca ggc atc tgt cac acc gaa 499
 Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly Ile Cys His Thr Glu
 120 125 130

gtt tcc gcc acc tcc acc acg att ctg cat ggt ctg cag ttg tgg aca 547
 Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly Leu Gln Leu Trp Thr
 135 140 145

gtt ctt ccc gac aaa gac cgc gaa gga cca cgc cgc ttt gat cac tac 595
 Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg Arg Phe Asp His Tyr
 150 155 160 165

gct cca gaa gaa atc aca ctc gaa ggc gga agt gca cgc gtt ttc cta 643
 Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser Ala Arg Val Phe Leu
 170 175 180

ggc tgc cta ttt ggt caa acc tcc cct gtt cat acg ttt act ggc tct 691
 Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His Thr Phe Thr Gly Ser
 185 190 195

tcc tgt ttt aga gtg cat tgatcttatg gaccaactgc cct
Ser Cys Phe Arg Val His
200

732

<210> 1122
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 1122
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Ala Pro Gly Thr Ala Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val
20 25 30
Glu Ile Ile Thr Ser Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met
35 40 45
Thr Val His Arg Thr Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala
50 55 60
Trp Cys Phe Val Asp His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly
65 70 75 80
Gly Met Asp Met Ala Ser His Pro His Thr Gly Leu Gln Thr Val Thr
85 90 95
Trp Leu Phe Glu Gly Glu Val Thr His His Asp Ser Gly Gly Asn His
100 105 110
Ala Val Val Leu Pro Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly
115 120 125
Ile Cys His Thr Glu Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly
130 135 140
Leu Gln Leu Trp Thr Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg
145 150 155 160
Arg Phe Asp His Tyr Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser
165 170 175
Ala Arg Val Phe Leu Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His
180 185 190
Thr Phe Thr Gly Ser Ser Cys Phe Arg Val His
195 200

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<212> DNA
<213> Corynebacterium glutamicum

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<223> FRXA02367

<400> 1123

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ggtcacgttt cctcagctca ggagaagttc ggagaagtcc atg tca aac gca gaa 115
                                         Met Ser Asn Ala Glu
                                         1                               5

att aat ccc gtt gaa tat gaa atc aac aac cac gcc cct ggt acc gcg 163
Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His Ala Pro Gly Thr Ala
                        10                               15                               20

cta aac cca cag tgc gaa gac ggc gcc aac gta gaa atc atc acc tcc 211
Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val Glu Ile Ile Thr Ser
                        25                               30                               35

cgt gaa gtc ccc ctc ggc gga cca cgc gcc atg acc gtg cac cgc aca 259
Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met Thr Val His Arg Thr
                        40                               45                               50

ctc ccc caa cgc cag cgc tcc ctc atc ggt gcc tgg tgt ttt gtg gat 307
Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala Trp Cys Phe Val Asp
                        55                               60                               65

cat tac ggc ccc gat gat gtc tca cta acc ggt ggc atg gat atg gcc 355
His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly Gly Met Asp Met Ala
                        70                               75                               80                               85

tcc cac ccg cac acc gga ttg caa aca gtc acg tgg ctt ttt gaa ggc 403
Ser His Pro His Thr Gly Leu Gln Thr Val Thr Trp Leu Phe Glu Gly
                        90                               95                               100

gaa gtc acc cac cat gat tcc ggc gga aat cac gca gtc gtg ctt cct 451
Glu Val Thr His His Asp Ser Gly Gly Asn His Ala Val Val Leu Pro
                        105                               110                               115

ggc gaa gtc aac ctc atg acc gcc ggc gca ggc atc tgt cac acc gaa 499
Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly Ile Cys His Thr Glu
                        120                               125                               130

gtt tcc gcc acc tcc acc acg att ctg cat ggt ctg cag ttg tgg aca 547
Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly Leu Gln Leu Trp Thr
                        135                               140                               145

gtt ctt ccc gac aaa gac cgc gaa gga cca cgc cgc ttt gat cac tac 595
Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg Arg Phe Asp His Tyr
                        150                               155                               160                               165

gct cca gaa gaa atc aca ctc gaa ggc gga agt gca cgc gtt ttc cta 643
Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser Ala Arg Val Phe Leu
                        170                               175                               180

ggg tcg cta ttt ggt caa acc tcc cct gtt cat acg ttt act ggc tct 691
Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His Thr Phe Thr Gly Ser
                        185                               190                               195

tcc tgt ttt aga gtg cat tgatcttatg gaccaactgc cct 732
Ser Cys Phe Arg Val His
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<210> 1124

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

Met Ser Asn Ala Glu Ile Asn Pro Val Glu Tyr Glu Ile Asn Asn His
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Ala Pro Gly Thr Ala Leu Asn Pro Gln Cys Glu Asp Gly Ala Asn Val
 20 25 30

Glu Ile Ile Thr Ser Arg Glu Val Pro Leu Gly Gly Pro Arg Ala Met
 35 40 45

Thr Val His Arg Thr Leu Pro Gln Arg Gln Arg Ser Leu Ile Gly Ala
 50 55 60

Trp Cys Phe Val Asp His Tyr Gly Pro Asp Asp Val Ser Leu Thr Gly
 65 70 75 80

Gly Met Asp Met Ala Ser His Pro His Thr Gly Leu Gln Thr Val Thr
 85 90 95

Trp Leu Phe Glu Gly Glu Val Thr His His Asp Ser Gly Gly Asn His
 100 105 110

Ala Val Val Leu Pro Gly Glu Val Asn Leu Met Thr Ala Gly Ala Gly
 115 120 125

Ile Cys His Thr Glu Val Ser Ala Thr Ser Thr Thr Ile Leu His Gly
 130 135 140

Leu Gln Leu Trp Thr Val Leu Pro Asp Lys Asp Arg Glu Gly Pro Arg
 145 150 155 160

Arg Phe Asp His Tyr Ala Pro Glu Glu Ile Thr Leu Glu Gly Gly Ser
 165 170 175

Ala Arg Val Phe Leu Gly Ser Leu Phe Gly Gln Thr Ser Pro Val His
 180 185 190

Thr Phe Thr Gly Ser Ser Cys Phe Arg Val His
 195 200

<210> 1125

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXN02368

<400> 1125

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 Met Ile Val Leu Ala
 1 5

gga gcc act cga gtt acc tat gaa gta gaa cct tgg ctg gcg atc cca 163
 Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro Trp Leu Ala Ile Pro
 10 15 20

tta ttc att ttg gct ttt gca tcg ata ttg atc cca ttc ccg atc tct 211
 Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile Pro Phe Pro Ile Ser
 25 30 35

aag aca aaa gga ctc cgt gat atc gat gcc tgg aaa atc cac acc acg 259
 Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp Lys Ile His Thr Thr
 40 45 50

caa ggc gat aaa aag cgt gcc atc cgc caa ctg atc att ccg gct acg 307
 Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu Ile Ile Pro Ala Thr
 55 60 65

gct ttg gcc atc gac atc att ggg ctg ccg aca tta ttt aat gcc cct 355
 Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr Leu Phe Asn Ala Pro
 70 75 80 85

ccc ctt gct tcc gct gca ctt ttt ggc ggt gtt tac ggc gct tcc cta 403
 Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val Tyr Gly Ala Ser Leu
 90 95 100

gct tgg gct gcg tac aga gct gat cag ctt cca cgc att cga acg aag 451
 Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro Arg Ile Arg Thr Lys
 105 110 115

gaa cgc ctc gca gaa ctt tca caa aat gca tct ctg gat gat gtg cgc 499
 Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser Leu Asp Asp Val Arg
 120 125 130

tca gat gac tta gat gtt cta gag cag ccg gaa tcc cgt gaa tta gtg 547
 Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu Ser Arg Glu Leu Val
 135 140 145

cgc tgt ctg ctt gcc cac ggt gcg atg gat ggc act cgg gtg atg gcc 595
 Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly Thr Arg Val Met Ala
 150 155 160 165

aga cag gtc gcg cga gta ctg gat acc gag gta gac gaa gta cat cag 643
 Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val Asp Glu Val His Gln
 170 175 180

gta gca cgc tca cta gaa cag cat ggt ttg gtt agt cgc tcc acc atc 691
 Val Ala Arg Ser Leu Glu Gln His Gly Leu Val Ser Arg Ser Thr Ile
 185 190 195

atg ccg ggt ggg gat cca gga aaa gta ttc atc gaa gtt tcc ctg aaa 739
 Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile Glu Val Ser Leu Lys
 200 205 210

ggg atc tca gcc atc aag gca ctt gaa tcc gga cgc taagttgttg 785
 Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly Arg
 215 220 225

atacatcaac tta 798

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

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Trp Leu Ala Ile Pro Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile
20 25 30

Pro Phe Pro Ile Ser Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp
35 40 45

Lys Ile His Thr Thr Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu
50 55 60

Ile Ile Pro Ala Thr Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr
65 70 75 80

Leu Phe Asn Ala Pro Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val
85 90 95

Tyr Gly Ala Ser Leu Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro
100 105 110

Arg Ile Arg Thr Lys Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser
115 120 125

Leu Asp Asp Val Arg Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu
130 135 140

Ser Arg Glu Leu Val Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly
145 150 155 160

Thr Arg Val Met Ala Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val
165 170 175

Asp Glu Val His Gln Val Ala Arg Ser Leu Glu Gln His Gly Leu Val
180 185 190

Ser Arg Ser Thr Ile Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile
195 200 205

Glu Val Ser Leu Lys Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly
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Arg

225

<210> 1127

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(775)

<223> FRXA02368

<400> 1127

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                                     Met Ile Val LeuAla
                                     1 5

gga gcc act cga gtt acc tat gaa gta gaa cct tgg ctg gcg atc cca 163
Gly Ala Thr Arg Val Thr Tyr Glu Val Glu Pro Trp Leu Ala Ile Pro
                        10 15 20

tta ttc att ttg gct ttt gca tcg ata ttg atc cca ttc ccg atc tct 211
Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile Pro Phe Pro Ile Ser
                        25 30 35

aag aca aaa gga ctc cgt gat atc gat gcc tgg aaa atc cac acc acg 259
Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp Lys Ile His Thr Thr
                        40 45 50

caa ggc gat aaa aag cgt gcc atc cgc caa ctg atc att ccg gct acg 307
Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu Ile Ile Pro Ala Thr
                        55 60 65

gct ttg gcc atc gac atc att ggg ctg ccg aca tta ttt aat gcc cct 355
Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr Leu Phe Asn Ala Pro
                        70 75 80 85

ccc ctt gct tcc gct gca ctt ttt ggc ggt gtt tac ggc gct tcc cta 403
Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val Tyr Gly Ala Ser Leu
                        90 95 100

gct tgg gct gcg tac aga gct gat cag ctt cca cgc att cga acg aag 451
Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro Arg Ile Arg Thr Lys
                        105 110 115

gaa cgc ctc gca gaa ctt tca caa aat gca tct ctg gat gat gtg cgc 499
Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser Leu Asp Asp Val Arg
                        120 125 130

tca gat gac tta gat gtt cta gag cag ccg gaa tcc cgt gaa tta gtg 547
Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu Ser Arg Glu Leu Val
                        135 140 145

cgc tgt ctg ctt gcc cac ggt gcg atg gat ggc act ccg gtg atg gcc 595
Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly Thr Arg Val Met Ala
                        150 155 160 165

aga cag gtc gcg cga gta ctg gat acc gag gta gac gaa gta cat cag 643
Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val Asp Glu Val His Gln
                        170 175 180

gta gca cgc tca cta gaa cag cat ggt ttg gtt agt cgc tcc acc atc 691
Val Ala Arg Ser Leu Glu Gln His Gly Leu Val Ser Arg Ser Thr Ile
                        185 190 195

atg ccg ggt ggg gat cca gga aaa gta ttc atc gaa gtt tcc ctg aaa 739
Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile Glu Val Ser Leu Lys
                        200 205 210

ggg atc tca gcc atc aag gca ctt gaa tcc gga cgc taagtgtgtg 785
Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly Arg

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215

220

225

atacatcaac tta

798

<210> 1128

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 1128

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Trp Leu Ala Ile Pro Leu Phe Ile Leu Ala Phe Ala Ser Ile Leu Ile
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Pro Phe Pro Ile Ser Lys Thr Lys Gly Leu Arg Asp Ile Asp Ala Trp
 35 40 45

Lys Ile His Thr Thr Gln Gly Asp Lys Lys Arg Ala Ile Arg Gln Leu
 50 55 60

Ile Ile Pro Ala Thr Ala Leu Ala Ile Asp Ile Ile Gly Leu Pro Thr
 65 70 75 80

Leu Phe Asn Ala Pro Pro Leu Ala Ser Ala Ala Leu Phe Gly Gly Val
 85 90 95

Tyr Gly Ala Ser Leu Ala Trp Ala Ala Tyr Arg Ala Asp Gln Leu Pro
 100 105 110

Arg Ile Arg Thr Lys Glu Arg Leu Ala Glu Leu Ser Gln Asn Ala Ser
 115 120 125

Leu Asp Asp Val Arg Ser Asp Asp Leu Asp Val Leu Glu Gln Pro Glu
 130 135 140

Ser Arg Glu Leu Val Arg Cys Leu Leu Ala His Gly Ala Met Asp Gly
 145 150 155 160

Thr Arg Val Met Ala Arg Gln Val Ala Arg Val Leu Asp Thr Glu Val
 165 170 175

Asp Glu Val His Gln Val Ala Arg Ser Leu Glu Gln His Gly Leu Val
 180 185 190

Ser Arg Ser Thr Ile Met Pro Gly Gly Asp Pro Gly Lys Val Phe Ile
 195 200 205

Glu Val Ser Leu Lys Gly Ile Ser Ala Ile Lys Ala Leu Glu Ser Gly
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Arg

225

<210> 1129

<211> 1146

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1123)

<223> RXN02381

<400> 1129

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                                         Met Ser Val Thr Asn
                                         1           5

ttc cgt cgg ttt ctt gct ggc ata gcg gtc atc gcg gcg tgt gtt gct 163
Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile Ala Ala Cys Val Ala
                10                15                20

gcg act cca aca gct cag gca caa agc agt ggc tct tct gga tcc tct 211
Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly Ser Ser Gly Ser Ser
                25                30                35

ggt tct tca gcg gga tct agc ggg ctg tgg gat tta ctt ttt cca gaa 259
Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp Leu Leu Phe Pro Glu
                40                45                50

tcc cat gag tct ttt atc gag cgg ctt ctt gat cct ttg gat gac agc 307
Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp Pro Leu Asp Asp Ser
                55                60                65

cat ata tct att cac cct gac ctc acc cca gac ctg tat gaa gag gtg 355
His Ile Ser Ile His Pro Asp Leu Thr Pro Asp Leu Tyr Glu Glu Val
                70                75                80                85

ttt gat cca ccg caa att ggt gaa tgc cca gcc gtt gtt gct gtg gtc 403
Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala Val Val Ala Val Val
                90                95                100

gca cga ggc agt gaa caa aac ctt caa atc cga ccc gcg cga tac agc 451
Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg Pro Ala Arg Tyr Ser
                105                110                115

gag gaa tct cca tgg aca tcc aat gga ttt gag gaa aaa aac ttt cgt 499
Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu Glu Lys Asn Phe Arg
                120                125                130

agt ttc ttt ggc cga atg gaa aaa cac tac cgt gaa tcg act ggc gag 547
Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg Glu Ser Thr Gly Glu
                135                140                145

tcg ttg atg aaa gac gtc tac gtg atg ggt ctg aat aat atc gaa tac 595
Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu Asn Asn Ile Glu Tyr
                150                155                160                165

cct gct tct ttg cca ctg tct tcg gag gga agc agc gcc att gaa ttg 643
Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser Ser Ala Ile Glu Leu
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ggc act tcc att tct agt ggt cgc gac aat gtc atc agc gcg att gat 691
Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val Ile Ser Ala Ile Asp
                185                190                195

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cgc ttt gaa tca gcg aca ggg tgc acg ccg aag tac ctg ttg gcg ggt 739
 Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys Tyr Leu Leu Ala Gly
 200 205 210
 tat tct caa ggt gtc ctc atc gtt gat ggc tat gaa gag gag ttg att 787
 Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr Glu Glu Glu Leu Ile
 215 220 225
 gcg agg gat cag tac ctc ggc acc ctg cac atc gcg aat cca gcg caa 835
 Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile Ala Asn Pro Ala Gln
 230 235 240 245
 caa gtt gat gat cca aca ctt gtt ggg cat gaa gta acc acg gga ggc 883
 Gln Val Asp Asp Pro Thr Leu Val Gly His Glu Val Thr Thr Gly Gly
 250 255 260
 ttg gct agt tcc gtg gag ccc gtc gag gac aat cct ttc aag gtg agc 931
 Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn Pro Phe Lys Val Ser
 265 270 275
 tac tgc ctg cct gga gac atc gtg tgc gat cgt tct ttt gaa cag ttc 979
 Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg Ser Phe Glu Gln Phe
 280 285 290
 tct gct gcg gga tcc tct ata gca gct gcg caa ttg agc acc gga aat 1027
 Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln Leu Ser Thr Gly Asn
 295 300 305
 atc cgt cca ggt cga gta cac gtg caa tac ttc gtt acc acc caa ccg 1075
 Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe Val Thr Thr Gln Pro
 310 315 320 325
 tgg gat gag cag att ttt gac gaa gtc gca tcg tgg att gaa gct gcc 1123
 Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser Trp Ile Glu Ala Ala
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 taaaaactcg cgaggacgca tgc 1146

<210> 1130

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1130

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Ala Ala Cys Val Ala Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly
 20 25 30

Ser Ser Gly Ser Ser Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp
 35 40 45

Leu Leu Phe Pro Glu Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp
 50 55 60

Pro Leu Asp Asp Ser His Ile Ser Ile His Pro Asp Leu Thr Pro Asp
 65 70 75 80

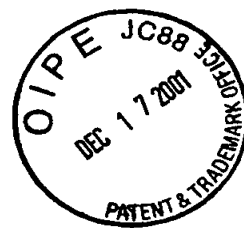
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<222> (101)..(1123)
<223> FRXA02381
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<400> 1131

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Met Ser Val Thr Asn
1 5
ttc cgt cgg ttt ctt gct ggc ata gcg gtc atc gcg gcg tgt gtt gct 163
Phe Arg Arg Phe Leu Ala Gly Ile Ala Val Ile Ala Ala Cys Val Ala
10 15 20
gcg act cca aca gct cag gca caa agc agt ggc tct tct gga tcc tct 211
Ala Thr Pro Thr Ala Gln Ala Gln Ser Ser Gly Ser Ser Gly Ser Ser
25 30 35
ggg tct tca gcg gga tct agc ggg ctg tgg gat tta ctt ttt cca gaa 259
Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp Leu Leu Phe Pro Glu
40 45 50
tcc cat gag tct ttt atc gag cgg ctt ctt gat cct ttg gat gac agc 307
Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp Pro Leu Asp Asp Ser
55 60 65
cat ata tct att cac cct gac ctc acc cca gac ctg tat gaa gag gtg 355
His Ile Ser Ile His Pro Asp Leu Thr Pro Asp Leu Tyr Glu Glu Val
70 75 80 85
ttt gat cca ccg caa att ggt gaa tgc cca gcc gtt gtt gct gtg gtc 403
Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala Val Val Ala Val Val
90 95 100
gca cga ggc agt gaa caa aac ctt caa atc cga ccc gcg cga tac agc 451
Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg Pro Ala Arg Tyr Ser
105 110 115
gag gaa tct cca tgg aca tcc aat gga ttt gag gaa aaa aac ttt cgt 499
Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu Glu Lys Asn Phe Arg
120 125 130
agt ttc ttt ggc cga atg gaa aaa cac tac cgt gaa tcg act ggc gag 547
Ser Phe Phe Gly Arg Met Glu Lys His Tyr Arg Glu Ser Thr Gly Glu
135 140 145
tcg ttg atg aaa gac gtc tac gtg atg ggt ctg aat aat atc gaa tac 595
Ser Leu Met Lys Asp Val Tyr Val Met Gly Leu Asn Asn Ile Glu Tyr
150 155 160 165
cct gct tct ttg cca ctg tct tcg gag gga agc agc gcc att gaa ttg 643
Pro Ala Ser Leu Pro Leu Ser Ser Glu Gly Ser Ser Ala Ile Glu Leu
170 175 180
ggc act tcc att tct agt ggt cgc gac aat gtc atc agc gcg att gat 691
Gly Thr Ser Ile Ser Ser Gly Arg Asp Asn Val Ile Ser Ala Ile Asp
185 190 195
cgc ttt gaa tca gcg aca ggg tgc acg ccg aag tac ctg ttg gcg ggt 739
Arg Phe Glu Ser Ala Thr Gly Cys Thr Pro Lys Tyr Leu Leu Ala Gly
200 205 210
tat tct caa ggt gtc ctc atc gtt gat ggc tat gaa gag gag ttg att 787
Tyr Ser Gln Gly Val Leu Ile Val Asp Gly Tyr Glu Glu Glu Leu Ile



215	220	225	
gcg agg gat cag tac ctc ggc acc ctg cac atc gcg aat cca gcg caa Ala Arg Asp Gln Tyr Leu Gly Thr Leu His Ile Ala Asn Pro Ala Gln 230 235 240 245			835
caa gtt gat gat cca aca ctt gtt ggg cat gaa gta acc acg gga ggc Gln Val Asp Asp Pro Thr Leu Val Gly His Glu Val Thr Thr Gly Gly 250 255 260			883
ttg gct agt tcc gtg gag ccc gtc gag gac aat cct ttc aag gtg agc Leu Ala Ser Ser Val Glu Pro Val Glu Asp Asn Pro Phe Lys Val Ser 265 270 275			931
tac tgc ctg cct gga gac atc gtg tgc gat cgt tct ttt gaa cag ttc Tyr Cys Leu Pro Gly Asp Ile Val Cys Asp Arg Ser Phe Glu Gln Phe 280 285 290			979
tct gct gcg gga tcc tct ata gca gct gcg caa ttg agc acc gga aat Ser Ala Ala Gly Ser Ser Ile Ala Ala Ala Gln Leu Ser Thr Gly Asn 295 300 305			1027
atc cgt cca ggt cga gta cac gtg caa tac ttc gtt acc acc caa ccg Ile Arg Pro Gly Arg Val His Val Gln Tyr Phe Val Thr Thr Gln Pro 310 315 320 325			1075
tgg gat gag cag att ttt gac gaa gtc gca tgc tgg att gaa gct gcc Trp Asp Glu Gln Ile Phe Asp Glu Val Ala Ser Trp Ile Glu Ala Ala 330 335 340			1123
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<213> Corynebacterium glutamicum

<400> 1132

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20 25 30

Ser Ser Gly Ser Ser Gly Ser Ser Ala Gly Ser Ser Gly Leu Trp Asp
35 40 45

Leu Leu Phe Pro Glu Ser His Glu Ser Phe Ile Glu Arg Leu Leu Asp
50 55 60

Pro Leu Asp Asp Ser His Ile Ser Ile His Pro Asp Leu Thr Pro Asp
65 70 75 80

Leu Tyr Glu Glu Val Phe Asp Pro Pro Gln Ile Gly Glu Cys Pro Ala
85 90 95

Val Val Ala Val Val Ala Arg Gly Ser Glu Gln Asn Leu Gln Ile Arg
100 105 110

Pro Ala Arg Tyr Ser Glu Glu Ser Pro Trp Thr Ser Asn Gly Phe Glu

att gtt gat tcc tcc gca tgc ttg cca acg cat gtg gcc gag gac ctc 163
 Ile Val Asp Ser Ser Ala Cys Leu Pro Thr His Val Ala Glu Asp Leu
 10 15 20

gac atc acg gtg att aac ttg cac gtg atg aat aac ggt gaa gaa cgc 211
 Asp Ile Thr Val Ile Asn Leu His Val Met Asn Asn Gly Glu Glu Arg
 25 30 35

agt aca tcc ggg ttg tcg tcg ttg gaa ctt gca gca agt tac gcc cgc 259
 Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala Ala Ser Tyr Ala Arg
 40 45 50

cag ctt gaa cgc ggt ggc gat gac ggt gtg ctt gcg ctg cat att tct 307
 Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu Ala Leu His Ile Ser
 55 60 65

aaa gag ctc tcg tcc acg tgg tcc gca gcg gtg aca gca gcc gct gtg 355
 Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val Thr Ala Ala Val
 70 75 80 85

ttt gat gat gat tct gtg cgc gtg gtg gat acc agt tcg ctc ggt atg 403
 Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr Ser Ser Leu Gly Met
 90 95 100

gct gtg ggt gct gcc gcg atg gct gct gcc cgc atg gct aaa gat ggc 451
 Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg Met Ala Lys Asp Gly
 105 110 115

gcg tct ttg cag gaa tgc tac gac atc gcg gtg gat acc ttg aag cgt 499
 Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val Asp Thr Leu Lys Arg
 120 125 130

tca gaa acc tgg atc tac ctg cac cgc att gat gaa atc tgg aag tcg 547
 Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp Glu Ile Trp Lys Ser
 135 140 145

gga cgg att tcc act gca acc gcc atg gtg tca acg gct ctg gca acc 595
 Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser Thr Ala Leu Ala Thr
 150 155 160 165

cgc ccc atc atg cgt ttc aac ggt ggt cgc atg gag atc gcc gct aag 643
 Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met Glu Ile Ala Ala Lys
 170 175 180

acc cgc acc caa tct aaa gcg ttt gcc aaa ttg gtg gaa tta gcc cag 691
 Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu Val Glu Leu Ala Gln
 185 190 195

atc agg gca gat ggt gaa ccc gta ttc att gcg att ggc caa aac 736
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 200 205 210

<210> 1134

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 1134

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25	30	35	
agt aca tcc ggg ttg tcg tcg ttg gaa ctt gca gca agt tac gcc cgc Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala Ala Ser Tyr Ala Arg			259
40	45	50	
cag ctt gaa cgc ggt ggc gat gac ggt gtg ctt gcg ctg cat att tct Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu Ala Leu His Ile Ser			307
55	60	65	
aaa gag ctc tcg tcc acg tgg tcc gca gcg gtg aca gca gcc gct gtg Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val Thr Ala Ala Ala Val			355
70	75	80	85
ttt gat gat gat tct gtg cgc gtg gtg gat acc agt tcg ctc ggt atg Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr Ser Ser Leu Gly Met			403
90	95	100	
gct gtg ggt gct gcc gcg atg gct gct gcc cgc atg gct aaa gat ggc Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg Met Ala Lys Asp Gly			451
105	110	115	
gcg tct ttg cag gaa tgc tac gac atc gcg gtg gat acc ttg aag cgt Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val Asp Thr Leu Lys Arg			499
120	125	130	
tca gaa acc tgg atc tac ctg cac cgc att gat gaa atc tgg aag tcg Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp Glu Ile Trp Lys Ser			547
135	140	145	
gga cgg att tcc act gca acc gcc atg gtg tca acg gct ctg gca acc Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser Thr Ala Leu Ala Thr			595
150	155	160	165
cgc ccc atc atg cgt ttc aac ggt ggt cgc atg gag atc gcc gct aag Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met Glu Ile Ala Ala Lys			643
170	175	180	
acc cgc acc caa tct aaa gcg ttt gcc aaa ttg gtg gaa tta gcc cag Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu Val Glu Leu Ala Gln			691
185	190	195	
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200			

<210> 1136

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1136

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Val Ala Glu Asp Leu Asp Ile Thr Val Ile Asn Leu His Val Met Asn

20	25	30
Asn Gly Glu Glu Arg Ser Thr Ser Gly Leu Ser Ser Leu Glu Leu Ala 35 40 45		
Ala Ser Tyr Ala Arg Gln Leu Glu Arg Gly Gly Asp Asp Gly Val Leu 50 55 60		
Ala Leu His Ile Ser Lys Glu Leu Ser Ser Thr Trp Ser Ala Ala Val 65 70 75 80		
Thr Ala Ala Ala Val Phe Asp Asp Asp Ser Val Arg Val Val Asp Thr 85 90 95		
Ser Ser Leu Gly Met Ala Val Gly Ala Ala Ala Met Ala Ala Ala Arg 100 105 110		
Met Ala Lys Asp Gly Ala Ser Leu Gln Glu Cys Tyr Asp Ile Ala Val 115 120 125		
Asp Thr Leu Lys Arg Ser Glu Thr Trp Ile Tyr Leu His Arg Ile Asp 130 135 140		
Glu Ile Trp Lys Ser Gly Arg Ile Ser Thr Ala Thr Ala Met Val Ser 145 150 155 160		
Thr Ala Leu Ala Thr Arg Pro Ile Met Arg Phe Asn Gly Gly Arg Met 165 170 175		
Glu Ile Ala Ala Lys Thr Arg Thr Gln Ser Lys Ala Phe Ala Lys Leu 180 185 190		
Val Glu Leu Ala Gln Ile Arg Ala Asp 195 200		

<210> 1137

<211> 885

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(862)

<223> RXN02387

<400> 1137

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ttgttgatg cgtaagccc atccttggtt gctgaagacc gtg tgg tgg tgc tta	115
Val Trp Trp Cys Leu	
1 5	

cca aca tgg atc aaa gca ggc caa gat gct gta gat cta gcc tta tcc	163
Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val Asp Leu Ala Leu Ser	
10 15 20	

gca gca gtt gat ccc agc cct ggt acc tac ttg atc gtc atg cac tct	211
Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu Ile Val Met His Ser	
25 30 35	

ggc ggt gga cgc tct aag tcg atg gtg aag aag ctg gaa aaa gtc gcg 259
 Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys Leu Glu Lys Val Ala
 40 45 50

gtg gtg cac gat gcc gca aag ctg aaa gac cgg gat cgt cca ggt tgg 307
 Val Val His Asp Ala Ala Lys Leu Lys Asp Arg Asp Arg Pro Gly Trp
 55 60 65

gta aaa caa gag ttc aaa aac cac aaa gtc cag gtc acc cca gat gtc 355
 Val Lys Gln Glu Phe Lys Asn His Lys Val Gln Val Thr Pro Asp Val
 70 75 80 85

att cat gct ctt tta gag ggc gtg ggt tca gat ctt aga gag ctg gcg 403
 Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp Leu Arg Glu Leu Ala
 90 95 100

tcc gcc gta tcc caa ttg gtt gag gac acc caa ggc aac gtg acg gtg 451
 Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln Gly Asn Val Thr Val
 105 110 115

gaa aaa gtc cgt gcc tat tac gtg ggt gtt gct gag gta tcg ggt ttc 499
 Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala Glu Val Ser Gly Phe
 120 125 130

gac atc gcc gat tct gca tgc gcc ggt caa atg tca aag gcc gtg gcc 547
 Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met Ser Lys Ala Val Ala
 135 140 145

agc acc aga cgt gcc ctt caa ttg ggt acc agc ccg gtt gca ttg gca 595
 Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser Pro Val Ala Leu Ala
 150 155 160 165

gct gcg ttg agt atg aaa gtt ggc cag atc gcc agg ctg tat tcc acc 643
 Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala Arg Leu Tyr Ser Thr
 170 175 180

agg gga cgc atc aac ggt ttt gag ctg gcc aaa gaa ttg ggc atg ccg 691
 Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys Glu Leu Gly Met Pro
 185 190 195

ccg ttc gtg gtg gag aag act gcg aaa gtg gcc cga aac tgg tcg gga 739
 Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala Arg Asn Trp Ser Gly
 200 205 210

gat gcg gtc agc gag gcc gtg att ttg atg gcc gat ctg gat gcc gct 787
 Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala Asp Leu Asp Ala Ala
 215 220 225

gta aaa gga caa agt ggc gat cct gaa ttt gcc atc gaa tct gcc gtg 835
 Val Lys Gly Gln Ser Gly Asp Pro Glu Phe Ala Ile Glu Ser Ala Val
 230 235 240 245

aga aga gtt gca gag ctg gcg agg cgg taacgctgaa cggcggcggg 882
 Arg Arg Val Ala Glu Leu Ala Arg Arg
 250

taa 885

<210> 1138

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 1138

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Ile Val Met His Ser Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys
35 40 45
Leu Glu Lys Val Ala Val Val His Asp Ala Ala Lys Leu Lys Asp Arg
50 55 60
Asp Arg Pro Gly Trp Val Lys Gln Glu Phe Lys Asn His Lys Val Gln
65 70 75 80
Val Thr Pro Asp Val Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp
85 90 95
Leu Arg Glu Leu Ala Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln
100 105 110
Gly Asn Val Thr Val Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala
115 120 125
Glu Val Ser Gly Phe Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met
130 135 140
Ser Lys Ala Val Ala Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser
145 150 155 160
Pro Val Ala Leu Ala Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala
165 170 175
Arg Leu Tyr Ser Thr Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys
180 185 190
Glu Leu Gly Met Pro Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala
195 200 205
Arg Asn Trp Ser Gly Asp Ala Val Ser Glu Ala Val Ile Leu Met Ala
210 215 220
Asp Leu Asp Ala Ala Val Lys Gly Gln Ser Gly Asp Pro Glu Phe Ala
225 230 235 240
Ile Glu Ser Ala Val Arg Arg Val Ala Glu Leu Ala Arg Arg
245 250

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<211> 778

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(778)

<400> 1139

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1 5

cca aca tgg atc aaa gca ggc caa gat gct gta gat cta gcc tta tcc 163
Pro Thr Trp Ile Lys Ala Gly Gln Asp Ala Val Asp Leu Ala Leu Ser
10 15 20

gca gca gtt gat ccc agc cct ggt acc tac ttg atc gtc atg cac tct 211
Ala Ala Val Asp Pro Ser Pro Gly Thr Tyr Leu Ile Val Met His Ser
25 30 35

ggc ggt gga cgc tct aag tcg atg gtg aag aag ctg gaa aaa gtc gcg 259
Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys Leu Glu Lys Val Ala
40 45 50

gtg gtg cac gat gcc gca aag ctg aaa gac cgg gat cgt cca ggt tgg 307
Val Val His Asp Ala Ala Lys Leu Lys Asp Arg Asp Arg Pro Gly Trp
55 60 65

gta aaa caa gag ttc aaa aac cac aaa gtc cag gtc acc cca gat gtc 355
Val Lys Gln Glu Phe Lys Asn His Lys Val Gln Val Thr Pro Asp Val
70 75 80 85

att cat gct ctt tta gag ggc gtg ggt tca gat ctt aga gag ctg gcg 403
Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp Leu Arg Glu Leu Ala
90 95 100

tcc gcc gta tcc caa ttg gtt gag gac acc caa ggc aac gtg acg gtg 451
Ser Ala Val Ser Gln Leu Val Glu Asp Thr Gln Gly Asn Val Thr Val
105 110 115

gaa aaa gtc cgt gcc tat tac gtg ggt gtt gct gag gta tcg ggt ttc 499
Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala Glu Val Ser Gly Phe
120 125 130

gac atc gcc gat tct gca tgc gcc ggt caa atg tca aag gcc gtg gcc 547
Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met Ser Lys Ala Val Ala
135 140 145

agc acc aga cgt gcc ctt caa ttg ggt acc agc ccg gtt gca ttg gca 595
 Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser Pro Val Ala Leu Ala
 150 155 160 165

gct gcg ttg agt atg aaa gtt ggc cag atc gcc agg ctg tat tcc acc 643
Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala Arg Leu Tyr Ser Thr
170 175 180

agg gga cgc atc aac ggt ttt gag ctg gcc aaa gaa ttg ggc atg ccg 691
Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys Glu Leu Gly Met Pro
185 190 195

ccg ttc gtg gtg gag aag act gcg aaa gtg gcc cga aac tgg tcg gga 739
Pro Phe Val Val Glu Lys Thr Ala Lys Val Ala Arg Asn Trp Ser Gly
200 205 210

gat gcg gtc agc gag gcc gtg att ttg atg gcc gat ctg
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778

<210> 1140
 <211> 226
 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Ile Val Met His Ser Gly Gly Gly Arg Ser Lys Ser Met Val Lys Lys
 35 40 45
 Leu Glu Lys Val Ala Val Val His Asp Ala Ala Lys Leu Lys Asp Arg
 50 55 60
 Asp Arg Pro Gly Trp Val Lys Gln Glu Phe Lys Asn His Lys Val Gln
 65 70 75 80
 Val Thr Pro Asp Val Ile His Ala Leu Leu Glu Gly Val Gly Ser Asp
 85 90 95
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 100 105 110
 Gly Asn Val Thr Val Glu Lys Val Arg Ala Tyr Tyr Val Gly Val Ala
 115 120 125
 Glu Val Ser Gly Phe Asp Ile Ala Asp Ser Ala Cys Ala Gly Gln Met
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 Ser Lys Ala Val Ala Ser Thr Arg Arg Ala Leu Gln Leu Gly Thr Ser
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 Pro Val Ala Leu Ala Ala Ala Leu Ser Met Lys Val Gly Gln Ile Ala
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 Arg Leu Tyr Ser Thr Arg Gly Arg Ile Asn Gly Phe Glu Leu Ala Lys
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 Asp Leu
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<220>

<221> CDS

<222> (101)..(1702)

<223> RXN02398

<400> 1141

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aag cgt aat ctc ctc gta gct ccc ctc act gct tcc ctg gtg ttc tgt 163
Lys Arg Asn Leu Leu Val Ala Pro Leu Thr Ala Ser Leu Val Phe Cys
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aac ttg gct gtt gca gca aac gcc gtt gaa gtt gag gcc gaa tca cca 211
Asn Leu Ala Val Ala Ala Asn Ala Val Glu Val Glu Ala Glu Ser Pro
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gtt gtc atc aat gaa gtt gaa tcc aac agc gac cca gtt ggt gac tgg 259
Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp Pro Val Gly Asp Trp
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gtg gag ttg gct aac acc gac aac aac aac tcc atc gac att tcc ggt 307
Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser Ile Asp Ile Ser Gly
                55                60                65

tgg tcc tta gtc gat gac aag gaa gac ctg gaa aat gcc ctc gtc ctt 355
Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu Asn Ala Leu Val Leu
                70                75                80                85

cct gaa ggc act gag att gag tcc ggt gga tac ttt gtt atc tac acc 403
Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr Phe Val Ile Tyr Thr
                90                95                100

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Asp Ser Ala Asp Tyr Val Pro Thr Asn Asn Thr Phe Gly Gly Gln Glu
                105                110                115

tac ttc ggc ctc ggc aaa gat gac act gtt act ctg cgc aac gct gaa 499
Tyr Phe Gly Leu Gly Lys Asp Asp Thr Val Thr Leu Arg Asn Ala Glu
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Gly Glu Val Val Ala Thr Tyr Ser Trp Lys Asp Leu Gly Glu His Ala
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gaa aac acc tat ggt cgc atc cca gat atg act ggt gat ttc gca aac 595
Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr Gly Asp Phe Ala Asn
                150                155                160                165

acc ggc gtt cca acc cca ggt gca aag aat gtt gct gct gaa ggc tcc 643
Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val Ala Ala Glu Gly Ser
                170                175                180

ggc gaa gaa gaa ggc gtt gtt gca aac gcc cag ctt cca ttc cac aac 691
Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln Leu Pro Phe His Asn
                185                190                195

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aat gac att gga aag atc tac tcc ctc gcc cac gac ata gct aac aac Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His Asp Ile Ala Asn Asn 230 235 240 245	835
acc tac aag ctg act ggc gaa tgg gaa acc ggc tac cca gaa ggc ggc Thr Tyr Lys Leu Thr Gly Glu Trp Glu Thr Gly Tyr Pro Glu Gly Gly 250 255 260	883
gga gag cca gac gct gaa ggc atc gtc gca gct acc aac ggt gac atc Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala Thr Asn Gly Asp Ile 265 270 275	931
tac ctg tcc acc gag cgc aac aac gct gac aag aac gtc tct cgc cca Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys Asn Val Ser Arg Pro 280 285 290	979
tcc atc ctg cgt ttt gct acc cca act ggc aag act ggc gta caa aac Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys Thr Gly Val Gln Asn 295 300 305	1027
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Leu Gly Glu His Ala Glu Asn Thr Tyr Gly Arg Ile Pro Asp Met Thr
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 Gly Asp Phe Ala Asn Thr Gly Val Pro Thr Pro Gly Ala Lys Asn Val
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 Ala Ala Glu Gly Ser Gly Glu Glu Glu Gly Val Val Ala Asn Ala Gln
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 Leu Pro Phe His Asn Val Glu Ile Thr Pro Ile His Leu Gly Gly Asp
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 Phe Thr Gly Glu Asp Met Ser Gly Val Asp Phe Asp Ala Asn Ser Thr
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 Ala Trp Ile Ala Asn Asn Asp Ile Gly Lys Ile Tyr Ser Leu Ala His
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 Tyr Pro Glu Gly Gly Gly Glu Pro Asp Ala Glu Gly Ile Val Ala Ala
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 Thr Asn Gly Asp Ile Tyr Leu Ser Thr Glu Arg Asn Asn Ala Asp Lys
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 Asn Val Ser Arg Pro Ser Ile Leu Arg Phe Ala Thr Pro Thr Gly Lys
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 Thr Gly Val Gln Asn Ala Val Gln Glu Trp Asp Leu Ser Glu Phe Val
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 Gly Asp Ile Gln Pro Asn Gly Gly Leu Glu Ala Ile Ala Gln Leu Glu
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 Asp Asn Ile Phe Val Val Gly Val Glu Glu Thr Gly Asp Val Ile Val
 340 345 350
 Val Asp Leu Ser Ala Asp Gln Pro Val Leu Val Gln Arg Tyr Glu Ser
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 405 410 415
 Arg Pro Ala Asn Leu Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr
 420 425 430
 Thr Ser Glu Leu Lys Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser
 435 440 445
 Tyr Leu Trp Ala Asp Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn
 450 455 460
 Ser Ala Gln Val Ile Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly

Tyr	Phe	Gly	Leu	Gly	Lys	Asp	Asp	Thr	Val	Thr	Leu	Arg	Asn	Ala	Glu		
		120					125					130					
ggc	gaa	gta	gtt	gct	acc	tat	tcc	tgg	aag	gat	ctg	ggc	gag	cac	gca	547	
Gly	Glu	Val	Val	Ala	Thr	Tyr	Ser	Trp	Lys	Asp	Leu	Gly	Glu	His	Ala		
	135					140					145						
gaa	aac	acc	tat	ggt	cgc	atc	cca	gat	atg	act	ggt	gat	ttc	gca	aac	595	
Glu	Asn	Thr	Tyr	Gly	Arg	Ile	Pro	Asp	Met	Thr	Gly	Asp	Phe	Ala	Asn		
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acc	ggc	gtt	cca	acc	cca	ggt	gca	aag	aat	gtt	gct	gct	gaa	ggc	tcc	643	
Thr	Gly	Val	Pro	Thr	Pro	Gly	Ala	Lys	Asn	Val	Ala	Ala	Glu	Gly	Ser		
				170					175					180			
ggc	gaa	gaa	gaa	ggc	gtt	gtt	gca	aac	gcc	cag	ctt	cca	ttc	cac	aac	691	
Gly	Glu	Glu	Glu	Gly	Val	Val	Ala	Asn	Ala	Gln	Leu	Pro	Phe	His	Asn		
		185					190						195				
gtt	gaa	atc	acc	cca	att	cac	ctc	ggt	gga	gat	ttc	acc	ggt	gaa	gat	739	
Val	Glu	Ile	Thr	Pro	Ile	His	Leu	Gly	Gly	Asp	Phe	Thr	Gly	Glu	Asp		
	200						205					210					
atg	tcc	ggc	gtt	gat	ttc	gat	gca	aac	agc	acc	gca	tgg	atc	gcc	aac	787	
Met	Ser	Gly	Val	Asp	Phe	Asp	Ala	Asn	Ser	Thr	Ala	Trp	Ile	Ala	Asn		
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aat	gac	att	gga	aag	atc	tac	tcc	ctc	gcc	cac	gac	ata	gct	aac	aac	835	
Asn	Asp	Ile	Gly	Lys	Ile	Tyr	Ser	Leu	Ala	His	Asp	Ile	Ala	Asn	Asn		
230					235					240					245		
acc	tac	aag	ctg	act	ggc	gaa	tgg	gaa	acc	ggc	tac	cca	gaa	ggc	ggc	883	
Thr	Tyr	Lys	Leu	Thr	Gly	Glu	Trp	Glu	Thr	Gly	Tyr	Pro	Glu	Gly	Gly		
			250					255						260			
gga	gag	cca	gac	gct	gaa	ggc	atc	gtc	gca	gct	acc	aac	ggt	gac	atc	931	
Gly	Glu	Pro	Asp	Ala	Glu	Gly	Ile	Val	Ala	Ala	Thr	Asn	Gly	Asp	Ile		
		265						270					275				
tac	ctg	tcc	acc	gag	cgc	aac	aac	gct	gac	aag	aac	gtc	tct	cgc	cca	979	
Tyr	Leu	Ser	Thr	Glu	Arg	Asn	Asn	Ala	Asp	Lys	Asn	Val	Ser	Arg	Pro		
		280					285					290					
tcc	atc	ctg	cgt	ttt	gct	acc	cca	act	ggc	aag	act	ggc	gta	caa	aac	1027	
Ser	Ile	Leu	Arg	Phe	Ala	Thr	Pro	Thr	Gly	Lys	Thr	Gly	Val	Gln	Asn		
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Ala	Val	Gln	Glu	Trp	Asp	Leu	Ser	Glu	Phe	Val	Gly	Asp	Ile	Gln	Pro		
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Asn	Gly	Gly	Leu	Glu	Ala	Ile	Ala	Gln	Leu	Glu	Asp	Asn	Ile	Phe	Val		
			330						335					340			
gtc	ggt	gtc	gaa	gag	aca	ggt	gat	gtc	atc	gtt	gtt	gat	ctt	tcc	gct	1171	
Val	Gly	Val	Glu	Glu	Thr	Gly	Asp	Val	Ile	Val	Val	Asp	Leu	Ser	Ala		
			345					350					355				
gac	cag	cca	gtt	ctg	gtt	caa	agg	tac	gaa	tct	tcc	ttc	gac	ggt	gtc	1219	
Asp	Gln	Pro	Val	Leu	Val	Gln	Arg	Tyr	Glu	Ser	Ser	Phe	Asp	Gly	Val		

360	365	370	
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Met Ser Leu Asp Tyr Asn Ala Ala Thr Lys Gln Leu Ser Val Val Cys			
375	380	385	
gac gaa gca tgt gac ggc ttg tct gaa atc ctc gaa tgg gat ggc gag			1315
Asp Glu Ala Cys Asp Gly Leu Ser Glu Ile Leu Glu Trp Asp Gly Glu			
390	395	400	405
aag ctg tac aag tcc gac gac aag atc tac gag cgt cca gca aac ctg			1363
Lys Leu Tyr Lys Ser Asp Asp Lys Ile Tyr Glu Arg Pro Ala Asn Leu			
410	415		420
ggc aac tgg gct aac gaa ggc ttc ggc acc tac acc tca gag ctt aaa			1411
Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr Thr Ser Glu Leu Lys			
425	430		435
tgc gag aac ggc aac acc gtt tct gtc acc agc tac ctc tgg gct gac			1459
Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser Tyr Leu Trp Ala Asp			
440	445		450
gat gca gca acc aac gaa ggc acc tcc ctc aac tcc gca cag gtc atc			1507
Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn Ser Ala Gln Val Ile			
455	460		465
aac gga gat tgc ggc gac gtc aac atc cct gga gag tcc tct tcc gac			1555
Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly Glu Ser Ser Ser Asp			
470	475	480	485
aat tcc tct tct gac ttt gca acc ggc agc atc gca ggc gcc ttt gca			1603
Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile Ala Gly Ala Phe Ala			
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Thr Ala Val Leu Ala Val Val Gly Ile			
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Glu Ala Glu Ser Pro Val Val Ile Asn Glu Val Glu Ser Asn Ser Asp			
35	40		45
Pro Val Gly Asp Trp Val Glu Leu Ala Asn Thr Asp Asn Asn Asn Ser			
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Ile Asp Ile Ser Gly Trp Ser Leu Val Asp Asp Lys Glu Asp Leu Glu			
65	70	75	80
Asn Ala Leu Val Leu Pro Glu Gly Thr Glu Ile Glu Ser Gly Gly Tyr			

Arg Pro Ala Asn Leu Gly Asn Trp Ala Asn Glu Gly Phe Gly Thr Tyr
 420 425 430

Thr Ser Glu Leu Lys Cys Glu Asn Gly Asn Thr Val Ser Val Thr Ser
 435 440 445

Tyr Leu Trp Ala Asp Asp Ala Ala Thr Asn Glu Gly Thr Ser Leu Asn
 450 455 460

Ser Ala Gln Val Ile Asn Gly Asp Cys Gly Asp Val Asn Ile Pro Gly
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Glu Ser Ser Ser Asp Asn Ser Ser Ser Asp Phe Ala Thr Gly Ser Ile
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<210> 1145

<211> 672

<212> DNA

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<220>

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<222> (101)..(649)

<223> RXN02406

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 Met Glu Thr Leu Ala
 1 5

gca caa gcg cgc acc ctg cta gaa aaa tgg ggc gtc gcg ccg acg cac 163
 Ala Gln Ala Arg Thr Leu Leu Glu Lys Trp Gly Val Ala Pro Thr His
 10 15 20

gca tct ttc gtc gaa tcc att gca aag gcc atc ccg att ctg tcg atc 211
 Ala Ser Phe Val Glu Ser Ile Ala Lys Ala Ile Pro Ile Leu Ser Ile
 25 30 35

ctg ctg acg ctg att gtc acc gtg aat gga att tca agc gga aat ccg 259
 Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile Ser Ser Gly Asn Pro
 40 45 50

gtc cag cca cca gca ctg gaa cag gta cgg acc gat gta gtg aac aag 307
 Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr Asp Val Val Asn Lys
 55 60 65

atc aac tac gaa cgc aac cta aag ggc ctc gtc tcg atc agc ccg gag 355
 Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val Ser Ile Ser Pro Glu
 70 75 80 85

ctt gaa tta cac acg gca gcc caa aca att gcg cag cga aat gca gac 403
 Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala Gln Arg Asn Ala Asp
 90 95 100

Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr Lys Gly Asp His Ala
 150 155 160 165

tgg ata gtg gtg gag ttc act gta gct ccc gct gat tcc gta gaa tca 643
 Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala Asp Ser Val Glu Ser
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aca gag tgaataccaa tccgtctgaa ttc 672
 Thr Glu

<210> 1148

<211> 183

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1148

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 20 25 30

Pro Ile Leu Ser Ile Leu Leu Thr Leu Ile Val Thr Val Asn Gly Ile
 35 40 45

Ser Ser Gly Asn Pro Val Gln Pro Pro Ala Leu Glu Gln Val Arg Thr
 50 55 60

Asp Val Val Asn Lys Ile Asn Tyr Glu Arg Asn Leu Lys Gly Leu Val
 65 70 75 80

Ser Ile Ser Pro Glu Leu Glu Leu His Thr Ala Ala Gln Thr Ile Ala
 85 90 95

Gln Arg Asn Ala Asp Ser Asp Ser Glu Glu Lys Val Pro Asp Pro Glu
 100 105 110

Gly Thr Leu Val Val Leu Gln Gln Asn Leu Pro Tyr Ala Asn Ala Asn
 115 120 125

Ala Asp Thr Ile Val Asp Arg Phe Leu Asn Ser Pro Asp His Val Lys
 130 135 140

Leu Leu Leu Ala Asn Asp Tyr Glu Ala Ile Gly Val Gly Val Ala Tyr
 145 150 155 160

Lys Gly Asp His Ala Trp Ile Val Val Glu Phe Thr Val Ala Pro Ala
 165 170 175

Asp Ser Val Glu Ser Thr Glu
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<210> 1149

<211> 495

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<400> 1149

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                                         Met Asn Arg Gln Asn
                                         1           5
caa ctt cac tac ccg cag gaa gtg aag gca gtg gaa agt gtg gaa tca 163
Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val Glu Ser Val Glu Ser
                10                15                20
agc ttg aac atg tcg tca cct tct gca ccg ctt gcc acg cca gat gtt 211
Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu Ala Thr Pro Asp Val
                25                30                35
gag ctt gat gtg cac acg ttg tcg agc gaa aac ctg cct tgg ttg tgc 259
Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn Leu Pro Trp Leu Cys
                40                45                50
atc gtg tgg gat gat ccg gtc aat ttg atg agc tat gtc acc tac gtt 307
Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser Tyr Val Thr Tyr Val
                55                60                65
ttt cag act gtg ttg ggc ttc agt aag aag agg gcc act gag ctg atg 355
Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg Ala Thr Glu Leu Met
                70                75                80                85
atg cag gtg cac acc gaa ggt aaa gcc gtg gtg agt tct ggc gag aag 403
Met Gln Val His Thr Glu Gly Lys Ala Val Val Ser Ser Gly Glu Lys
                90                95                100
gac aaa gtg gag ggt gat gtg aag aaa ctc cac acc gca ggg ctg tgg 451
Asp Lys Val Glu Gly Asp Val Lys Lys Leu His Thr Ala Gly Leu Trp
                105                110                115
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<400> 1150

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  20                25                30
Ala Thr Pro Asp Val Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn
  35                40                45
Leu Pro Trp Leu Cys Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser
  50                55                60

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Tyr Val Thr Tyr Val Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg
 65 70 75 80
 Ala Thr Glu Leu Met Met Gln Val His Thr Glu Gly Lys Ala Val Val
 85 90 95
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 Thr Ala Gly Leu Trp Ala Thr Met Gln Gln Ala Gly
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 <223> FRXA02407

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 Met Asn Arg Gln Asn
 1 5
 caa ctt cac tac ccg cag gaa gtg aag gca gtg gaa agt gtg gaa tca 163
 Gln Leu His Tyr Pro Gln Glu Val Lys Ala Val Glu Ser Val Glu Ser
 10 15 20
 agc ttg aac atg tcg tca cct tct gca ccg ctt gcc acg cca gat gtt 211
 Ser Leu Asn Met Ser Ser Pro Ser Ala Pro Leu Ala Thr Pro Asp Val
 25 30 35
 gag ctt gat gtg cac acg ttg tcg agc gaa aac ctg cct tgg ttg tgc 259
 Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn Leu Pro Trp Leu Cys
 40 45 50
 atc gtg tgg gat gat ccg gtc aat ttg atg agc tat gtc acc tac gtt 307
 Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser Tyr Val Thr Tyr Val
 55 60 65
 ttt cag act gtg ttg ggc ttc agt aag aag agg gcc act gag ctg atg 355
 Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg Ala Thr Glu Leu Met
 70 75 80 85
 atg cag gtg cac acc gaa ggt aaa gcc gtg gtg agt tct ggc gag aag 403
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 Asp

<210> 1152

<211> 102

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

Ala Thr Pro Asp Val Glu Leu Asp Val His Thr Leu Ser Ser Glu Asn
 35 40 45

Leu Pro Trp Leu Cys Ile Val Trp Asp Asp Pro Val Asn Leu Met Ser
 50 55 60

Tyr Val Thr Tyr Val Phe Gln Thr Val Leu Gly Phe Ser Lys Lys Arg
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Ala Thr Glu Leu Met Met Gln Val His Thr Glu Gly Lys Ala Val Val
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Ser Ser Gly Glu Lys Asp
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<210> 1153

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<220>

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<222> (101)..(1012)

<223> RXN02408

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 Met Leu Ile Asp Val
 1 5

gcg ggc ttc ctt tta ggc cac gtc acg aag ggg gat acg ggt tgc tca 163
 Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly Asp Thr Gly Cys Ser
 10 15 20

gtg gtc att gca cct aac ggt gca ttt gcg ggc gtc gat gtc cgt ggg 211
 Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly Val Asp Val Arg Gly
 25 30 35

gga ggc cca ggc acc agg gaa acc gac ctt cta gaa cca cac aat tct 259
 Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu Glu Pro His Asn Ser
 40 45 50

gtg cag caa gca cat gcc gtg gtg ttg tgt ggc ggt tcg gcg ttc ggg 307
 Val Gln Gln Ala His Ala Val Val Leu Cys Gly Gly Ser Ala Phe Gly
 55 60 65

ttg gct gct gcc gat gga gtg atg aca gcc cta gaa aac cgc ggt att 355

[illegible]

<210> 1154

<211> 304

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1154

Met Leu Ile Asp Val Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly
1 5 10 15
Asp Thr Gly Cys Ser Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly
20 25 30
Val Asp Val Arg Gly Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu
35 40 45
Glu Pro His Asn Ser Val Gln Gln Ala His Ala Val Val Leu Cys Gly
50 55 60
Gly Ser Ala Phe Gly Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu
65 70 75 80
Glu Asn Arg Gly Ile Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val
85 90 95
Pro Ile Val Pro Gly Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro
100 105 110
Lys Asn Arg Pro Thr Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala
115 120 125
Phe Ala Gly Thr His Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly
130 135 140
Ala Thr Ala Gly Arg Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg
145 150 155 160
Val Gly Lys Tyr Thr Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly
165 170 175
Glu Val Val Asp Leu Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val
180 185 190
Met Gly Val Gly Val Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn
195 200 205
Thr Thr Ile Gly Val Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln
210 215 220
Ala Lys Arg Leu Ala Leu Val Ala His Asp Gly Leu Ala Arg Ala Val
225 230 235 240
Arg Pro Ser His Ser Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser
245 250 255
Ser Gly Asp Gly Ser Gly Val Thr Pro Val Glu Leu Ala Glu Leu Ser
260 265 270
Ala His Ala Ala Asp Cys Val Gln Asp Ala Ile Ile Asp Ala Ile Leu
275 280 285

atc gcg gca ggg gtc gtg gcg aat cct gtt ggg gaa gtc gtg gac cta 643
 Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly Glu Val Val Asp Leu
 170 175 180

aca act gga gct ttg ttt ggt agg ccc gaa gtg atg ggg gtg ggc gtc 691
 Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val Met Gly Val Gly Val
 185 190 195

gat aag cta aaa agc gcg gca gag acg ctg aac acg acc atc ggc gtc 739
 Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn Thr Thr Ile Gly Val
 200 205 210

gtg gca act gac gcg ccg gtg aca aaa gcc caa gcg aag cgc ttg gcg 787
 Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln Ala Lys Arg Leu Ala
 215 220 225

ctg gtg gcc cat gat ggt ttg gcg agg gca gtg cgg ccg tcg cat tca 835
 Leu Val Ala His Asp Gly Leu Ala Arg Ala Val Arg Pro Ser His Ser
 230 235 240 245

ccg atg gac ggt gac aca ttt ttc gcc atg tca tcg ggt gat ggt agt 883
 Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser Ser Gly Asp Gly Ser
 250 255 260

ggc gtt acc ccg gtt gag ctg ggg gaa ttg tcg gct cat gct gca 928
 Gly Val Thr Pro Val Glu Leu Gly Glu Leu Ser Ala His Ala Ala
 265 270 275

<210> 1156

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 1156

Met Leu Ile Asp Val Ala Gly Phe Leu Leu Gly His Val Thr Lys Gly
 1 5 10 15

Asp Thr Gly Cys Ser Val Val Ile Ala Pro Asn Gly Ala Phe Ala Gly
 20 25 30

Val Asp Val Arg Gly Gly Gly Pro Gly Thr Arg Glu Thr Asp Leu Leu
 35 40 45

Glu Pro His Asn Ser Val Gln Gln Ala His Ala Val Val Leu Cys Gly
 50 55 60

Gly Ser Ala Phe Gly Leu Ala Ala Ala Asp Gly Val Met Thr Ala Leu
 65 70 75 80

Glu Asn Arg Gly Ile Gly Phe Pro Val Arg Pro Glu Gly Pro Ile Val
 85 90 95

Pro Ile Val Pro Gly Ala Val Ile Phe Asp Leu Leu Val Gly Asp Pro
 100 105 110

Lys Asn Arg Pro Thr Ala Ala Asp Gly Glu Gln Ala Val Glu Asn Ala
 115 120 125

Phe Ala Gly Thr His Asn Gly Ser Gly Ser Val Gly Ala Gly Thr Gly
 130 135 140

Ala Thr Ala Gly Arg Leu Arg Gly Gly Phe Gly Gln Ser Ser Arg Arg
 145 150 155 160

Val Gly Lys Tyr Thr Ile Ala Ala Gly Val Val Ala Asn Pro Val Gly
 165 170 175

Glu Val Val Asp Leu Thr Thr Gly Ala Leu Phe Gly Arg Pro Glu Val
 180 185 190

Met Gly Val Gly Val Asp Lys Leu Lys Ser Ala Ala Glu Thr Leu Asn
 195 200 205

Thr Thr Ile Gly Val Val Ala Thr Asp Ala Pro Val Thr Lys Ala Gln
 210 215 220

Ala Lys Arg Leu Ala Leu Val Ala His Asp Gly Leu Ala Arg Ala Val
 225 230 235 240

Arg Pro Ser His Ser Pro Met Asp Gly Asp Thr Phe Phe Ala Met Ser
 245 250 255

Ser Gly Asp Gly Ser Gly Val Thr Pro Val Glu Leu Gly Glu Leu Ser
 260 265 270

Ala His Ala Ala
 275

<210> 1157

<211> 660

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(637)

<223> RXN02409

<400> 1157

gagttctggc gagaaggaca aagtggaggg tgatgtgaag aaactccaca ccgcagggct 60

gtgggcgaca atgcagcagg cagggtaggg gagaattttc atg cag cag tgg aag 115
 Met Gln Gln Trp Lys
 1 5

aag aaa aaa ggg ctg atg cgc cag gct cgt tac gcg gtg gtt ttt gag 163
 Lys Lys Lys Gly Leu Met Arg Gln Ala Arg Tyr Ala Val Val Phe Glu
 10 15 20

ccg atg gag cgg gaa gtg ttg ggt gat ttg tca gct gcg gtc agt gag 211
 Pro Met Glu Arg Glu Val Leu Gly Asp Leu Ser Ala Ala Val Ser Glu
 25 30 35

gcg ttg att cag cgt gca cag tct gtg ccg aag gat cct ctg gca gag 259
 Ala Leu Ile Gln Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu
 40 45 50

atg acc ggc atg aca agt gga cac aaa gaa gca cca acc gat ccg gcg 307
 Met Thr Gly Met Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala
 55 60 65

ctt gcg cgt ttg ctc cct gat ttt cag cac gag ggc gat gag gaa tac 355
 Leu Ala Arg Leu Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr
 70 75 80 85
 gac ggc gat aat tct ttc ctc cgt tca ctc cat gaa ggc gac atc acc 403
 Asp Gly Asp Asn Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr
 90 95 100
 cga gca aaa ctg gaa aat ctg cgc gtg att aac gat gcg ctg gga ccc 451
 Arg Ala Lys Leu Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro
 105 110 115
 gac gga aat gtt gcg gtc acc gcc tct gag gag gaa gcg cac gct tgg 499
 Asp Gly Asn Val Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp
 120 125 130
 ttg gct gcg ctc aat gac atc cgc ctg tac gtt gcc tcc ggt gat gta 547
 Leu Ala Ala Leu Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val
 135 140 145
 cgc ggc ggg gaa gcc gcc gag gaa gac cgc gaa aac ctc gtg cag tgg 595
 Arg Gly Gly Glu Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp
 150 155 160 165
 ctt gcc tac aat caa gag tcc ttg ctg gaa gcg atg atg aat 637
 Leu Ala Tyr Asn Gln Glu Ser Leu Leu Glu Ala Met Met Asn
 170 175
 taatgcttat cgacgtcgcg ggc 660

<210> 1158

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 1158

Met Gln Gln Trp Lys Lys Lys Lys Gly Leu Met Arg Gln Ala Arg Tyr
 1 5 10 15
 Ala Val Val Phe Glu Pro Met Glu Arg Glu Val Leu Gly Asp Leu Ser
 20 25 30
 Ala Ala Val Ser Glu Ala Leu Ile Gln Arg Ala Gln Ser Val Pro Lys
 35 40 45
 Asp Pro Leu Ala Glu Met Thr Gly Met Thr Ser Gly His Lys Glu Ala
 50 55 60
 Pro Thr Asp Pro Ala Leu Ala Arg Leu Leu Pro Asp Phe Gln His Glu
 65 70 75 80
 Gly Asp Glu Glu Tyr Asp Gly Asp Asn Ser Phe Leu Arg Ser Leu His
 85 90 95
 Glu Gly Asp Ile Thr Arg Ala Lys Leu Glu Asn Leu Arg Val Ile Asn
 100 105 110
 Asp Ala Leu Gly Pro Asp Gly Asn Val Ala Val Thr Ala Ser Glu Glu
 115 120 125

Glu Ala His Ala Trp Leu Ala Ala Leu Asn Asp Ile Arg Leu Tyr Val
 130 135 140

Ala Ser Gly Asp Val Arg Gly Gly Glu Ala Ala Glu Glu Asp Arg Glu
 145 150 155 160

Asn Leu Val Gln Trp Leu Ala Tyr Asn Gln Glu Ser Leu Leu Glu Ala
 165 170 175

Met Met Asn

<210> 1159
 <211> 437
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(414)
 <223> FRXA02409

<400> 1159

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Arg Ala Gln Ser Val Pro Lys Asp Pro Leu Ala Glu Met Thr Gly Met	
1 5 10 15	
aca agt gga cac aaa gaa gca cca acc gat ccg gcg ctt gcg cgt ttg	96
Thr Ser Gly His Lys Glu Ala Pro Thr Asp Pro Ala Leu Ala Arg Leu	
20 25 30	
ctc cct gat ttt cag cac gag ggc gat gag gaa tac gac ggc gat aat	144
Leu Pro Asp Phe Gln His Glu Gly Asp Glu Glu Tyr Asp Gly Asp Asn	
35 40 45	
tct ttc ctc cgt tca ctc cat gaa ggc gac atc acc cga gca aaa ctg	192
Ser Phe Leu Arg Ser Leu His Glu Gly Asp Ile Thr Arg Ala Lys Leu	
50 55 60	
gaa aat ctg cgc gtg att aac gat gcg ctg gga ccc gac gga aat gtt	240
Glu Asn Leu Arg Val Ile Asn Asp Ala Leu Gly Pro Asp Gly Asn Val	
65 70 75 80	
gcg gtc acc gcc tct gag gag gaa gcg cac gct tgg ttg gct gcg ctc	288
Ala Val Thr Ala Ser Glu Glu Glu Ala His Ala Trp Leu Ala Ala Leu	
85 90 95	
aat gac atc cgc ctg tac gtt gcc tcc ggt gat gta cgc ggc ggg gaa	336
Asn Asp Ile Arg Leu Tyr Val Ala Ser Gly Asp Val Arg Gly Gly Glu	
100 105 110	
gcc gcc gag gaa gac cgc gaa aac ctc gtg cag tgg ctt gcc tac aat	384
Ala Ala Glu Glu Asp Arg Glu Asn Leu Val Gln Trp Leu Ala Tyr Asn	
115 120 125	
caa gag tcc ttg ctg gaa gcg atg atg aat taatgcttat cgacgtcgcg	434
Gln Glu Ser Leu Leu Glu Ala Met Met Asn	
130 135	

ggc

437

<210> 1160

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 1160

Arg	Ala	Gln	Ser	Val	Pro	Lys	Asp	Pro	Leu	Ala	Glu	Met	Thr	Gly	Met
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Thr	Ser	Gly	His	Lys	Glu	Ala	Pro	Thr	Asp	Pro	Ala	Leu	Ala	Arg	Leu
			20					25					30		

Leu	Pro	Asp	Phe	Gln	His	Glu	Gly	Asp	Glu	Glu	Tyr	Asp	Gly	Asp	Asn
		35					40					45			

Ser	Phe	Leu	Arg	Ser	Leu	His	Glu	Gly	Asp	Ile	Thr	Arg	Ala	Lys	Leu
	50					55					60				

Glu	Asn	Leu	Arg	Val	Ile	Asn	Asp	Ala	Leu	Gly	Pro	Asp	Gly	Asn	Val
65					70					75					80

Ala	Val	Thr	Ala	Ser	Glu	Glu	Glu	Ala	His	Ala	Trp	Leu	Ala	Ala	Leu
				85					90					95	

Asn	Asp	Ile	Arg	Leu	Tyr	Val	Ala	Ser	Gly	Asp	Val	Arg	Gly	Gly	Glu
			100					105					110		

Ala	Ala	Glu	Glu	Asp	Arg	Glu	Asn	Leu	Val	Gln	Trp	Leu	Ala	Tyr	Asn
		115					120					125			

Gln	Glu	Ser	Leu	Leu	Glu	Ala	Met	Met	Asn
130						135			

<210> 1161

<211> 1257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1234)

<223> RXN02428

<400> 1161

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ttcagtttagc	gtgaagggtgc	catcatcaca	agggttgatg	atg	gcc	gcg	acg	tta	115
				Met	Ala	Ala	Thr	Leu	
				1				5	

gat	ctt	cca	gat	aca	gat	ccc	att	gcc	tat	gca	atg	ttt	gcc	cac	tgt	163
Asp	Leu	Pro	Asp	Thr	Asp	Pro	Ile	Ala	Tyr	Ala	Met	Phe	Ala	His	Cys	
			10					15					20			

ttc	acc	ggc	tca	cgg	ttc	acg	cca	gcc	gcc	gcg	cga	gtc	agt	aaa	aca	211
Phe	Thr	Gly	Ser	Arg	Phe	Thr	Pro	Ala	Ala	Ala	Arg	Val	Ser	Lys	Thr	
			25					30					35			

ctc gca gaa tcc ggc gtc gcc tgc ctg cgt ttc gat ttc cca gga ctg	259
Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe Asp Phe Pro Gly Leu	
40 45 50	
agc caa tca gaa ggt gac ttc tcc aaa acc acc ttc aac tcc aat gtg	307
Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr Phe Asn Ser Asn Val	
55 60 65	
gac gat atc gtg gcg gcc tcg cag tgg ttg acg gaa cac tac tcc gct	355
Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr Glu His Tyr Ser Ala	
70 75 80 85	
cca cag ttg ctc att gga cac tcc ttg ggt ggt gca gca tca ctg aaa	403
Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly Ala Ala Ser Leu Lys	
90 95 100	
gct gcc acc aaa atc tcc tgc ctc aaa gca gta gca acg ata ggt gca	451
Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val Ala Thr Ile Gly Ala	
105 110 115	
cct ttt gat cct gcg cac gca gtc ctg cac ttt gct gat cgc ata tgt	499
Pro Phe Asp Pro Ala His Ala Val Leu His Phe Ala Asp Arg Ile Cys	
120 125 130	
gat gta gat gat caa ggt gct gtc act ctg cag ctc gga ggc cgg gat	547
Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln Leu Gly Gly Arg Asp	
135 140 145	
gtc acc att tcc cgc gaa ttc ctc gaa gac ctt gca gag gtc aac ccc	595
Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu Ala Glu Val Asn Pro	
150 155 160 165	
gaa gat cac ctc cgc agg ctc cgc aaa cca ctg ctt tta ctg cat tcc	643
Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu Leu Leu Leu His Ser	
170 175 180	
ccc acc gac caa acc gtc ggc gtg gac aac gcg cag ctc atc ttc aga	691
Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala Gln Leu Ile Phe Arg	
185 190 195	
gtc act cgc tac cct aaa tcc ttg atg act ttg gac aag gca gat cac	739
Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu Asp Lys Ala Asp His	
200 205 210	
ctg ctc acc aaa gat ggc acc gca cag cgt gca gcc cgg atc atc gcg	787
Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala Ala Arg Ile Ile Ala	
215 220 225	
aac tgg gtc gag ccc tac ctg gtt cca gaa aac gtc tgt gag gat ctt	835
Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn Val Cys Glu Asp Leu	
230 235 240 245	
ccg gag ttt gtc gcc gaa gcc tca acc atc aaa gcc agc aaa tac ggc	883
Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys Ala Ser Lys Tyr Gly	
250 255 260	
gca gcc atc cgc acc ggt ggt cac aat ttc atc acc gac cgc gac aaa	931
Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile Thr Asp Arg Asp Lys	
265 270 275	

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<210> 1162
<211> 378
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1162
Met Ala Ala Thr Leu Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala
  1             5             10             15
Met Phe Ala His Cys Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala
          20             25             30
Arg Val Ser Lys Thr Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe
      35             40             45
Asp Phe Pro Gly Leu Ser Gln Ser Glu Gly Asp Phe Ser Lys Thr Thr
      50             55             60
Phe Asn Ser Asn Val Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr
  65             70             75             80
Glu His Tyr Ser Ala Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly
          85             90             95
Ala Ala Ser Leu Lys Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val
          100             105             110
Ala Thr Ile Gly Ala Pro Phe Asp Pro Ala His Ala Val Leu His Phe
      115             120             125
Ala Asp Arg Ile Cys Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln
      130             135             140

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Leu Gly Gly Arg Asp Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu
 145 150 155 160
 Ala Glu Val Asn Pro Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu
 165 170 175
 Leu Leu Leu His Ser Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala
 180 185 190
 Gln Leu Ile Phe Arg Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu
 195 200 205
 Asp Lys Ala Asp His Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala
 210 215 220
 Ala Arg Ile Ile Ala Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn
 225 230 235 240
 Val Cys Glu Asp Leu Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys
 245 250 255
 Ala Ser Lys Tyr Gly Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile
 260 265 270
 Thr Asp Arg Asp Lys Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro
 275 280 285
 Thr Ser Leu Leu Val Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile
 290 295 300
 Lys Gln Ala Ala Ile Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys
 305 310 315 320
 Val Thr Ile Ser Gln Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu
 325 330 335
 Arg Arg Lys Ile Ser Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala
 340 345 350
 Ser Leu Arg Ala Ala Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala
 355 360 365
 Gln Gly Ile Val Ile Asp Asp Glu Val Asn
 370 375

<210> 1163

<211> 1257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1234)

<223> FRXA02428

<400> 1163

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 ttcagtttagc gtgaagggtgc catcatcaca agggttgatg atg gcc gcg acg tta 115

	Met	Ala	Ala	Thr	Leu	
	1				5	
gat ctt cca gat aca gat ccc att gcc tat gca atg ttt gcc cac tgt	163					
Asp Leu Pro Asp Thr Asp Pro Ile Ala Tyr Ala Met Phe Ala His Cys						
	10			15		20
ttc acc ggc tca cgg ttc acg cca gcc gcc gcg cga gtc agt aaa aca	211					
Phe Thr Gly Ser Arg Phe Thr Pro Ala Ala Ala Arg Val Ser Lys Thr						
	25		30		35	
ctc gca gaa tcc ggc gtc gcc tgc ctg cgt ttc gat ttc cca gga ctg	259					
Leu Ala Glu Ser Gly Val Ala Cys Leu Arg Phe Asp Phe Pro Gly Leu						
	40		45		50	
agc caa tca gaa ggt gac ttc tcc aaa acc acc ttc aac tcc aat gtg	307					
Ser Gln Ser Ser Glu Gly Asp Phe Ser Lys Thr Thr Phe Asn Ser Asn Val						
	55		60		65	
gac gat atc gtg gcg gcc tcg cag tgg ttg acg gaa cac tac tcc gct	355					
Asp Asp Ile Val Ala Ala Ser Gln Trp Leu Thr Glu His Tyr Ser Ala						
	70		75		80	85
cca cag ttg ctc att gga cac tcc ttg ggt ggt gca gca tca ctg aaa	403					
Pro Gln Leu Leu Ile Gly His Ser Leu Gly Gly Ala Ala Ser Leu Lys						
	90		95		100	
gct gcc acc aaa atc tcc tgc ctc aaa gca gta gca acg ata ggt gca	451					
Ala Ala Thr Lys Ile Ser Cys Leu Lys Ala Val Ala Thr Ile Gly Ala						
	105		110		115	
cct ttt gat cct gcg cac gca gtc ctg cac ttt gct gat cgc ata tgt	499					
Pro Phe Asp Pro Ala His Ala Val Leu His Phe Ala Asp Arg Ile Cys						
	120		125		130	
gat gta gat gat caa ggt gct gtc act ctg cag ctc gga ggc cgg gat	547					
Asp Val Asp Asp Gln Gly Ala Val Thr Leu Gln Leu Gly Gly Arg Asp						
	135		140		145	
gtc acc att tcc cgc gaa ttc ctc gaa gac ctt gca gag gtc aac ccc	595					
Val Thr Ile Ser Arg Glu Phe Leu Glu Asp Leu Ala Glu Val Asn Pro						
	150		155		160	165
gaa gat cac ctc cgc agg ctc cgc aaa cca ctg ctt tta ctg cat tcc	643					
Glu Asp His Leu Arg Arg Leu Arg Lys Pro Leu Leu Leu Leu His Ser						
	170		175		180	
ccc acc gac caa acc gtc ggc gtg gac aac gcg cag ctc atc ttc aga	691					
Pro Thr Asp Gln Thr Val Gly Val Asp Asn Ala Gln Leu Ile Phe Arg						
	185		190		195	
gtc act cgc tac cct aaa tcc ttg atg act ttg gac aag gca gat cac	739					
Val Thr Arg Tyr Pro Lys Ser Leu Met Thr Leu Asp Lys Ala Asp His						
	200		205		210	
ctg ctc acc aaa gat ggc acc gca cag cgt gca gcc cgg atc atc gcg	787					
Leu Leu Thr Lys Asp Gly Thr Ala Gln Arg Ala Ala Arg Ile Ile Ala						
	215		220		225	
aac tgg gtc gag ccc tac ctg gtt cca gaa aac gtc tgt gag gat ctt	835					
Asn Trp Val Glu Pro Tyr Leu Val Pro Glu Asn Val Cys Glu Asp Leu						

230	235	240	245	
ccg gag ttt gtc gcc gaa gcc tca acc atc aaa gcc agc aaa tac ggc				883
Pro Glu Phe Val Ala Glu Ala Ser Thr Ile Lys Ala Ser Lys Tyr Gly				
	250	255	260	
gca gcc atc cgc acc ggt ggt cac aat ttc atc acc gac cgc gac aaa				931
Ala Ala Ile Arg Thr Gly Gly His Asn Phe Ile Thr Asp Arg Asp Lys				
	265	270	275	
tcc cag ggt ggc aaa aac ctc ggc ttc acc cct act tcc ctg ctg gtt				979
Ser Gln Gly Gly Lys Asn Leu Gly Phe Thr Pro Thr Ser Leu Leu Val				
	280	285	290	
tcc gcg ctt gct gct gca aac tct caa acg atc aaa caa gca gcc atc				1027
Ser Ala Leu Ala Ala Ala Asn Ser Gln Thr Ile Lys Gln Ala Ala Ile				
	295	300	305	
gac aac cgc atc aaa ggc ctt gac gat gtc aaa gtg acg atc tcc cag				1075
Asp Asn Arg Ile Lys Gly Leu Asp Asp Val Lys Val Thr Ile Ser Gln				
	310	315	320	325
gaa caa tca gcc gac cac ggc cag atc aaa ctc cgc cga aag atc tct				1123
Glu Gln Ser Ala Asp His Gly Gln Ile Lys Leu Arg Arg Lys Ile Ser				
	330	335	340	
ttg atc ggc aac ctc agc gat gct gac agt gct tca ctt cgg gcc gca				1171
Leu Ile Gly Asn Leu Ser Asp Ala Asp Ser Ala Ser Leu Arg Ala Ala				
	345	350	355	
tct aat tcc tgc tcg att acc caa ctg ctc gcg cag gga atc gtc atc				1219
Ser Asn Ser Cys Ser Ile Thr Gln Leu Leu Ala Gln Gly Ile Val Ile				
	360	365	370	
gac gac gag gtg aac tagcgtggat tttgagttgg gta				1257
Asp Asp Glu Val Asn				
	375			

<210> 1164

<211> 378

<212> PRT

<213> Corynebacterium glutamicum

<400> 1164

Met	Ala	Ala	Thr	Leu	Asp	Leu	Pro	Asp	Thr	Asp	Pro	Ile	Ala	Tyr	Ala
1				5					10					15	

Met	Phe	Ala	His	Cys	Phe	Thr	Gly	Ser	Arg	Phe	Thr	Pro	Ala	Ala	Ala
			20					25					30		

Arg	Val	Ser	Lys	Thr	Leu	Ala	Glu	Ser	Gly	Val	Ala	Cys	Leu	Arg	Phe
		35					40					45			

Asp	Phe	Pro	Gly	Leu	Ser	Gln	Ser	Glu	Gly	Asp	Phe	Ser	Lys	Thr	Thr
	50					55					60				

Phe	Asn	Ser	Asn	Val	Asp	Asp	Ile	Val	Ala	Ala	Ser	Gln	Trp	Leu	Thr
65					70				75					80	

Glu	His	Tyr	Ser	Ala	Pro	Gln	Leu	Leu	Ile	Gly	His	Ser	Leu	Gly	Gly
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<210> 1165
<211> 1365
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (101)..(1342)

<223> RXN02454

<400> 1165

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gttctagcca taatcagcag aaaaggtgga gtgattcgcc atg aaa gag tcc atg 115
 Met Lys Glu Ser Met
 1 5

agc atc acc tcg tcg acg tac gcg tcg gca ctg ctg aca ctg ccc tgg 163
 Ser Ile Thr Ser Ser Thr Tyr Ala Ser Ala Leu Leu Thr Leu Pro Trp
 10 15 20

ggt aca ccc ctg gaa cag tgg ccc gat aat ctc atc gcc gcg ctg ccc 211
 Gly Thr Pro Leu Glu Gln Trp Pro Asp Asn Leu Ile Ala Ala Leu Pro
 25 30 35

agg ggt att tcc cgg cac atc gtg cgt ttc gtg ggg atc aac cgt ggc 259
 Arg Gly Ile Ser Arg His Ile Val Arg Phe Val Gly Ile Asn Arg Gly
 40 45 50

atc gtc gcg gtc aaa gaa att ggt gcg cgt acc gcc cac cac gag tac 307
 Ile Val Ala Val Lys Glu Ile Gly Ala Arg Thr Ala His His Glu Tyr
 55 60 65

aag atg ctg cgt gaa ctg cag cgc ctt ggt gcc ccc agt gtg cgc ccc 355
 Lys Met Leu Arg Glu Leu Gln Arg Leu Gly Ala Pro Ser Val Arg Pro
 70 75 80 85

gta gcc gtg atc acc gga cgc cat ccg gca gag gaa gac tac ggg gag 403
 Val Ala Val Ile Thr Gly Arg His Pro Ala Glu Glu Asp Tyr Gly Glu
 90 95 100

ctc acc gca gct ttg gtg acc gag cac ttg gag ttt tcc ctg ccc tat 451
 Leu Thr Ala Ala Leu Val Thr Glu His Leu Glu Phe Ser Leu Pro Tyr
 105 110 115

cgc gag atc ttt tct cgg cac ctc acg gtc gtg gaa tcg gag aag ctc 499
 Arg Glu Ile Phe Ser Arg His Leu Thr Val Val Glu Ser Glu Lys Leu
 120 125 130

atc cgc gcc ctg tcc gtg ctg ttg gtg cgg atg cat ctg ctc aac ttc 547
 Ile Arg Ala Leu Ser Val Leu Leu Val Arg Met His Leu Leu Asn Phe
 135 140 145

tac tgg gga gat gtg tca ctg tct aat act ctc ttt cgt cgc gat gct 595
 Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr Leu Phe Arg Arg Asp Ala
 150 155 160 165

gaa acc tat tcc gcc tat ctc gtc gat gcc gaa acc ggg gag ttc cag 643
 Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala Glu Thr Gly Glu Phe Gln
 170 175 180

ccc aac ctc tct gaa tca cgc agg ctt tac gac gtc gac atc gcc cgc 691
 Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr Asp Val Asp Ile Ala Arg
 185 190 195

gtc aac atc att ggc gaa ctc atg gac cta cag gcg ggt gaa tgc cta 739
 Val Asn Ile Ile Gly Glu Leu Met Asp Leu Gln Ala Gly Glu Cys Leu
 200 205 210

gat aag tcc atc gat gtc atc gcc cta gga ggc ctt gtc gaa agc tct 787
 Asp Lys Ser Ile Asp Val Ile Ala Leu Gly Gly Leu Val Glu Ser Ser
 215 220 225

tat ctt gaa ttg tgg acg gag ctc acc gcg gag gaa tcc gtc gat gcc 835
 Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala Glu Glu Ser Val Asp Ala
 230 235 240 245

agt gaa tat tgg cgc ctc tct gag aga att gac cgg ctc aat caa ctg 883
 Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile Asp Arg Leu Asn Gln Leu
 250 255 260

ggc ttt gac gta ggg gag ctc aag gtc acg aag gac gat tcg cgg cag 931
 Gly Phe Asp Val Gly Glu Leu Lys Val Thr Lys Asp Asp Ser Arg Gln
 265 270 275

gtt gtg cgc att cgc cct gta gtg gtg gat ccg ggc cac tat cgt gca 979
 Val Val Arg Ile Arg Pro Val Val Val Asp Pro Gly His Tyr Arg Ala
 280 285 290

gag cta ttg agc tta acc ggg ctg agc gtc gag gaa cac cag gcc caa 1027
 Glu Leu Leu Ser Leu Thr Gly Leu Ser Val Glu Glu His Gln Ala Gln
 295 300 305

cgc cta ttg ggc tcg atc cag gcc tat cag gcc gtc gaa tgc gga ccg 1075
 Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln Ala Val Glu Cys Gly Pro
 310 315 320 325

cat gta ggt ctt acc caa gcc gcg cat ctc tgg atg acg aat gaa tac 1123
 His Val Gly Leu Thr Gln Ala Ala His Leu Trp Met Thr Asn Glu Tyr
 330 335 340

gaa ccg act atc gcc gcc gtc ccc gtg gag atg tta gac aag ctg gag 1171
 Glu Pro Thr Ile Ala Ala Val Pro Val Glu Met Leu Asp Lys Leu Glu
 345 350 355

cca gca caa atc ttc cac gaa atc gtc gac cac cgc tgg ttc ctc gcc 1219
 Pro Ala Gln Ile Phe His Glu Ile Val Asp His Arg Trp Phe Leu Ala
 360 365 370

caa gaa agg gga ggg gct gtc acc ctc cca gag gcc acg gca tcc tat 1267
 Gln Glu Arg Gly Gly Ala Val Thr Leu Pro Glu Ala Thr Ala Ser Tyr
 375 380 385

ctt gaa tcc gtg ctt ccg gcc cgc cgc gac gag gct cgc ctc ctc agc 1315
 Leu Glu Ser Val Leu Pro Ala Arg Arg Asp Glu Ala Arg Leu Leu Ser
 390 395 400 405

aca aac cct tca gac gaa gac ttg tca taacctctcg cgtgccccaa 1362
 Thr Asn Pro Ser Asp Glu Asp Leu Ser
 410

cgg 1365

<210> 1166

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 1166

Met Lys Glu Ser Met Ser Ile Thr Ser Ser Thr Tyr Ala Ser Ala Leu
1 5 10 15
Leu Thr Leu Pro Trp Gly Thr Pro Leu Glu Gln Trp Pro Asp Asn Leu
20 25 30
Ile Ala Ala Leu Pro Arg Gly Ile Ser Arg His Ile Val Arg Phe Val
35 40 45
Gly Ile Asn Arg Gly Ile Val Ala Val Lys Glu Ile Gly Ala Arg Thr
50 55 60
Ala His His Glu Tyr Lys Met Leu Arg Glu Leu Gln Arg Leu Gly Ala
65 70 75 80
Pro Ser Val Arg Pro Val Ala Val Ile Thr Gly Arg His Pro Ala Glu
85 90 95
Glu Asp Tyr Gly Glu Leu Thr Ala Ala Leu Val Thr Glu His Leu Glu
100 105 110
Phe Ser Leu Pro Tyr Arg Glu Ile Phe Ser Arg His Leu Thr Val Val
115 120 125
Glu Ser Glu Lys Leu Ile Arg Ala Leu Ser Val Leu Leu Val Arg Met
130 135 140
His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr Leu
145 150 155 160
Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala Glu
165 170 175
Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr Asp
180 185 190
Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu Gln
195 200 205
Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly Gly
210 215 220
Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala Glu
225 230 235 240
Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile Asp
245 250 255
Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr Lys
260 265 270
Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp Pro
275 280 285
Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val Glu
290 295 300

Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln Ala
305 310 315 320

Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu Trp
325 330 335

Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu Met
340 345 350

Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp His
355 360 365

Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro Glu
370 375 380

Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp Glu
385 390 395 400

Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
405 410

<210> 1167

<211> 836

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(813)

<223> FRXA02454

<400> 1167

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Met His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr	
1 5 10 15	
ctc ttt cgt cgc gat gct gaa acc tat tcc gcc tat ctc gtc gat gcc	96
Leu Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala	
20 25 30	
gaa acc ggg gag ttc cag ccc aac ctc tct gaa tca cgc agg ctt tac	144
Glu Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr	
35 40 45	
gac gtc gac atc gcc cgc gtc aac atc att ggc gaa ctc atg gac cta	192
Asp Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu	
50 55 60	
cag gcg ggt gaa tgc cta gat aag tcc atc gat gtc atc gcc cta gga	240
Gln Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly	
65 70 75 80	
ggc ctt gtc gaa agc tct tat ctt gaa ttg tgg acg gag ctc acc gcg	288
Gly Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala	
85 90 95	
gag gaa tcc gtc gat gcc agt gaa tat tgg cgc ctc tct gag aga att	336
Glu Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile	
100 105 110	

gac cgg ctc aat caa ctg ggc ttt gac gta ggg gag ctc aag gtc acg 384
 Asp Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr
 115 120 125
 aag gac gat tcg cgg cag gtt gtg cgc att cgc cct gta gtg gtg gat 432
 Lys Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp
 130 135 140
 ccg ggc cac tat cgt gca gag cta ttg agc tta acc ggg ctg agc gtc 480
 Pro Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val
 145 150 155 160
 gag gaa cac cag gcc caa cgc cta ttg ggc tcg atc cag gcc tat cag 528
 Glu Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln
 165 170 175
 gcc gtc gaa tgc gga ccg cat gta ggt ctt acc caa gcc gcg cat ctc 576
 Ala Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu
 180 185 190
 tgg atg acg aat gaa tac gaa ccg act atc gcc gcc gtc ccc gtg gag 624
 Trp Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu
 195 200 205
 atg tta gac aag ctg gag cca gca caa atc ttc cac gaa atc gtc gac 672
 Met Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp
 210 215 220
 cac cgc tgg ttc ctc gcc caa gaa agg gga ggg gct gtc acc ctc cca 720
 His Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro
 225 230 235 240
 gag gcc acg gca tcc tat ctt gaa tcc gtg ctt ccg gcc cgc cgc gac 768
 Glu Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp
 245 250 255
 gag gct cgc ctc ctc agc aca aac cct tca gac gaa gac ttg tca 813
 Glu Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
 260 265 270
 taacctctcg cgtgccccaa cgg 836

<210> 1168

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 1168

Met His Leu Leu Asn Phe Tyr Trp Gly Asp Val Ser Leu Ser Asn Thr
 1 5 10 15

Leu Phe Arg Arg Asp Ala Glu Thr Tyr Ser Ala Tyr Leu Val Asp Ala
 20 25 30

Glu Thr Gly Glu Phe Gln Pro Asn Leu Ser Glu Ser Arg Arg Leu Tyr
 35 40 45

Asp Val Asp Ile Ala Arg Val Asn Ile Ile Gly Glu Leu Met Asp Leu
 50 55 60

Gln Ala Gly Glu Cys Leu Asp Lys Ser Ile Asp Val Ile Ala Leu Gly
 65 70 75 80
 Gly Leu Val Glu Ser Ser Tyr Leu Glu Leu Trp Thr Glu Leu Thr Ala
 85 90 95
 Glu Glu Ser Val Asp Ala Ser Glu Tyr Trp Arg Leu Ser Glu Arg Ile
 100 105 110
 Asp Arg Leu Asn Gln Leu Gly Phe Asp Val Gly Glu Leu Lys Val Thr
 115 120 125
 Lys Asp Asp Ser Arg Gln Val Val Arg Ile Arg Pro Val Val Val Asp
 130 135 140
 Pro Gly His Tyr Arg Ala Glu Leu Leu Ser Leu Thr Gly Leu Ser Val
 145 150 155 160
 Glu Glu His Gln Ala Gln Arg Leu Leu Gly Ser Ile Gln Ala Tyr Gln
 165 170 175
 Ala Val Glu Cys Gly Pro His Val Gly Leu Thr Gln Ala Ala His Leu
 180 185 190
 Trp Met Thr Asn Glu Tyr Glu Pro Thr Ile Ala Ala Val Pro Val Glu
 195 200 205
 Met Leu Asp Lys Leu Glu Pro Ala Gln Ile Phe His Glu Ile Val Asp
 210 215 220
 His Arg Trp Phe Leu Ala Gln Glu Arg Gly Gly Ala Val Thr Leu Pro
 225 230 235 240
 Glu Ala Thr Ala Ser Tyr Leu Glu Ser Val Leu Pro Ala Arg Arg Asp
 245 250 255
 Glu Ala Arg Leu Leu Ser Thr Asn Pro Ser Asp Glu Asp Leu Ser
 260 265 270

<210> 1169

<211> 1233

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> RXN02457

<400> 1169

ctgtaaagcc acgtgagctg ttgcttagac tttactctac cccgcgtgt ccaccacatc 60

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 Met Phe Tyr Phe Thr
 1 5

gtc aat aat ccg cag gat cct tta agc acc gaa att gtt gag act aat 163
 Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu Ile Val Glu Thr Asn
 10 15 20

cgc cgt gac ctc gca ttt tgg cat cga tta cgc ccc aaa gat gac gat	211
Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg Pro Lys Asp Asp	
25 30 35	
gat tta gcc aca gcc atc aac aaa ata tgc gtg cgc aca ggc tta tcc	259
Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val Arg Thr Gly Leu Ser	
40 45 50	
cgc aaa ctg atc gcc gct tgt tta ttt agc atc tgc ttc ctg ccg tac	307
Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile Cys Phe Leu Pro Tyr	
55 60 65	
tta ccc aac ttc cac aaa ctc gtc gaa aag ctt ggt cat ctc gac atg	355
Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu Gly His Leu Asp Met	
70 75 80 85	
gcg cgc atc aac gcg atc act aaa gct ggc gaa aaa gtg cca agc gag	403
Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu Lys Val Pro Ser Glu	
90 95 100	
aag aga gag ctt ttc gac gcc tac ctc gtc gat tac ctg acg cct cga	451
Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp Tyr Leu Thr Pro Arg	
105 110 115	
gcg gag gct cag tgc ttg ccc cag gca agc tca att tcc gca atg atg	499
Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser Ile Ser Ala Met Met	
120 125 130	
cgg aaa ttt atc gca caa cac tgc ccc gac gac aag gcc tcc tca gcc	547
Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp Lys Ala Ser Ser Ala	
135 140 145	
acc aat gat ggc tcc atc cgc tac cgc aga aac aac aaa ggc ggg atc	595
Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn Asn Lys Gly Gly Ile	
150 155 160 165	
agt atc acc gtc gat gcc acc gcc agc gaa gta aca gaa atc aaa gct	643
Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val Thr Glu Ile Lys Ala	
170 175 180	
gcc ctg gaa caa atg tcc aaa gat aag gac tgc aca cca ggc act tcc	691
Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys Thr Pro Gly Thr Ser	
185 190 195	
cta ctc cac atc att cgt ggc ctg ccg aca aaa gtc gta ctc aac acc	739
Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys Val Val Leu Asn Thr	
200 205 210	
tac ggc acc aaa gac agc cct gaa tac tta gaa gga gga acc tgg ctg	787
Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu Gly Gly Thr Trp Leu	
215 220 225	
tca aag gaa cag tct gag ttc tgg aaa acc cga acc acg tcc agt cgg	835
Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg Thr Thr Ser Ser Arg	
230 235 240 245	
gat atg gac gcc gcc cac ttc tct tac acc acc gcc tac gct cca acc	883
Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr Ala Tyr Ala Pro Thr	
250 255 260	
cga gaa atg cgc gtc tac atc aaa ggt cta cgc acc acc tgt agc gtc	931

Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg Thr Thr Cys Ser Val
 265 270 275
 cct ggc tgc agt gta gcg gtc gaa aac tgc caa ctg gac cac atc atc 979
 Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln Leu Asp His Ile Ile
 280 285 290
 ccc tgg ggt gaa gga ggg ccg aca aca ccg tgg aat att cat ccc ctg 1027
 Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp Asn Ile His Pro Leu
 295 300 305
 tgt gtc ttc cac cac atc cag aag act gaa ggg agg ctc cag tgc tat 1075
 Cys Val Phe His His Ile Gln Lys Thr Glu Gly Arg Leu Gln Cys Tyr
 310 315 320 325
 cca cta ccg gac ggc acc gtc cta ttc cta gtg gat gga ata ccg gtg 1123
 Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val Asp Gly Ile Pro Val
 330 335 340
 ttc tcc atc ccc gac ggg cct tta tct aaa tcg aat aaa acc tgg ggg 1171
 Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser Asn Lys Thr Trp Gly
 345 350 355
 aca aag ttc ggc aaa tac atg gag cgt cga atc gcc gcc taatccagca 1220
 Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile Ala Ala
 360 365 370
 agccagcgtg atc 1233

<210> 1170

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 1170

Met Phe Tyr Phe Thr Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu
 1 5 10 15
 Ile Val Glu Thr Asn Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg
 20 25 30
 Pro Lys Asp Asp Asp Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val
 35 40 45
 Arg Thr Gly Leu Ser Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile
 50 55 60
 Cys Phe Leu Pro Tyr Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu
 65 70 75 80
 Gly His Leu Asp Met Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu
 85 90 95
 Lys Val Pro Ser Glu Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp
 100 105 110
 Tyr Leu Thr Pro Arg Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser
 115 120 125
 Ile Ser Ala Met Met Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp

130 135 140
Lys Ala Ser Ser Ala Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn
145 150 155 160
Asn Lys Gly Gly Ile Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val
165 170 175
Thr Glu Ile Lys Ala Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys
180 185 190
Thr Pro Gly Thr Ser Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys
195 200 205
Val Val Leu Asn Thr Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu
210 215 220
Gly Gly Thr Trp Leu Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg
225 230 235 240
Thr Thr Ser Ser Arg Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr
245 250 255
Ala Tyr Ala Pro Thr Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg
260 265 270
Thr Thr Cys Ser Val Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln
275 280 285
Leu Asp His Ile Ile Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp
290 295 300
Asn Ile His Pro Leu Cys Val Phe His His Ile Gln Lys Thr Glu Gly
305 310 315 320
Arg Leu Gln Cys Tyr Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val
325 330 335
Asp Gly Ile Pro Val Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser
340 345 350
Asn Lys Thr Trp Gly Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile
355 360 365
Ala Ala
370

<210> 1171

<211> 1233

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> FRXA02457

<400> 1171

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agttagaaca tatgtaccac ttcaaattcta ggggggaaaca atg ttc tac ttc acc 115
Met Phe Tyr Phe Thr
1 5

gtc aat aat ccg cag gat cct tta agc acc gaa att gtt gag act aat 163
Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu Ile Val Glu Thr Asn
10 15 20

cgc cgt gac ctc gca ttt tgg cat cga tta cgc ccc aaa gat gac gat 211
Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg Pro Lys Asp Asp Asp
25 30 35

gat tta gcc aca gcc atc aac aaa ata tgc gtg cgc aca ggc tta tcc 259
Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val Arg Thr Gly Leu Ser
40 45 50

cgc aaa ctg atc gcc gct tgt tta ttt agc atc tgc ttc ctg ccg tac 307
Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile Cys Phe Leu Pro Tyr
55 60 65

tta ccc aac ttc cac aaa ctc gtc gaa aag ctt ggt cat ctc gac atg 355
Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu Gly His Leu Asp Met
70 75 80 85

gcg cgc atc aac gcg atc act aaa gct ggc gaa aaa gtg cca agc gag 403
Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu Lys Val Pro Ser Glu
90 95 100

aag aga gag ctt ttc gac gcc tac ctc gtc gat tac ctg acg cct cga 451
Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp Tyr Leu Thr Pro Arg
105 110 115

gcg gag gct cag tgc ttg ccc cag gca agc tca att tcc gca atg atg 499
Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser Ile Ser Ala Met Met
120 125 130

cgg aaa ttt atc gca caa cac tgc ccc gac gac aag gcc tcc tca gcc 547
Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp Lys Ala Ser Ser Ala
135 140 145

acc aat gat ggc tcc atc cgc tac cgc aga aac aac aaa ggc ggg atc 595
Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn Asn Lys Gly Gly Ile
150 155 160 165

agt atc acc gtc gat gcc acc gcc agc gaa gta aca gaa atc aaa gct 643
Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val Thr Glu Ile Lys Ala
170 175 180

gcc ctg gaa caa atg tcc aaa gat aag gac tgc aca cca ggc act tcc 691
Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys Thr Pro Gly Thr Ser
185 190 195

cta ctc cac atc att cgt ggc ctg ccg aca aaa gtc gta ctc aac acc 739
Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys Val Val Leu Asn Thr
200 205 210

tac ggc acc aaa gac agc cct gaa tac tta gaa gga gga acc tgg ctg 787
Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu Gly Gly Thr Trp Leu
215 220 225

tca aag gaa cag tct gag ttc tgg aaa acc cga acc acg tcc agt cgg 835

Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg Thr Thr Ser Ser Arg
 230 235 240 245

gat atg gac gcc gcc cac ttc tct tac acc acc gcc tac gct cca acc 883
 Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr Ala Tyr Ala Pro Thr
 250 255 260

cga gaa atg cgc gtc tac atc aaa ggt cta cgc acc acc tgt agc gtc 931
 Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg Thr Thr Cys Ser Val
 265 270 275

cct ggc tgc agt gta gcg gtc gaa aac tgc caa ctg gac cac atc atc 979
 Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln Leu Asp His Ile Ile
 280 285 290

ccc tgg ggt gaa gga ggg ccg aca aca ccg tgg aat att cat ccc ctg 1027
 Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp Asn Ile His Pro Leu
 295 300 305

tgt gtc ttc cac cac atc cag aag act gaa ggg agg ctc cag tgc tat 1075
 Cys Val Phe His His Ile Gln Lys Thr Glu Gly Arg Leu Gln Cys Tyr
 310 315 320 325

cca cta ccg gac ggc acc gtc cta ttc cta gtg gat gga ata ccg gtg 1123
 Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val Asp Gly Ile Pro Val
 330 335 340

ttc tcc atc ccc gac ggg cct tta tct aaa tcg aat aaa acc tgg ggg 1171
 Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser Asn Lys Thr Trp Gly
 345 350 355

aca aag ttc ggc aaa tac atg gag cgt cga atc gcc gcc taatccagca 1220
 Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile Ala Ala
 360 365 370

agccagcgtg atc 1233

<210> 1172

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 1172

Met Phe Tyr Phe Thr Val Asn Asn Pro Gln Asp Pro Leu Ser Thr Glu
 1 5 10 15

Ile Val Glu Thr Asn Arg Arg Asp Leu Ala Phe Trp His Arg Leu Arg
 20 25 30

Pro Lys Asp Asp Asp Asp Leu Ala Thr Ala Ile Asn Lys Ile Cys Val
 35 40 45

Arg Thr Gly Leu Ser Arg Lys Leu Ile Ala Ala Cys Leu Phe Ser Ile
 50 55 60

Cys Phe Leu Pro Tyr Leu Pro Asn Phe His Lys Leu Val Glu Lys Leu
 65 70 75 80

Gly His Leu Asp Met Ala Arg Ile Asn Ala Ile Thr Lys Ala Gly Glu
 85 90 95

Lys Val Pro Ser Glu Lys Arg Glu Leu Phe Asp Ala Tyr Leu Val Asp
100 105 110

Tyr Leu Thr Pro Arg Ala Glu Ala Gln Cys Leu Pro Gln Ala Ser Ser
115 120 125

Ile Ser Ala Met Met Arg Lys Phe Ile Ala Gln His Cys Pro Asp Asp
130 135 140

Lys Ala Ser Ser Ala Thr Asn Asp Gly Ser Ile Arg Tyr Arg Arg Asn
145 150 155 160

Asn Lys Gly Gly Ile Ser Ile Thr Val Asp Ala Thr Ala Ser Glu Val
165 170 175

Thr Glu Ile Lys Ala Ala Leu Glu Gln Met Ser Lys Asp Lys Asp Cys
180 185 190

Thr Pro Gly Thr Ser Leu Leu His Ile Ile Arg Gly Leu Pro Thr Lys
195 200 205

Val Val Leu Asn Thr Tyr Gly Thr Lys Asp Ser Pro Glu Tyr Leu Glu
210 215 220

Gly Gly Thr Trp Leu Ser Lys Glu Gln Ser Glu Phe Trp Lys Thr Arg
225 230 235 240

Thr Thr Ser Ser Arg Asp Met Asp Ala Ala His Phe Ser Tyr Thr Thr
245 250 255

Ala Tyr Ala Pro Thr Arg Glu Met Arg Val Tyr Ile Lys Gly Leu Arg
260 265 270

Thr Thr Cys Ser Val Pro Gly Cys Ser Val Ala Val Glu Asn Cys Gln
275 280 285

Leu Asp His Ile Ile Pro Trp Gly Glu Gly Gly Pro Thr Thr Pro Trp
290 295 300

Asn Ile His Pro Leu Cys Val Phe His His Ile Gln Lys Thr Glu Gly
305 310 315 320

Arg Leu Gln Cys Tyr Pro Leu Pro Asp Gly Thr Val Leu Phe Leu Val
325 330 335

Asp Gly Ile Pro Val Phe Ser Ile Pro Asp Gly Pro Leu Ser Lys Ser
340 345 350

Asn Lys Thr Trp Gly Thr Lys Phe Gly Lys Tyr Met Glu Arg Arg Ile
355 360 365

Ala Ala
370

<210> 1173

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXN02460

<400> 1173

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aaatcgctcgg actgttcggg ctagaaggag aattctaate ttg cgc gtc tac atc 115
                                   Leu Arg Val Tyr Ile
                                   1 5

cca gca acg ttt tcc aca ctc cgc gga ctc aat gaa tcc cgc gtc atc 163
Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn Glu Ser Arg Val Ile
              10              15              20

aca gca cgc tcc gga tac ggt ttc gca gtc acc cca gca ctc ctt gac 211
Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr Pro Ala Leu Leu Asp
              25              30              35

ttc tac acc gac ggt gac gaa gaa gaa atc gca cat gca gcc ttc caa 259
Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala His Ala Ala Phe Gln
              40              45              50

gac gcc gca gaa gcc tcc atc cga ctc ctc gca atc ggc gac gaa gaa 307
Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala Ile Gly Asp Glu Glu
              55              60              65

aca ttt ccc tac cgc aga gtc gtc gtc tca gta gat gtt gac gac tcc 355
Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val Asp Val Asp Asp Ser
              70              75              80              85

gtg gtg acc tac cag cct gaa aac ggc gaa tcc gta gtc aaa ctc agc 403
Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser Val Val Lys Leu Ser
              90              95              100

cca gcg cac atc aac ctc gac gac gtg gca gca atc cac atc gac gtt 451
Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala Ile His Ile Asp Val
              105              110              115

gaa gcc tcc gaa gca gac acc aaa aaa gct atc gaa gtc atc gac gaa 499
Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile Glu Val Ile Asp Glu
              120              125              130

tcc gac ctc ggc gaa gaa gac gcc gaa ctc acc gtc gga gac gcc caa 547
Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr Val Gly Asp Ala Gln
              135              140              145

gac aac ttc atg gcc tgg tac gac cca gaa gag ctc ccc ttc cta gtc 595
Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu Leu Pro Phe Leu Val
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<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 1174

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 20 25 30
 Pro Ala Leu Leu Asp Phe Tyr Thr Asp Gly Asp Glu Glu Glu Ile Ala
 35 40 45
 His Ala Ala Phe Gln Asp Ala Ala Glu Ala Ser Ile Arg Leu Leu Ala
 50 55 60
 Ile Gly Asp Glu Glu Thr Phe Pro Tyr Arg Arg Val Val Val Ser Val
 65 70 75 80
 Asp Val Asp Asp Ser Val Val Thr Tyr Gln Pro Glu Asn Gly Glu Ser
 85 90 95
 Val Val Lys Leu Ser Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala
 100 105 110
 Ile His Ile Asp Val Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile
 115 120 125
 Glu Val Ile Asp Glu Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr
 130 135 140
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 145 150 155 160
 Leu Pro Phe Leu Val Glu Leu Leu
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 Leu Arg Val Tyr Ile
 1 5
 cca gca acg ttt tcc aca ctc cgc gga ctc aat gaa tcc cgc gtc atc 163
 Pro Ala Thr Phe Ser Thr Leu Arg Gly Leu Asn Glu Ser Arg Val Ile
 10 15 20
 aca gca cgc tcc gga tac ggt ttc gca gtc acc cca gca ctc ctt gac 211
 Thr Ala Arg Ser Gly Tyr Gly Phe Ala Val Thr Pro Ala Leu Leu Asp
 25 30 35

Val Val Lys Leu Ser Pro Ala His Ile Asn Leu Asp Asp Val Ala Ala
 100 105 110

Ile His Ile Asp Val Glu Ala Ser Glu Ala Asp Thr Lys Lys Ala Ile
 115 120 125

Glu Val Ile Asp Glu Ser Asp Leu Gly Glu Glu Asp Ala Glu Leu Thr
 130 135 140

Val Gly Asp Ala Gln Asp Asn Phe Met Ala Trp Tyr Asp Pro Glu Glu
 145 150 155 160

Leu Pro Phe Leu Val Glu Leu Leu
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<210> 1177

<211> 1323

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1300)

<223> RXN02464

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aacagcccca cgaccaccac gccgcacccg gaaataactt atg gca gca aag ctt 115
 Met Ala Ala Lys Leu
 1 5

caa cca ctc aaa cgc acc aaa aaa gac ctc atc gca acc ggt gtc atc 163
 Gln Pro Leu Lys Arg Thr Lys Lys Asp Leu Ile Ala Thr Gly Val Ile
 10 15 20

aca gca cta gca gtc att ggc gtc ggc acg gtc tgg gca acc gca cca 211
 Thr Ala Leu Ala Val Ile Gly Val Gly Thr Val Trp Ala Thr Ala Pro
 25 30 35

ata cga gga tct gaa ctc acc ccc gcc gac gaa cca ttc att ggc tca 259
 Ile Arg Gly Ser Glu Leu Thr Pro Ala Asp Glu Pro Phe Ile Gly Ser
 40 45 50

acc aca ctg gac gcc atc ccc gaa aca ctc agc gaa cat tgg cga gcc 307
 Thr Thr Leu Asp Ala Ile Pro Glu Thr Leu Ser Glu His Trp Arg Ala
 55 60 65

acc gac acc tta aca aac cac aaa ccc ctc atc acc ggc gga gtc atc 355
 Thr Asp Thr Leu Thr Asn His Lys Pro Leu Ile Thr Gly Gly Val Ile
 70 75 80 85

ttc acc gcc gac ggc aac acc att aag acc tac acc ccc gac ggc gcc 403
 Phe Thr Ala Asp Gly Asn Thr Ile Lys Thr Tyr Thr Pro Asp Gly Ala
 90 95 100

ctc ctg tgg agc tac gaa cgc gac aaa gaa ctc tgc agc ctc tcc gta 451
 Leu Leu Trp Ser Tyr Glu Arg Asp Lys Glu Leu Cys Ser Leu Ser Val
 105 110 115

gga ttc gac gcc gcc gtc gcc acc tac aaa acc gga atc gga tgt ggc 499
 Gly Phe Asp Ala Ala Val Ala Thr Tyr Lys Thr Gly Ile Gly Cys Gly
 120 125 130

gac gtc acc gcc atc aac gcc aac gac ggc caa tac caa gca aca cgc 547
 Asp Val Thr Ala Ile Asn Ala Asn Asp Gly Gln Tyr Gln Ala Thr Arg
 135 140 145

agc gca atc tcc agc gac cac gta gca ccg atc tcc tcg aac gat cgg 595
 Ser Ala Ile Ser Ser Asp His Val Ala Pro Ile Ser Ser Asn Asp Arg
 150 155 160 165

atc ggt gtt ctc ggg aca gaa cgc ttg gag ctt tgg cga tcc gat ctg 643
 Ile Gly Val Leu Gly Thr Glu Arg Leu Glu Leu Trp Arg Ser Asp Leu
 170 175 180

gtg cga acc atc gaa tac ggc gat gtg gaa gct cct caa gaa tct ggg 691
 Val Arg Thr Ile Glu Tyr Gly Asp Val Glu Ala Pro Gln Glu Ser Gly
 185 190 195

caa caa cca cat ccg gaa tgc tcg att acg tcc gcc atg aca cgc aaa 739
 Gln Gln Pro His Pro Glu Cys Ser Ile Thr Ser Ala Met Thr Arg Lys
 200 205 210

gat cta ttg gct atc acc gag gat tgc cct gac gga tct tct tac ttg 787
 Asp Leu Leu Ala Ile Thr Glu Asp Cys Pro Asp Gly Ser Ser Tyr Leu
 215 220 225

agg ttc atg ggc aca aca cca gac gat tcc cga act cct gaa atc acc 835
 Arg Phe Met Gly Thr Thr Pro Asp Asp Ser Arg Thr Pro Glu Ile Thr
 230 235 240 245

caa gac ata gaa ata acc gat ggc agg atc gtt gcc atc ggt caa tca 883
 Gln Asp Ile Glu Ile Thr Asp Gly Arg Ile Val Ala Ile Gly Gln Ser
 250 255 260

gtg gct gcg gtg tat aca aac gat cct tcg cct cga atc gtc tcc tac 931
 Val Ala Ala Val Tyr Thr Asn Asp Pro Ser Pro Arg Ile Val Ser Tyr
 265 270 275

aac gat gat ggt gaa cta gtt gga gaa caa gca gtc gat gag gtt gag 979
 Asn Asp Asp Gly Glu Leu Val Gly Glu Gln Ala Val Asp Glu Val Glu
 280 285 290

ttc ccg gat ccg ccg ttt caa agc gcg acc gct gat ctt cca cac cat 1027
 Phe Pro Asp Pro Pro Phe Gln Ser Ala Thr Ala Asp Leu Pro His His
 295 300 305

atg agt tgg ttc aac gga gac agc ctc gta ctg ttc tct ccc act cag 1075
 Met Ser Trp Phe Asn Gly Asp Ser Leu Val Leu Phe Ser Pro Thr Gln
 310 315 320 325

ctc aat gta cga caa agc ttc aat gat gct tta gga acc ggc att gcg 1123
 Leu Asn Val Arg Gln Ser Phe Asn Asp Ala Leu Gly Thr Gly Ile Ala
 330 335 340

ttg aac gga agt ctc ctc tac ccc acc gct gag ggc atc acg gta gct 1171
 Leu Asn Gly Ser Leu Leu Tyr Pro Thr Ala Glu Gly Ile Thr Val Ala
 345 350 355

aat tgg gac acc gga gag gtg cag cgc acc att ccg gtg gac cgt gcg 1219

Asn Trp Asp Thr Gly Glu Val Gln Arg Thr Ile Pro Val Asp Arg Ala
 360 365 370

ggc tac gac ggt gaa gtt gcg ctc ggc gtt gta ggg cag gtg atc gtc 1267
 Gly Tyr Asp Gly Glu Val Ala Leu Gly Val Val Gly Gln Val Ile Val
 375 380 385

gaa aag cgt ggc tct gag atc gtt gct cta ggc tagatctcgt tgtagccca 1320
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aag 1323

<210> 1178

<211> 400

<212> PRT

<213> Corynebacterium glutamicum

<400> 1178

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 20 25 30

Trp Ala Thr Ala Pro Ile Arg Gly Ser Glu Leu Thr Pro Ala Asp Glu
 35 40 45

Pro Phe Ile Gly Ser Thr Thr Leu Asp Ala Ile Pro Glu Thr Leu Ser
 50 55 60

Glu His Trp Arg Ala Thr Asp Thr Leu Thr Asn His Lys Pro Leu Ile
 65 70 75 80

Thr Gly Gly Val Ile Phe Thr Ala Asp Gly Asn Thr Ile Lys Thr Tyr
 85 90 95

Thr Pro Asp Gly Ala Leu Leu Trp Ser Tyr Glu Arg Asp Lys Glu Leu
 100 105 110

Cys Ser Leu Ser Val Gly Phe Asp Ala Ala Val Ala Thr Tyr Lys Thr
 115 120 125

Gly Ile Gly Cys Gly Asp Val Thr Ala Ile Asn Ala Asn Asp Gly Gln
 130 135 140

Tyr Gln Ala Thr Arg Ser Ala Ile Ser Ser Asp His Val Ala Pro Ile
 145 150 155 160

Ser Ser Asn Asp Arg Ile Gly Val Leu Gly Thr Glu Arg Leu Glu Leu
 165 170 175

Trp Arg Ser Asp Leu Val Arg Thr Ile Glu Tyr Gly Asp Val Glu Ala
 180 185 190

Pro Gln Glu Ser Gly Gln Gln Pro His Pro Glu Cys Ser Ile Thr Ser
 195 200 205

Ala Met Thr Arg Lys Asp Leu Leu Ala Ile Thr Glu Asp Cys Pro Asp
 210 215 220

Gly Ser Ser Tyr Leu Arg Phe Met Gly Thr Thr Pro Asp Asp Ser Arg
 225 230 235 240
 Thr Pro Glu Ile Thr Gln Asp Ile Glu Ile Thr Asp Gly Arg Ile Val
 245 250 255
 Ala Ile Gly Gln Ser Val Ala Ala Val Tyr Thr Asn Asp Pro Ser Pro
 260 265 270
 Arg Ile Val Ser Tyr Asn Asp Asp Gly Glu Leu Val Gly Glu Gln Ala
 275 280 285
 Val Asp Glu Val Glu Phe Pro Asp Pro Pro Phe Gln Ser Ala Thr Ala
 290 295 300
 Asp Leu Pro His His Met Ser Trp Phe Asn Gly Asp Ser Leu Val Leu
 305 310 315 320
 Phe Ser Pro Thr Gln Leu Asn Val Arg Gln Ser Phe Asn Asp Ala Leu
 325 330 335
 Gly Thr Gly Ile Ala Leu Asn Gly Ser Leu Leu Tyr Pro Thr Ala Glu
 340 345 350
 Gly Ile Thr Val Ala Asn Trp Asp Thr Gly Glu Val Gln Arg Thr Ile
 355 360 365
 Pro Val Asp Arg Ala Gly Tyr Asp Gly Glu Val Ala Leu Gly Val Val
 370 375 380
 Gly Gln Val Ile Val Glu Lys Arg Gly Ser Glu Ile Val Ala Leu Gly
 385 390 395 400

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<211> 630

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(607)

<223> FRXA02464

<400> 1179

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 Met Gly Thr Thr Pro
 1 5
 gac gat tcc cga act cct gaa atc acc caa gac ata gaa ata acc gat 163
 Asp Asp Ser Arg Thr Pro Glu Ile Thr Gln Asp Ile Glu Ile Thr Asp
 10 15 20
 ggc agg atc gtt gcc atc ggt caa tca gtg gct gcg gtg tat aca aac 211
 Gly Arg Ile Val Ala Ile Gly Gln Ser Val Ala Ala Val Tyr Thr Asn
 25 30 35
 gat cct tcg cct cga atc gtc tcc tac aac gat gat ggt gaa cta gtt 259

Asp Pro Ser Pro Arg Ile Val Ser Tyr Asn Asp Asp Gly Glu Leu Val
 40 45 50
 gga gaa caa gca gtc gat gag gtt gag ttc ccg gat ccg ccg ttt caa 307
 Gly Glu Gln Ala Val Asp Glu Val Glu Phe Pro Asp Pro Pro Phe Gln
 55 60 65
 agc gcg acc gct gat ctt cca cac cat atg agt tgg ttc aac gga gac 355
 Ser Ala Thr Ala Asp Leu Pro His His Met Ser Trp Phe Asn Gly Asp
 70 75 80 85
 agc ctc gta ctg ttc tct ccc act cag ctc aat gta cga caa agc ttc 403
 Ser Leu Val Leu Phe Ser Pro Thr Gln Leu Asn Val Arg Gln Ser Phe
 90 95 100
 aat gat gct tta gga acc ggc att gcg ttg aac gga agt ctc ctc tac 451
 Asn Asp Ala Leu Gly Thr Gly Ile Ala Leu Asn Gly Ser Leu Leu Tyr
 105 110 115
 ccc acc gct gag ggc atc acg gta gct aat tgg gac acc gga gag gtg 499
 Pro Thr Ala Glu Gly Ile Thr Val Ala Asn Trp Asp Thr Gly Glu Val
 120 125 130
 cag cgc acc att ccg gtg gac cgt gcg ggc tac gac ggt gaa gtt gcg 547
 Gln Arg Thr Ile Pro Val Asp Arg Ala Gly Tyr Asp Gly Glu Val Ala
 135 140 145
 ctc ggc gtt gta ggg cag gtg atc gtc gaa aag cgt ggc tct gag atc 595
 Leu Gly Val Val Gly Gln Val Ile Val Glu Lys Arg Gly Ser Glu Ile
 150 155 160 165
 gtt gct cta ggc tagatctcgt tgtagccca aag 630
 Val Ala Leu Gly

 <210> 1180
 <211> 169
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1180
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 Ile Glu Ile Thr Asp Gly Arg Ile Val Ala Ile Gly Gln Ser Val Ala
 20 25 30
 Ala Val Tyr Thr Asn Asp Pro Ser Pro Arg Ile Val Ser Tyr Asn Asp
 35 40 45
 Asp Gly Glu Leu Val Gly Glu Gln Ala Val Asp Glu Val Glu Phe Pro
 50 55 60
 Asp Pro Pro Phe Gln Ser Ala Thr Ala Asp Leu Pro His His Met Ser
 65 70 75 80
 Trp Phe Asn Gly Asp Ser Leu Val Leu Phe Ser Pro Thr Gln Leu Asn
 85 90 95
 Val Arg Gln Ser Phe Asn Asp Ala Leu Gly Thr Gly Ile Ala Leu Asn

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<222> (101)..(499)  
<223> RXN02465
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<210> 1182

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 1182

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Thr Ile Gly Phe Gly Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr
 20 25 30

Gly Glu Thr Asp Pro Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr
 35 40 45

Trp Val Gly Tyr Gly Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr
 50 55 60

Val Val Ala Gly Ala Ile Asn Met Met Lys Gly His Arg Trp Gly Arg
 65 70 75 80

Gly Ala Val Val Met Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr
 85 90 95

Met Phe Ile Glu Gly Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser
 100 105 110

Ala Leu Phe Val Leu Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp
 115 120 125

Ala Asn Asn Glu Ile
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<210> 1183

<211> 522

<212> DNA

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<220>

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<222> (101)..(499)

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 Met Pro Ala Ser Ile
 1 5

cgc tgg ggc ggc atc gtc gcc ctc att caa tcc acc atc gga ttc ggt 163
 Arg Trp Gly Gly Ile Val Ala Leu Ile Gln Ser Thr Ile Gly Phe Gly
 10 15 20

tac gcc ttt ttc ctt att tac agg gaa gct acg ggc gag acg gat cca 211
 Tyr Ala Phe Phe Leu Ile Tyr Arg Glu Ala Thr Gly Glu Thr Asp Pro
 25 30 35

agc atc gtc tac gaa acc gat aac gcc aac acg tgg gtt ggc tac ggt 259
 Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr Trp Val Gly Tyr Gly
 40 45 50

acc gct gca ttc ttc atc att gtg ttc gga acg gtt gtt gca ggc gca 307
 Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr Val Val Ala Gly Ala
 55 60 65

atc aac atg atg aag ggg cat cgc tgg gga cgc gga gct gtc gtc atg 355
 Ile Asn Met Met Lys Gly His Arg Trp Gly Arg Gly Ala Val Val Met
 70 75 80 85

ctg aat att att ttg ttg ccg gct gcg tat tac atg ttt atc gaa ggc 403
 Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr Met Phe Ile Glu Gly
 90 95 100

cga ttc tcc tgg gcg atc gtc aca gga atc tca gct ctc ttc gtt ttg 451
 Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser Ala Leu Phe Val Leu
 105 110 115

ggc gca ctg ttt aat aag cgc gcc gtc ctt tgg gct aac aac gag atc 499
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<210> 1184
 <211> 133
 <212> PRT
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Gly Glu Thr Asp Pro Ser Ile Val Tyr Glu Thr Asp Asn Ala Asn Thr
 35 40 45

Trp Val Gly Tyr Gly Thr Ala Ala Phe Phe Ile Ile Val Phe Gly Thr
 50 55 60

Val Val Ala Gly Ala Ile Asn Met Met Lys Gly His Arg Trp Gly Arg
 65 70 75 80

Gly Ala Val Val Met Leu Asn Ile Ile Leu Leu Pro Ala Ala Tyr Tyr
 85 90 95

Met Phe Ile Glu Gly Arg Phe Ser Trp Ala Ile Val Thr Gly Ile Ser
 100 105 110

Ala Leu Phe Val Leu Gly Ala Leu Phe Asn Lys Arg Ala Val Leu Trp
 115 120 125

Ala Asn Asn Glu Ile
130

<210> 1185
<211> 187
<212> DNA
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<220>
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<222> (101)..(187)
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tgctggcact ttccgccagg tcggcgctgc ttttctctgc gtg ggc gag ggg cag 115
Val Gly Glu Gly Gln
1 5
gaa caa act ttt acg tac gtc att gag att gag gat ggc gtc aac acg 163
Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu Asp Gly Val Asn Thr
10 15 20
gcc gct tat ggt ggc gac gat gcg 187
Ala Ala Tyr Gly Gly Asp Asp Ala
25

<210> 1186
<211> 29
<212> PRT
<213> Corynebacterium glutamicum

<400> 1186
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Asp Gly Val Asn Thr Ala Ala Tyr Gly Gly Asp Asp Ala
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<211> 187
<212> DNA
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<220>
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Val Gly Glu Gly Gln
1 5
gaa caa act ttt acg tac gtc att gag att gag gat ggc gtc aac acg 163

Glu Gln Thr Phe Thr Tyr Val Ile Glu Ile Glu Asp Gly Val Asn Thr
 10 15 20

gcc gct tat ggt ggc gac gat gcg
 Ala Ala Tyr Gly Gly Asp Asp Ala
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 187

<210> 1188
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 <212> PRT
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(271)
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cattaagcgc actggtcgtt tgcgtattcc ggggggtcttt gtg gct ggc act cat 115
 Val Ala Gly Thr His
 1 5

gcg tat gtc aat gaa act ctt tcg gaa aat gag ttc agc atg tgc cga 163
 Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu Phe Ser Met Cys Arg
 10 15 20

aag aat gaa cct ggt ttg gtc att gag ctg gag aac atc agc atc gat 211
 Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu Asn Ile Ser Ile Asp
 25 30 35

cgc att gtc att tcc aca cca gat gcc cac cgc tat gcg gat gag ctc 259
 Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg Tyr Ala Asp Glu Leu
 40 45 50

atg gcg gct gtt tagaactcag tttccgtcaa taa 294
 Met Ala Ala Val
 55

<210> 1190
 <211> 57
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1190

Val Ala Gly Thr His Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu
 1 5 10 15
 Phe Ser Met Cys Arg Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu
 20 25 30
 Asn Ile Ser Ile Asp Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg
 35 40 45
 Tyr Ala Asp Glu Leu Met Ala Ala Val
 50 55

<210> 1191
 <211> 294
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(271)
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 Val Ala Gly Thr His
 1 5
 gcg tat gtc aat gaa act ctt tcg gaa aat gag ttc agc atg tgc cga 163
 Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu Phe Ser Met Cys Arg
 10 15 20
 aag aat gaa cct ggt ttg gtc att gag ctg gag aac atc agc atc gat 211
 Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu Asn Ile Ser Ile Asp
 25 30 35
 cgc att gtc att tcc aca cca gat gcc cac cgc tat gcg gat gag ctc 259
 Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg Tyr Ala Asp Glu Leu
 40 45 50
 atg gcg gct gtt tagaactcag tttccgtcaa taa 294
 Met Ala Ala Val
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<210> 1192
 <211> 57
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1192
 Val Ala Gly Thr His Ala Tyr Val Asn Glu Thr Leu Ser Glu Asn Glu
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 Phe Ser Met Cys Arg Lys Asn Glu Pro Gly Leu Val Ile Glu Leu Glu
 20 25 30
 Asn Ile Ser Ile Asp Arg Ile Val Ile Ser Thr Pro Asp Ala His Arg
 35 40 45

Tyr Ala Asp Glu Leu Met Ala Ala Val
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<210> 1193

<211> 759

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> RXN02510

<400> 1193

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                                         Met Asp Ser Ser Asp
                                         1 5
agc cac gtt ggt cag gat gta tat gtt gat caa ggt cta ggg gag ccc 163
Ser His Val Gly Gln Asp Val Tyr Val Asp Gln Gly Leu Gly Glu Pro
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gac aga ctg gaa cgt ctg tgg gcg ccc tac cgg atg agc tac atc aac 211
Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg Met Ser Tyr Ile Asn
                        25 30 35
act cga tct ggc ggt aag caa tca act acc gcc aag cgg gac ccc ttc 259
Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala Lys Arg Asp Pro Phe
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att gag gtt ccc aaa atg agt gat gag gac gcc ctg atc gtt gcg cgg 307
Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly Leu Ile Val Ala Arg
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Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr Pro Tyr Asn Ala Gly
                        70 75 80 85
cac atg atg gtg atc cca ttc cgt aag gaa aag aat cta gag gat ttg 403
His Met Met Val Ile Pro Phe Arg Lys Glu Lys Asn Leu Glu Asp Leu
                        90 95 100
agc ttg gca gaa tct gcg gag ttg atg ctc ttt acc caa acg gcc atc 451
Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe Thr Gln Thr Ala Ile
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Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala Val Asn Val Gly Leu
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Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly Asp His Leu His Val
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cat gtg gtg cct agg tgg tcg ggt gat gct aat ttc atg act gtg att 595
His Val Val Pro Arg Trp Ser Gly Asp Ala Asn Phe Met Thr Val Ile
                        150 155 160 165

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 170 175 180

ctt gcg caa gca tgg ggc acc att gat ggg gca cca ggc act gtc gac 691
 Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala Pro Gly Thr Val Asp
 185 190 195

cca acg ctg act tca gcg atc cgt acc gca gca ccg aag gag cac 736
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<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 1194

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 20 25 30

Met Ser Tyr Ile Asn Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala
 35 40 45

Lys Arg Asp Pro Phe Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly
 50 55 60

Leu Ile Val Ala Arg Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr
 65 70 75 80

Pro Tyr Asn Ala Gly His Met Met Val Ile Pro Phe Arg Lys Glu Lys
 85 90 95

Asn Leu Glu Asp Leu Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe
 100 105 110

Thr Gln Thr Ala Ile Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala
 115 120 125

Val Asn Val Gly Leu Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly
 130 135 140

Asp His Leu His Val His Val Val Pro Arg Trp Ser Gly Asp Ala Asn
 145 150 155 160

Phe Met Thr Val Ile Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg
 165 170 175

Gln Thr Arg Ala Met Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala
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Pro Gly Thr Val Asp Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala
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Pro Lys Glu His
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<211> 759
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(736)
<223> FRXA02510

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Met Asp Ser Ser Asp
1 5
agc cac gtt ggt cag gat gta tat gtt gat caa ggt cta ggg gag ccc 163
Ser His Val Gly Gln Asp Val Tyr Val Asp Gln Gly Leu Gly Glu Pro
10 15 20
gac aga ctg gaa cgt ctg tgg gcg ccc tac cgg atg agc tac atc aac 211
Asp Arg Leu Glu Arg Leu Trp Ala Pro Tyr Arg Met Ser Tyr Ile Asn
25 30 35
act cga tct ggc ggt aag caa tca act acc gcc aag cgg gac ccc ttc 259
Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala Lys Arg Asp Pro Phe
40 45 50
att gag gtt ccc aaa atg agt gat gag gac ggc ctg atc gtt gcg cgg 307
Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly Leu Ile Val Ala Arg
55 60 65
ggc gag ctg gtg tat tgc gta ctc aac ttg tat ccc tac aac gct gga 355
Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr Pro Tyr Asn Ala Gly
70 75 80 85
cac atg atg gtg atc cca ttc cgt aag gaa aag aat cta gag gat ttg 403
His Met Met Val Ile Pro Phe Arg Lys Glu Lys Asn Leu Glu Asp Leu
90 95 100
agc ttg gca gaa tct gcg gag ttg atg ctc ttt acc caa acg gcc atc 451
Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe Thr Gln Thr Ala Ile
105 110 115
aag gcg ctg aag cag gtg tca aac cct gat gct gtc aat gtt ggt tta 499
Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala Val Asn Val Gly Leu
120 125 130
aac ctt ggc aaa gca tcg ggt ggc tca gtg gga gat cac ctt cat gtc 547
Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly Asp His Leu His Val
135 140 145
cat gtg gtg cct agg tgg tcg ggt gat gct aat ttc atg act gtg att 595
His Val Val Pro Arg Trp Ser Gly Asp Ala Asn Phe Met Thr Val Ile
150 155 160 165

gac ggt gtc aaa gtg cta ccg cag acc ctg cgt caa acc agg gcc atg 643
 Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg Gln Thr Arg Ala Met
 170 175 180

ctt gcg caa gca tgg ggc acc att gat ggg gca cca ggc act gtc gac 691
 Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala Pro Gly Thr Val Asp
 185 190 195

cca acg ctg act tca gcg atc cgt acc gca gca ccg aag gag cac 736
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<210> 1196

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 1196

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Met Ser Tyr Ile Asn Thr Arg Ser Gly Gly Lys Gln Ser Thr Thr Ala
 35 40 45

Lys Arg Asp Pro Phe Ile Glu Val Pro Lys Met Ser Asp Glu Asp Gly
 50 55 60

Leu Ile Val Ala Arg Gly Glu Leu Val Tyr Cys Val Leu Asn Leu Tyr
 65 70 75 80

Pro Tyr Asn Ala Gly His Met Met Val Ile Pro Phe Arg Lys Glu Lys
 85 90 95

Asn Leu Glu Asp Leu Ser Leu Ala Glu Ser Ala Glu Leu Met Leu Phe
 100 105 110

Thr Gln Thr Ala Ile Lys Ala Leu Lys Gln Val Ser Asn Pro Asp Ala
 115 120 125

Val Asn Val Gly Leu Asn Leu Gly Lys Ala Ser Gly Gly Ser Val Gly
 130 135 140

Asp His Leu His Val His Val Val Pro Arg Trp Ser Gly Asp Ala Asn
 145 150 155 160

Phe Met Thr Val Ile Asp Gly Val Lys Val Leu Pro Gln Thr Leu Arg
 165 170 175

Gln Thr Arg Ala Met Leu Ala Gln Ala Trp Gly Thr Ile Asp Gly Ala
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Pro Gly Thr Val Asp Pro Thr Leu Thr Ser Ala Ile Arg Thr Ala Ala
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Pro Lys Glu His

210

<210> 1197

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXN02519

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Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser
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atc aac gac cgc gat acc gac gcc tca ggg ctt gag cct gaa aag att 211
Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile
                25                30                35

cgc cga ttt gca tgg ctg cgc ctg atc ggc acc atg ggt gcg tta atg 259
Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met
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atc gcg ttt ggt gcg ctg ggc gcg ggt gca ctt ccg gtg gtg aat aat 307
Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn
                55                60                65

ccg tat gtg gat ttc cct ggc gga aac ttc atg agc cga atg ctg cag 355
Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln
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acc tct tcc atg atc gtg ctc atc ggc gtg gga ttt ttg gtg ctg gcg 403
Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala
                90                95                100

tgg gtg tta atg gca ccg ctg gtg ggt att cct ttt aaa cgc agc gga 451
Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly
                105                110                115

aac aga aca gcc agc gtg agt ttg tcc atg ctg cgc cgc aca ttt ggc 499
Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly
                120                125                130

gcc tgg gta gcg ccc atc atg ctc acc gcc cca ctg ttt act caa gac 547
Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp
                135                140                145

att tat tct tat ctg gca caa ggc tct gtg acc gcg cag gga atg gat 595
Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp
                150                155                160                165

gcc tac gcc ggt gga ccg ctt gaa cta ttg ggg ccc gat aat cat ctg 643

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Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser Pro Ser Pro Tyr Gly	
185 190 195	
cct gtt gcg ctg agc atc gcg gcg tcg ata agc gtt att act aat gac	739
Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp	
200 205 210	
agc atc gtt gga ggc gtg ctg gcg cac cgt att gcg tcg ctg ctg ggc	787
Ser Ile Val Gly Gly Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly	
215 220 225	
gtt gtg gct gca ggc tgg gcg atc acc atg ctg gcc agg cgc tgt cgg	835
Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg	
230 235 240 245	
gta tct gaa gaa gcg tcc ttt tac ctg ggc gta ctt aat ccg ctg ctg	883
Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu	
250 255 260	
att ctg cac ctg atc ggc ggt att cac aac gaa tcc atc ctg ctg gga	931
Ile Leu His Leu Ile Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly	
265 270 275	
ttt tta ctt gtt ggc ctg gaa ctc gga ctg cgt ggc acc gac cgg att	979
Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg Gly Thr Asp Arg Ile	
280 285 290	
caa aca ggg ctg tgg ggg cct gcg tgg aca tat att gca ctg agt ggc	1027
Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly	
295 300 305	
gta ttg att tct tgc gca ggc ctg gtc aag gtg acc ggc ttt att ggg	1075
Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly	
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Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly	
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His Arg His Val Val Ala Ile Gly Val Ala Gly Leu Val Gln Val Ala	
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gcc ctg gtg atc acc gtg gtt gtt ctc agt gtg att acc gga atc agt	1219
Ala Leu Val Ile Thr Val Val Val Leu Ser Val Ile Thr Gly Ile Ser	
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Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp	
375 380 385	
atg tct atg acc acc aac att ggc gtt att tct gga ttc atc gga atg	1315
Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met	
390 395 400 405	
aat ttg ggg cta ggc gac cac acc gca gcc atg ctc gtt gtg acc cgt	1363
Asn Leu Gly Leu Gly Asp His Thr Ala Ala Met Leu Val Val Thr Arg	

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ggc gca gcg ctc gga ttc agc att ctc cta tta gtt gga tgg tgg agt Gly Ala Ala Leu Gly Phe Ser Ile Leu Leu Leu Val Gly Trp Trp Ser 520 525 530			1699
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Glu Pro Glu Lys Ile Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr 35 40 45			
Met Gly Ala Leu Met Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu 50 55 60			
Pro Val Val Asn Asn Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met 65 70 75 80			
Ser Arg Met Leu Gln Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly 85 90 95			

Phe Leu Val Leu Ala Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro
100 105 110

Phe Lys Arg Ser Gly Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu
115 120 125

Arg Arg Thr Phe Gly Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro
130 135 140

Leu Phe Thr Gln Asp Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr
145 150 155 160

Ala Gln Gly Met Asp Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly
165 170 175

Pro Asp Asn His Leu Ala Arg Ser Val Pro Phe Ile Trp Ala Gln Ser
180 185 190

Pro Ser Pro Tyr Gly Pro Val Ala Leu Ser Ile Ala Ala Ser Ile Ser
195 200 205

Val Ile Thr Asn Asp Ser Ile Val Gly Gly Val Leu Ala His Arg Ile
210 215 220

Ala Ser Leu Leu Gly Val Val Ala Ala Gly Trp Ala Ile Thr Met Leu
225 230 235 240

Ala Arg Arg Cys Arg Val Ser Glu Glu Ala Ser Phe Tyr Leu Gly Val
245 250 255

Leu Asn Pro Leu Leu Ile Leu His Leu Ile Gly Gly Ile His Asn Glu
260 265 270

Ser Ile Leu Leu Gly Phe Leu Leu Val Gly Leu Glu Leu Gly Leu Arg
275 280 285

Gly Thr Asp Arg Ile Gln Thr Gly Leu Trp Gly Pro Ala Trp Thr Tyr
290 295 300

Ile Ala Leu Ser Gly Val Leu Ile Ser Cys Ala Gly Leu Val Lys Val
305 310 315 320

Thr Gly Phe Ile Gly Leu Gly Phe Val Gly Met Ala Leu Ala Arg Ala
325 330 335

Phe His Ala Arg Gly His Arg His Val Val Ala Ile Gly Val Ala Gly
340 345 350

Leu Val Gln Val Ala Ala Leu Val Ile Thr Val Val Val Leu Ser Val
355 360 365

Ile Thr Gly Ile Ser Leu Gly Trp Ile Thr Gly Gln Gly Gly Ala Ala
370 375 380

Thr Ile Arg Ser Trp Met Ser Met Thr Thr Asn Ile Gly Val Ile Ser
385 390 395 400

Gly Phe Ile Gly Met Asp Leu Gly Leu Gly Asp His Thr Ala Ala Met
405 410 415

Leu Val Val Thr Arg Ala Ala Gly Ile Ala Val Ala Ala Ala Phe Met

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His Pro Trp Tyr Met Leu Trp Ala Ile Val Pro Leu Ala Ser Trp Ala 465 470 475 480		
Asn Arg Leu Phe Phe Gln Leu Gly Val Ile Ala Tyr Ser Thr Ala Phe 485 490 495		
Ser Phe Phe Val Leu Pro Arg Gly Leu Ala Leu Pro Val Gly Thr Val 500 505 510		
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<211> 1929

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<220>

<221> CDS

<222> (101)..(1906)

<223> FRXA02519

<400> 1199

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                                     Met Phe Ser Ala Pro
                                     1 5

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Ser Asn Ala Pro Glu Asn Arg Lys Trp Phe Pro Arg Ala Pro Arg Pro
      25 30 35

cta cgc caa ttt ctc gac act ttg ccg cgc atc ggc acc gct ggt tcc 259
Leu Arg Gln Phe Leu Asp Thr Leu Pro Arg Ile Gly Thr Ala Gly Ser
      40 45 50

aga tca gcg acc ctc cac gtg gaa gac gag cag agc cct tta ggg gca 307
Arg Ser Ala Thr Leu His Val Glu Asp Glu Gln Ser Pro Leu Gly Ala
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acg ctt ttc gac gtc gcg acc ggc gcg agc tcc atc aac gac cgc gat 355
Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser Ile Asn Asp Arg Asp
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 90 95 100

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 Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met Ile Ala Phe Gly Ala
 105 110 115

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 Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn Pro Tyr Val Asp Phe
 120 125 130

cct ggc gga aac ttc atg agc cga atg ctg cag acc tct tcc atg atc 547
 Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln Thr Ser Ser Met Ile
 135 140 145

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ccg ctg gtg ggt att cct ttt aaa cgc agc gga aac aga aca gcc agc 643
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 170 175 180

gtg agt ttg tcc atg ctg cgc cgc aca ttt ggc gcc tgg gta gcg ccc 691
 Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly Ala Trp Val Ala Pro
 185 190 195

atc atg ctc acc gcc cca ctg ttt act caa gac att tat tct tat ctg 739
 Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp Ile Tyr Ser Tyr Leu
 200 205 210

gca caa ggc tct gtg acc gcg cag gga atg gat gcc tac gcc ggt gga 787
 Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp Ala Tyr Ala Gly Gly
 215 220 225

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 250 255 260

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 Ile Ala Ala Ser Ile Ser Val Ile Thr Asn Asp Ser Ile Val Gly Gly
 265 270 275

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 Val Leu Ala His Arg Ile Ala Ser Leu Leu Gly Val Val Ala Ala Gly
 280 285 290

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 Trp Ala Ile Thr Met Leu Ala Arg Arg Cys Arg Val Ser Glu Glu Ala
 295 300 305

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 Ser Phe Tyr Leu Gly Val Leu Asn Pro Leu Leu Ile Leu His Leu Ile
 310 315 320 325

ggc ggt att cac aac gaa tcc atc ctg ctg gga ttt tta ctt gtt ggc 1123

Gly Gly Ile His Asn Glu Ser Ile Leu Leu Gly Phe Leu Leu Val Gly
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 Gly Pro Ala Trp Thr Tyr Ile Ala Leu Ser Gly Val Leu Ile Ser Cys
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 Ala Gly Leu Val Lys Val Thr Gly Phe Ile Gly Leu Gly Phe Val Gly
 375 380 385
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 Met Ala Leu Ala Arg Ala Phe His Ala Arg Gly His Arg His Val Val
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 410 415 420
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 Val Val Val Leu Ser Val Ile Thr Gly Ile Ser Leu Gly Trp Ile Thr
 425 430 435
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 Gly Gln Gly Gly Ala Ala Thr Ile Arg Ser Trp Met Ser Met Thr Thr
 440 445 450
 aac att ggc gtt att tct gga ttc atc gga atg aat ttg ggg cta ggc 1507
 Asn Ile Gly Val Ile Ser Gly Phe Ile Gly Met Asn Leu Gly Leu Gly
 455 460 465
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 Asp His Thr Ala Ala Met Leu Val Val Thr Arg Ala Ala Gly Ile Ala
 470 475 480 485
 gta gct gcc gcc ttc atg gtt cgt atg ttg ttt gcc aca tat aga ggt 1603
 Val Ala Ala Ala Phe Met Val Arg Met Leu Phe Ala Thr Tyr Arg Gly
 490 495 500
 cac att cac gct gtg ggc gga ctg ggc gtg gcg act ttc gtc ctc gtt 1651
 His Ile His Ala Val Gly Gly Leu Gly Val Ala Thr Phe Val Leu Val
 505 510 515
 atc ctc ttc ccc gtg gtg cat ccg tgg tac atg ctg tgg gct atc gtg 1699
 Ile Leu Phe Pro Val Val His Pro Trp Tyr Met Leu Trp Ala Ile Val
 520 525 530
 ccg cta gct tcc tgg gca aat aga ctg ttc ttc cag ctc gga gtg att 1747
 Pro Leu Ala Ser Trp Ala Asn Arg Leu Phe Phe Gln Leu Gly Val Ile
 535 540 545
 gcc tac tcc act gcc ttc agt ttc ttt gtg ctg cct cgc ggg ctt gca 1795
 Ala Tyr Ser Thr Ala Phe Ser Phe Phe Val Leu Pro Arg Gly Leu Ala
 550 555 560 565
 ctt cca gtc gga act gtc ttt tcc atc tac ttc ggc gca gcg ctc gga 1843
 Leu Pro Val Gly Thr Val Phe Ser Ile Tyr Phe Gly Ala Ala Leu Gly

570

575

580

ttc agc att ctc cta tta gtt gga tgg tgg agt ttg agg cgg aat cca 1891
 Phe Ser Ile Leu Leu Leu Val Gly Trp Trp Ser Leu Arg Arg Asn Pro
 585 590 595

acc ttt ggt tta cac tgatcaactg tgactactga ttt 1929
 Thr Phe Gly Leu His
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<210> 1200

<211> 602

<212> PRT

<213> Corynebacterium glutamicum

<400> 1200

Met Phe Ser Ala Pro Leu Arg Arg Met Met Arg Val Thr Lys Asp Glu
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Gln Ile Gln Pro Asn Ser Asn Ala Pro Glu Asn Arg Lys Trp Phe Pro
 20 25 30

Arg Ala Pro Arg Pro Leu Arg Gln Phe Leu Asp Thr Leu Pro Arg Ile
 35 40 45

Gly Thr Ala Gly Ser Arg Ser Ala Thr Leu His Val Glu Asp Glu Gln
 50 55 60

Ser Pro Leu Gly Ala Thr Leu Phe Asp Val Ala Thr Gly Ala Ser Ser
 65 70 75 80

Ile Asn Asp Arg Asp Thr Asp Ala Ser Gly Leu Glu Pro Glu Lys Ile
 85 90 95

Arg Arg Phe Ala Trp Leu Arg Leu Ile Gly Thr Met Gly Ala Leu Met
 100 105 110

Ile Ala Phe Gly Ala Leu Gly Ala Gly Ala Leu Pro Val Val Asn Asn
 115 120 125

Pro Tyr Val Asp Phe Pro Gly Gly Asn Phe Met Ser Arg Met Leu Gln
 130 135 140

Thr Ser Ser Met Ile Val Leu Ile Gly Val Gly Phe Leu Val Leu Ala
 145 150 155 160

Trp Val Leu Met Ala Pro Leu Val Gly Ile Pro Phe Lys Arg Ser Gly
 165 170 175

Asn Arg Thr Ala Ser Val Ser Leu Ser Met Leu Arg Arg Thr Phe Gly
 180 185 190

Ala Trp Val Ala Pro Ile Met Leu Thr Ala Pro Leu Phe Thr Gln Asp
 195 200 205

Ile Tyr Ser Tyr Leu Ala Gln Gly Ser Val Thr Ala Gln Gly Met Asp
 210 215 220

Ala Tyr Ala Gly Gly Pro Leu Glu Leu Leu Gly Pro Asp Asn His Leu
 225 230 235 240

135 140 145
 gaa gct ttt agt cgg cat ggt tat gca gca act gtc gat gcc act cga 595
 Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr Val Asp Ala Thr Arg
 150 155 160 165
 aac ggg ttg caa ctc tgc cag cat cac tgt cca ata tct aca gtc gcc 643
 Asn Gly Leu Gln Leu Cys Gln His His Cys Pro Ile Ser Thr Val Ala
 170 175 180
 acg gaa ttt ccg gaa ctg tgt gag gca gag cat caa gca gtc tca gaa 691
 Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His Gln Ala Val Ser Glu
 185 190 195
 ctt ttg ggg cag cac acg caa cca ttg gca aca atc gcg gac ggc cac 739
 Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr Ile Ala Asp Gly His
 200 205 210
 ggc atc tgc aca aca aat att gca ttg aca ccc atc aaa cac tcc 784
 Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro Ile Lys His Ser
 215 220 225
 tgatgaaagg agcggatcat gac 807

 <210> 1202
 <211> 228
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1202
 Val Gly Asp Val Val Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp
 1 5 10 15
 Thr Arg Arg Lys Ile Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile
 20 25 30
 Ala Ser Asp Ile Ala Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg
 35 40 45
 Arg His Leu Asp Asn Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn
 50 55 60
 Pro Arg Gln Asn Pro Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys
 65 70 75 80
 Thr Tyr Arg Leu Thr Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr
 85 90 95
 Asp Ser Leu Ala Ala Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly
 100 105 110
 Asp Asp Ala Val Arg Gln Phe Ala Arg Lys Arg Ile Glu Thr Ile Val
 115 120 125
 Glu Gly Ile Thr Pro Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr
 130 135 140
 Ala Lys Ser Leu Val Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr
 145 150 155 160

Val Asp Ala Thr Arg Asn Gly Leu Gln Leu Cys Gln His His Cys Pro
 165 170 175

Ile Ser Thr Val Ala Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His
 180 185 190

Gln Ala Val Ser Glu Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr
 195 200 205

Ile Ala Asp Gly His Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro
 210 215 220

Ile Lys His Ser
 225

<210> 1203

<211> 807

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02520

<400> 1203

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gtctaaaggt gaaagctaaa tcaagcagga ggtgacacca gtg gga gat gtt gta 115
 Val Gly Asp Val Val
 1 5

aaa ggc aac gac gcg cac acc gga gac ggt gat acg cgc cga aaa att 163
 Lys Gly Asn Asp Ala His Thr Gly Asp Gly Asp Thr Arg Arg Lys Ile
 10 15 20

ctt ctc atc ctg ttg gaa cgt gca ccg gtg atc gct tca gat att gct 211
 Leu Leu Ile Leu Leu Glu Arg Ala Pro Val Ile Ala Ser Asp Ile Ala
 25 30 35

gaa cag ctt cag ctt tca act gtg gga gtg cgc agg cac cta gac aac 259
 Glu Gln Leu Gln Leu Ser Thr Val Gly Val Arg Arg His Leu Asp Asn
 40 45 50

ttg gtt gaa gaa aat ctg gcg gag gcg gca aat ccg cgc cag aac cca 307
 Leu Val Glu Glu Asn Leu Ala Glu Ala Ala Asn Pro Arg Gln Asn Pro
 55 60 65

tat gag ccc aaa atg cgc ggt agg cca gca aaa act tat cgg ctt act 355
 Tyr Glu Pro Lys Met Arg Gly Arg Pro Ala Lys Thr Tyr Arg Leu Thr
 70 75 80 85

gat aaa ggt cgc tca atc ttc ggc cac gaa tat gat tcc ctt gct gcg 403
 Asp Lys Gly Arg Ser Ile Phe Gly His Glu Tyr Asp Ser Leu Ala Ala
 90 95 100

gca gct cta gcc act ctt cga gag gtc ggc gga gat gat gca gta agg 451
 Ala Ala Leu Ala Thr Leu Arg Glu Val Gly Gly Asp Asp Ala Val Arg
 105 110 115

Glu Gly Ile Thr Pro Ala Asp Val Thr Asp Gln Ser Ile Glu Asp Thr
 130 135 140
 Ala Lys Ser Leu Val Glu Ala Phe Ser Arg His Gly Tyr Ala Ala Thr
 145 150 155 160
 Val Asp Ala Thr Arg Asn Gly Leu Gln Leu Cys Gln His His Cys Pro
 165 170 175
 Ile Ser Thr Val Ala Thr Glu Phe Pro Glu Leu Cys Glu Ala Glu His
 180 185 190
 Gln Ala Val Ser Glu Leu Leu Gly Gln His Thr Gln Pro Leu Ala Thr
 195 200 205
 Ile Ala Asp Gly His Gly Ile Cys Thr Thr Asn Ile Ala Leu Thr Pro
 210 215 220
 Ile Lys His Ser
 225

<210> 1205
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXN02534

<400> 1205
 ttaccagtaa tctatgcaga ttactgtcc gttggggatc cgcgcctatc ggaagttgcc 60
 tacattataa aaactcagat tcaggaatac acagaccatg atg aat tca ccg aac 115
 Met Asn Ser Pro Asn
 1 5
 gcg gac att att tta gta gtt aac aag ctg tcc aag ttt att gat atc 163
 Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser Lys Phe Ile Asp Ile
 10 15 20
 gaa aat att atg ctc gtt gga gca cga tgt aga gac att cac cag caa 211
 Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg Asp Ile His Gln Gln
 25 30 35
 aaa tat cgc gat caa aca gcg ggt aga aga act aag gat gtt gac ttc 259
 Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr Lys Asp Val Asp Phe
 40 45 50
 gct tta gct tta gaa agc tgg gac gac ttc aat cta tta aag caa caa 307
 Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn Leu Leu Lys Gln Gln
 55 60 65
 ttc tca ccg act ggt aac gca tgg caa gga atc acc att gga aat att 355
 Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile Thr Ile Gly Asn Ile
 70 75 80 85
 cca gta gat ctc gtg cca ttc gga aat att gaa aac cca ccc ggt gaa 403
 Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu Asn Pro Pro Gly Glu

90	95	100	
gtc ttg tcc aga aaa ggt cat cta ctt aat gtc gct ggg ttc aag gaa Val Leu Ser Arg Lys Gly His Leu Leu Asn Val Ala Gly Phe Lys Glu 105 110 115			451
gta ttc gag caa gct gag cta tat ccc cta aat gat gcg ata gac att Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn Asp Ala Ile Asp Ile 120 125 130			499
aag ttg tct aca gtt ccc gga ctt act gcg cta aag cta cat gca tgg Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu Lys Leu His Ala Trp 135 140 145			547
ctc gac cgt aaa gaa aat aac atc aaa gat gca agc gat cta gca tta Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala Ser Asp Leu Ala Leu 150 155 160 165			595
atc ttg tcg tgg tac gaa gag gat gta gaa act tta tgg aat cgc tat Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr Leu Trp Asn Arg Tyr 170 175 180			643
ttt gcc ctg gaa aat caa gga tac ata ggt gaa cca gag gca atg gca Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu Pro Glu Ala Met Ala 185 190 195			691
gct gaa tta cta gga ctt gac act gga aga ata ctc ggc cac aag gaa Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile Leu Gly His Lys Glu 200 205 210			739
act caa gcc ctc ctt gat cga ttt aat gaa cag tct cct cct gag cta Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln Ser Pro Pro Glu Leu 215 220 225			787
aac caa ttt gct gaa tca ctt gaa gcc cct cct gaa cac agt cac cca Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro Glu His Ser His Pro 230 235 240 245			835
tta gaa cgg cgt cgt atc cag gtc gag gca ctg tta ggt gga ctt aga Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu Leu Gly Gly Leu Arg 250 255 260			883
gat tcc ctc ggt tac gat gaa tagcttccaa tcccgattg ttc Asp Ser Leu Gly Tyr Asp Glu 265			927

<210> 1206

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 1206

Met	Asn	Ser	Pro	Asn	Ala	Asp	Ile	Ile	Leu	Val	Val	Asn	Lys	Leu	Ser
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Lys	Phe	Ile	Asp	Ile	Glu	Asn	Ile	Met	Leu	Val	Gly	Ala	Arg	Cys	Arg
		20						25					30		

Asp	Ile	His	Gln	Gln	Lys	Tyr	Arg	Asp	Gln	Thr	Ala	Gly	Arg	Arg	Thr
	35						40					45			

Lys Asp Val Asp Phe Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn
 50 55 60
 Leu Leu Lys Gln Gln Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile
 65 70 75 80
 Thr Ile Gly Asn Ile Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu
 85 90 95
 Asn Pro Pro Gly Glu Val Leu Ser Arg Lys Gly His Leu Leu Asn Val
 100 105 110
 Ala Gly Phe Lys Glu Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn
 115 120 125
 Asp Ala Ile Asp Ile Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu
 130 135 140
 Lys Leu His Ala Trp Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala
 145 150 155 160
 Ser Asp Leu Ala Leu Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr
 165 170 175
 Leu Trp Asn Arg Tyr Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu
 180 185 190
 Pro Glu Ala Met Ala Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile
 195 200 205
 Leu Gly His Lys Glu Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln
 210 215 220
 Ser Pro Pro Glu Leu Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro
 225 230 235 240
 Glu His Ser His Pro Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu
 245 250 255
 Leu Gly Gly Leu Arg Asp Ser Leu Gly Tyr Asp Glu
 260 265

<210> 1207

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> FRXA02534

<400> 1207

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 tacattataa aaactcagat tcaggaatac acagaccatg atg aat tca ccg aac 115
 Met Asn Ser Pro Asn
 1 5

gcg gac att att tta gta gtt aac aag ctg tcc aag ttt att gat atc 163
Ala Asp Ile Ile Leu Val Val Asn Lys Leu Ser Lys Phe Ile Asp Ile
10 15 20

gaa aat att atg ctc gtt gga gca cga tgt aga gac att cac cag caa 211
Glu Asn Ile Met Leu Val Gly Ala Arg Cys Arg Asp Ile His Gln Gln
25 30 35

aaa tat cgc gat caa aca gcg ggt aga aga act aag gat gtt gac ttc 259
Lys Tyr Arg Asp Gln Thr Ala Gly Arg Arg Thr Lys Asp Val Asp Phe
40 45 50

gct tta gct tta gaa agc tgg gac gac ttc aat cta tta aag caa caa 307
Ala Leu Ala Leu Glu Ser Trp Asp Asp Phe Asn Leu Leu Lys Gln Gln
55 60 65

ttc tca ccg act ggt aac gca tgg caa gga atc acc att gga aat att 355
Phe Ser Pro Thr Gly Asn Ala Trp Gln Gly Ile Thr Ile Gly Asn Ile
70 75 80 85

cca gta gat ctc gtg cca ttc gga aat att gaa aac cca ccc ggt gaa 403
Pro Val Asp Leu Val Pro Phe Gly Asn Ile Glu Asn Pro Pro Gly Glu
90 95 100

gtc ttg tcc aga aaa ggt cat cta ctt aat gtc gct ggg ttc aag gaa 451
Val Leu Ser Arg Lys Gly His Leu Leu Asn Val Ala Gly Phe Lys Glu
105 110 115

gta ttc gag caa gct gag cta tat ccc cta aat gat gcg ata gac att 499
Val Phe Glu Gln Ala Glu Leu Tyr Pro Leu Asn Asp Ala Ile Asp Ile
120 125 130

aag ttg tct aca gtt ccc gga ctt act gcg cta aag cta cat gca tgg 547
Lys Leu Ser Thr Val Pro Gly Leu Thr Ala Leu Lys Leu His Ala Trp
135 140 145

ctc gac cgt aaa gaa aat aac atc aaa gat gca agc gat cta gca tta 595
Leu Asp Arg Lys Glu Asn Asn Ile Lys Asp Ala Ser Asp Leu Ala Leu
150 155 160 165

atc ttg tcg tgg tac gaa gag gat gta gaa act tta tgg aat cgc tat 643
Ile Leu Ser Trp Tyr Glu Glu Asp Val Glu Thr Leu Trp Asn Arg Tyr
170 175 180

ttt gcc ctg gaa aat caa gga tac ata ggt gaa cca gag gca atg gca 691
Phe Ala Leu Glu Asn Gln Gly Tyr Ile Gly Glu Pro Glu Ala Met Ala
185 190 195

gct gaa tta cta gga ctt gac act gga aga ata ctc ggc cac aag gaa 739
Ala Glu Leu Leu Gly Leu Asp Thr Gly Arg Ile Leu Gly His Lys Glu
200 205 210

act caa gcc ctc ctt gat cga ttt aat gaa cag tct cct cct gag cta 787
Thr Gln Ala Leu Leu Asp Arg Phe Asn Glu Gln Ser Pro Pro Glu Leu
215 220 225

aac caa ttt gct gaa tca ctt gaa gcc cct cct gaa cac agt cac cca 835
Asn Gln Phe Ala Glu Ser Leu Glu Ala Pro Pro Glu His Ser His Pro
230 235 240 245

tta gaa cgg cgt cgt atc cag gtc gag gca ctg tta ggt gga ctt aga 883

927

<213> *Corynebacterium glutamicum*

Glu His Ser His Pro Leu Glu Arg Arg Arg Ile Gln Val Glu Ala Leu
245 250 255

Leu Gly Gly Leu Arg Asp Ser Leu Gly Tyr Asp Glu
 260 265

<210> 1209
 <211> 585
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(562)
 <223> RXN02537

<400> 1209
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 tagacgtcga tcttggccac aactgaata agttgcaactg atg ctc gcc ctc aaa 115
 Met Leu Ala Leu Lys
 1 5
 agt tca gaa tta gaa ggc ata gcc aca tca ctc acc gcc gtg gcg ggt 163
 Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu Thr Ala Val Ala Gly
 10 15 20
 gcg ctc cac gaa tca aac act gac cgg ttg cag tcc tgg cag cag ctc 211
 Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln Ser Trp Gln Gln Leu
 25 30 35
 gaa acg atg acc tct gcc agc tcc ctt atc cag gcc ttt atc aag ctt 259
 Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln Gly Phe Ile Lys Leu
 40 45 50
 gtc gat tac aac cga ccc aca gtg aat atc gtg gaa caa atg cac aaa 307
 Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val Glu Gln Met His Lys
 55 60 65
 acc gca tcc acg ctt ttc aac acc gct gat ttc cta cgc act ttg gaa 355
 Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe Leu Arg Thr Leu Glu
 70 75 80 85
 ggc tat gtt gat gta ctg gaa aaa caa gcc gat aaa tct ata acg ctc 403
 Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp Lys Ser Ile Thr Leu
 90 95 100
 acc gtc atg ctt cga tat att gcc agc ttg agt agc ctt tta gac ctc 451
 Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser Ser Leu Leu Asp Leu
 105 110 115
 atg tgt gca cgc gag atc aac gcg ttg tgc aca gcg att act cca gaa 499
 Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr Ala Ile Thr Pro Glu
 120 125 130
 cca ttg aag cat ctg ggc gat ttt ggc act cta ccg cct cag caa tcc 547
 Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu Pro Pro Gln Gln Ser
 135 140 145
 acg agt ttc att tgg tgaatgcccc accagaaatc cgt 585
 Thr Ser Phe Ile Trp
 150

<210> 1210

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 1210

Met Leu Ala Leu Lys Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu
 1 5 10 15

Thr Ala Val Ala Gly Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln
 20 25 30

Ser Trp Gln Gln Leu Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln
 35 40 45

Gly Phe Ile Lys Leu Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val
 50 55 60

Glu Gln Met His Lys Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe
 65 70 75 80

Leu Arg Thr Leu Glu Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp
 85 90 95

Lys Ser Ile Thr Leu Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser
 100 105 110

Ser Leu Leu Asp Leu Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr
 115 120 125

Ala Ile Thr Pro Glu Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu
 130 135 140

Pro Pro Gln Gln Ser Thr Ser Phe Ile Trp
 145 150

<210> 1211

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> FRXA02537

<400> 1211

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tagacgtcga tcttggccac aactgaata agttgcactg atg ctc gcc ctc aaa 115
 Met Leu Ala Leu Lys
 1 5

agt tca gaa tta gaa ggc ata gcc aca tca ctc acc gcc gtg gcg ggt 163
 Ser Ser Glu Leu Glu Gly Ile Ala Thr Ser Leu Thr Ala Val Ala Gly
 10 15 20

gcg ctc cac gaa tca aac act gac cgg ttg cag tcc tgg cag cag ctc 211

Ala Leu His Glu Ser Asn Thr Asp Arg Leu Gln Ser Trp Gln Gln Leu
25 30 35

gaa acg atg acc tct gcc agc tcc ctt atc cag ggc ttt atc aag ctt 259
Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln Gly Phe Ile Lys Leu
40 45 50

gtc gat tac aac cga ccc aca gtg aat atc gtg gaa caa atg cac aaa 307
Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val Glu Gln Met His Lys
55 60 65

acc gca tcc acg ctt ttc aac acc gct gat ttc cta cgc act ttg gaa 355
Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe Leu Arg Thr Leu Glu
70 75 80 85

ggc tat gtt gat gta ctg gaa aaa caa gcc gat aaa tct ata acg ctc 403
Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp Lys Ser Ile Thr Leu
90 95 100

acc gtc atg ctt cga tat att gcc agc ttg agt agc ctt tta gac ctc 451
Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser Ser Leu Leu Asp Leu
105 110 115

atg tgt gca cgc gag atc aac gcg ttg tgc aca gcg att act cca gaa 499
Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr Ala Ile Thr Pro Glu
120 125 130

cca ttg aag cat ctg ggc gat ttt ggc act cta ccg cct cag caa tcc 547
Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu Pro Pro Gln Gln Ser
135 140 145

acg agt ttc att tgg tgaatgcccc accagaaatc cgt 585
Thr Ser Phe Ile Trp
150

<210> 1212
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 1212
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20 25 30

Ser Trp Gln Gln Leu Glu Thr Met Thr Ser Ala Ser Ser Leu Ile Gln
35 40 45

Gly Phe Ile Lys Leu Val Asp Tyr Asn Arg Pro Thr Val Asn Ile Val
50 55 60

Glu Gln Met His Lys Thr Ala Ser Thr Leu Phe Asn Thr Ala Asp Phe
65 70 75 80

Leu Arg Thr Leu Glu Gly Tyr Val Asp Val Leu Glu Lys Gln Ala Asp
85 90 95

Lys Ser Ile Thr Leu Thr Val Met Leu Arg Tyr Ile Ala Ser Leu Ser

100

105

110

Ser Leu Leu Asp Leu Met Cys Ala Arg Glu Ile Asn Ala Leu Cys Thr
 115 120 125

Ala Ile Thr Pro Glu Pro Leu Lys His Leu Gly Asp Phe Gly Thr Leu
 130 135 140

Pro Pro Gln Gln Ser Thr Ser Phe Ile Trp
 145 150

<210> 1213

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(772)

<223> RXN02538

<400> 1213

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 Val Asn Ala Pro Pro
 1 5
 gaa atc cgt gcc tta gcc gaa gcc cat ccc gat atg cag atc cta gaa 163
 Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp Met Gln Ile Leu Glu
 10 15 20
 gcc ggc gat ggt tca ttg gta gca tcg ttt ggg gat att gat agg gct 211
 Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly Asp Ile Asp Arg Ala
 25 30 35
 acg acc gtg acc acc atc gtg gca ggt gtg ggt tcc tcc aac cca gaa 259
 Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly Ser Ser Asn Pro Glu
 40 45 50
 ggg tgg aat aca tat gtt gac cgt gcc cgc aca gta tct gct tcc acc 307
 Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr Val Ser Ala Ser Thr
 55 60 65
 ggt tcc gca acg gtg ttg tgg ctg gga tat caa gca ccc gct tcg att 355
 Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln Ala Pro Ala Ser Ile
 70 75 80 85
 cct gct gcg gta tcc ggc gcg gca gcg aat cgc gct gcc gcg gat ctc 403
 Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg Ala Ala Ala Asp Leu
 90 95 100
 cag agg ttt caa gcg gca cta cag tcc cgc aat ccc cac caa aga aaa 451
 Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn Pro His Gln Arg Lys
 105 110 115
 gta gtg atg ggc tac agc tac ggt tcc aca gtg gtg gga aaa gct gcg 499
 Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val Val Gly Lys Ala Ala
 120 125 130

tct tcc ggc gag ctc agt gcc gat gcg ttg gta ttg gtt ggc agt ccc 547
 Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val Leu Val Gly Ser Pro
 135 140 145

ggc gcg ggt gtc tcg cac tct tcc cag ctt ggc gca cct gtg tat gcg 595
 Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly Ala Pro Val Tyr Ala
 150 155 160 165

gta aca ggg tct gct gat ccc atc ggt ttt gcc ggc acc caa tat gac 643
 Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala Gly Thr Gln Tyr Asp
 170 175 180

ggc atc cac ggc act gat ccc acc gct gcc cta ttc ggt gca aca gtg 691
 Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu Phe Gly Ala Thr Val
 185 190 195

tgg gat tcg ccc tca acg cat tcc ggt tat tgg aat gac cag gag ttc 739
 Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp Asn Asp Gln Glu Phe
 200 205 210

ctg ggc aat gtg gcg gag gtg gtt cgc ggc aaa tagaaaagcc gccgcacact 792
 Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
 215 220

gga 795

<210> 1214
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 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Asp Ile Asp Arg Ala Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly
 35 40 45
 Ser Ser Asn Pro Glu Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr
 50 55 60
 Val Ser Ala Ser Thr Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln
 65 70 75 80
 Ala Pro Ala Ser Ile Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg
 85 90 95
 Ala Ala Ala Asp Leu Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn
 100 105 110
 Pro His Gln Arg Lys Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val
 115 120 125
 Val Gly Lys Ala Ala Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val
 130 135 140
 Leu Val Gly Ser Pro Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly

145	150	155	160
Ala Pro Val Tyr	Ala Val Thr Gly Ser	Ala Asp Pro Ile Gly Phe Ala	
	165	170	175
Gly Thr Gln Tyr Asp Gly Ile His	Gly Thr Asp Pro Thr Ala Ala Leu		
	180	185	190
Phe Gly Ala Thr Val Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp			
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Asn Asp Gln Glu Phe Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys			
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<220>
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 <223> FRXA02538

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 Val Asn Ala Pro Pro
 1 5

gaa atc cgt gcc tta gcc gaa gcc cat ccc gat atg cag atc cta gaa 163
 Glu Ile Arg Ala Leu Ala Glu Ala His Pro Asp Met Gln Ile Leu Glu
 10 15 20

gcc gcc gat ggt tca ttg gta gca tcg ttt ggg gat att gat agg gct 211
 Ala Gly Asp Gly Ser Leu Val Ala Ser Phe Gly Asp Ile Asp Arg Ala
 25 30 35

acg acc gtg acc acc atc gtg gca ggt gtg ggt tcc tcc aac cca gaa 259
 Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly Ser Ser Asn Pro Glu
 40 45 50

ggg tgg aat aca tat gtt gac cgt gcc cgc aca gta tct gct tcc acc 307
 Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr Val Ser Ala Ser Thr
 55 60 65

ggt tcc gca acg gtg ttg tgg ctg gga tat caa gca ccc gct tcg att 355
 Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln Ala Pro Ala Ser Ile
 70 75 80 85

cct gct gcg gta tcc ggc gcg gca gcg aat cgc gct gcc gcg gat ctc 403
 Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg Ala Ala Ala Asp Leu
 90 95 100

cag agg ttt caa gcg gca cta cag tcc cgc aat ccc cac caa aga aaa 451
 Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn Pro His Gln Arg Lys
 105 110 115

gta gtg atg ggc tac agc tac ggt tcc aca gtg gtg gga aaa gct gcg 499

Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val Val Gly Lys Ala Ala
 120 125 130
 tct tcc ggc gag ctc agt gcc gat gcg ttg gta ttg gtt ggc agt ccc 547
 Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val Leu Val Gly Ser Pro
 135 140 145
 ggc gcg ggt gtc tcg cac tct tcc cag ctt ggc gca cct gtg tat gcg 595
 Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly Ala Pro Val Tyr Ala
 150 155 160 165
 gta aca ggg tct gct gat ccc atc ggt ttt gcc ggc acc caa tat gac 643
 Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala Gly Thr Gln Tyr Asp
 170 175 180
 ggc atc cac ggc act gat ccc acc gct gcc cta ttc ggt gca aca gtg 691
 Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu Phe Gly Ala Thr Val
 185 190 195
 tgg gat tcg ccc tca acg cat tcc ggt tat tgg aat gac cag gag ttc 739
 Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp Asn Asp Gln Glu Phe
 200 205 210
 ctg ggc aat gtg gcg gag gtg gtt cgc ggc aaa tagaaaagcc gccgcacact 792
 Leu Gly Asn Val Ala Glu Val Val Arg Gly Lys
 215 220
 gga 795

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 <213> Corynebacterium glutamicum

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 Asp Ile Asp Arg Ala Thr Thr Val Thr Thr Ile Val Ala Gly Val Gly
 35 40 45
 Ser Ser Asn Pro Glu Gly Trp Asn Thr Tyr Val Asp Arg Ala Arg Thr
 50 55 60
 Val Ser Ala Ser Thr Gly Ser Ala Thr Val Leu Trp Leu Gly Tyr Gln
 65 70 75 80
 Ala Pro Ala Ser Ile Pro Ala Ala Val Ser Gly Ala Ala Ala Asn Arg
 85 90 95
 Ala Ala Ala Asp Leu Gln Arg Phe Gln Ala Ala Leu Gln Ser Arg Asn
 100 105 110
 Pro His Gln Arg Lys Val Val Met Gly Tyr Ser Tyr Gly Ser Thr Val
 115 120 125
 Val Gly Lys Ala Ala Ser Ser Gly Glu Leu Ser Ala Asp Ala Leu Val

130

135

140

Leu Val Gly Ser Pro Gly Ala Gly Val Ser His Ser Ser Gln Leu Gly
 145 150 155 160

Ala Pro Val Tyr Ala Val Thr Gly Ser Ala Asp Pro Ile Gly Phe Ala
 165 170 175

Gly Thr Gln Tyr Asp Gly Ile His Gly Thr Asp Pro Thr Ala Ala Leu
 180 185 190

Phe Gly Ala Thr Val Trp Asp Ser Pro Ser Thr His Ser Gly Tyr Trp
 195 200 205

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<211> 726

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<222> (101)..(703)

<223> RXN02555

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 Met Gly Glu Gln Phe
 1 5

cca ggc gat aaa aac atc cga gtc agc gac acc gaa aga tca gca gca 163
 Pro Gly Asp Lys Asn Ile Arg Val Ser Asp Thr Glu Arg Ser Ala Ala
 10 15 20

cta gca gca ctc ggc cag ttc tac gca gaa ggt cgc ctc tcc cta gaa 211
 Leu Ala Ala Leu Gly Gln Phe Tyr Ala Glu Gly Arg Leu Ser Leu Glu
 25 30 35

gaa acc gac gac cgc tgc gaa gcc gtc gcc gac gcc aaa acc cgc ggc 259
 Glu Thr Asp Asp Arg Cys Glu Ala Val Ala Asp Ala Lys Thr Arg Gly
 40 45 50

gac ctc aac gcc atc ttc tac gat ctg ccc aac caa caa atc gca gtc 307
 Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn Gln Gln Ile Ala Val
 55 60 65

gtc gac cgc tcc gaa caa acc tac aca gcc acc gaa gtt gcc gaa ctc 355
 Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr Glu Val Ala Glu Leu
 70 75 80 85

cac cgc aaa ggc gca cgc cca cgc gcc gga atc ctc gga ctc acc aca 403
 His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile Leu Gly Leu Thr Thr
 90 95 100

gtt tta gcc atc acc ggt acc gct gct ttc gcc agc acc aca gct ttt 451
 Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala Ser Thr Thr Ala Phe

105 110 115
 gca aca gta ctt tta gcc ctg att ccg atc gtg ttc atc atg ctg tac 499
 Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val Phe Ile Met Leu Tyr
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 gtg atg aaa att ggt cct gaa tcc tgg cac gca cca aca cct cgc caa 547
 Val Met Lys Ile Gly Pro Glu Ser Trp His Ala Pro Thr Pro Arg Gln
 135 140 145
 ctt cag cga aag cgc atg atc gaa ctg cgt gaa aag gaa aaa ctc cgc 595
 Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu Lys Glu Lys Leu Arg
 150 155 160 165
 gac atg gag ctc aaa gcc cag cgc aag gaa cgc acc cac gca tta acc 643
 Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg Thr His Ala Leu Thr
 170 175 180
 aac cgc gcg ttg gat gct gct gaa act gct ttc aac acc aag ccc tgg 691
 Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe Asn Thr Lys Pro Trp
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 aag aag aac aaa tagggctttt gaagtgtgtc gcg 726
 Lys Lys Asn Lys
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 20 25 30
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 35 40 45
 Ala Lys Thr Arg Gly Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn
 50 55 60
 Gln Gln Ile Ala Val Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr
 65 70 75 80
 Glu Val Ala Glu Leu His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile
 85 90 95
 Leu Gly Leu Thr Thr Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala
 100 105 110
 Ser Thr Thr Ala Phe Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val
 115 120 125
 Phe Ile Met Leu Tyr Val Met Lys Ile Gly Pro Glu Ser Trp His Ala
 130 135 140
 Pro Thr Pro Arg Gln Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu

gtg atg aaa att ggt cct gaa tcc tgg cac gca cca aca cct cgc caa 547
 Val Met Lys Ile Gly Pro Glu Ser Trp His Ala Pro Thr Pro Arg Gln
 135 140 145

ctt cag cga aag cgc atg atc gaa ctg cgt gaa aag gaa aaa ctc cgc 595
 Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu Lys Glu Lys Leu Arg
 150 155 160 165

gac atg gag ctc aaa gcc cag cgc aag gaa cgc acc cac gca tta acc 643
 Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg Thr His Ala Leu Thr
 170 175 180

aac cgc gcg ttg gat gct gct gaa act gct ttc aac acc aag ccc tgg 691
 Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe Asn Thr Lys Pro Trp
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aag aag aac aaa tagggctttt gaagtgtgtc gcg 726
 Lys Lys Asn Lys
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<210> 1220

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1220

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 20 25 30

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 35 40 45

Ala Lys Thr Arg Gly Asp Leu Asn Ala Ile Phe Tyr Asp Leu Pro Asn
 50 55 60

Gln Gln Ile Ala Val Val Asp Arg Ser Glu Gln Thr Tyr Thr Ala Thr
 65 70 75 80

Glu Val Ala Glu Leu His Arg Lys Gly Ala Arg Pro Arg Ala Gly Ile
 85 90 95

Leu Gly Leu Thr Thr Val Leu Ala Ile Thr Gly Thr Ala Ala Phe Ala
 100 105 110

Ser Thr Thr Ala Phe Ala Thr Val Leu Leu Ala Leu Ile Pro Ile Val
 115 120 125

Phe Ile Met Leu Tyr Val Met Lys Ile Gly Pro Glu Ser Trp His Ala
 130 135 140

Pro Thr Pro Arg Gln Leu Gln Arg Lys Arg Met Ile Glu Leu Arg Glu
 145 150 155 160

Lys Glu Lys Leu Arg Asp Met Glu Leu Lys Ala Gln Arg Lys Glu Arg
 165 170 175

Thr His Ala Leu Thr Asn Arg Ala Leu Asp Ala Ala Glu Thr Ala Phe

180

185

190

Asn Thr Lys Pro Trp Lys Lys Asn Lys
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<210> 1221

<211> 1125

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1102)

<223> RXN02564

<400> 1221

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                                         Met Ala Glu Val Gly
                                         1 5

gca gaa ccc gca ggg tct gca caa tcc aaa act aaa caa ttt gtt gta 163
Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr Lys Gln Phe Val Val
                        10 15 20

ggt acc gca gcg gtg gtc atc act gca atc gct gcg ttt ttc tcc atc 211
Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala Ala Phe Phe Ser Ile
                        25 30 35

cag tct gca tcc ggt ggc gag gat att cgt tcc aac atg acg ctg att 259
Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser Asn Met Thr Leu Ile
                        40 45 50

gct cct gca gct gca ggt gga ggt tgg gat act ttc caa cgt gag cag 307
Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr Phe Gln Arg Glu Gln
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cag cag tct atg cgc gtg aat aag atc gtg aac aat att cag gtg gtc 355
Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn Asn Ile Gln Val Val
                        70 75 80 85

aac atc cct gga gct ggt gga acc att gca ctt ggc aaa ctg tct acc 403
Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu Gly Lys Leu Ser Thr
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atg act gca ccg aac acc ttg atg gtg ggt gga acg ggg cat atc gca 451
Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly Thr Gly His Ile Ala
                        105 110 115

gca caa att caa ttc gat acc cct gcg aaa atc cag gat gtc acc cca 499
Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile Gln Asp Val Thr Pro
                        120 125 130

att gct cgt gtg gtg gaa gag ttc gac atc atc acc gtg cca gcg gat 547
Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile Thr Val Pro Ala Asp
                        135 140 145

tct cca tac aac acc ctt gaa gag ctc att gaa ggt tgg aag gca gat 595
Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu Gly Trp Lys Ala Asp

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Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser Phe Asp Gln Leu Val	170	175	180	
atg aca gaa att gca ctg tct gca ggt ata gat cct aag caa acc acc				691
Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp Pro Lys Gln Thr Thr	185	190	195	
ttt att cct tct gat ggt ggt ggc gaa gcg att cag gcg cta ctg aac				739
Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile Gln Ala Leu Leu Asn	200	205	210	
gga acc gca aag gca tca act ggt ggt ttt gct gat atg tat ccg cag				787
Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala Asp Met Tyr Pro Gln	215	220	225	
gta gaa gcc ggt cga ttg aag gtt ttg gga att gct gca gaa gaa cgc				835
Val Glu Ala Gly Arg Leu Lys Val Leu Gly Ile Ala Ala Glu Glu Arg	230	235	240	245
ctt cca ggt tct gac att cca acg cta gtg gaa caa ggc tat gac gtg				883
Leu Pro Gly Ser Asp Ile Pro Thr Leu Val Glu Gln Gly Tyr Asp Val	250	255	260	
acc ttg acc aac tgg cgt gcc atg ttc gct cct cct ggt ttg agc gat				931
Thr Leu Thr Asn Trp Arg Ala Met Phe Ala Pro Pro Gly Leu Ser Asp	265	270	275	
gat caa att gcg gaa ctt cga gca atc gtt gcg gag tct gtg gag act				979
Asp Gln Ile Ala Glu Leu Arg Ala Ile Val Ala Glu Ser Val Glu Thr	280	285	290	
gct gaa tgg cag tcc gcg gtg gaa cga aac tac tgg atg aac gcc tca				1027
Ala Glu Trp Gln Ser Ala Val Glu Arg Asn Tyr Trp Met Asn Ala Ser	295	300	305	
ctt gaa ggc gaa gaa ctc gac cag ttt gtt gaa gat gaa att gac cga				1075
Leu Glu Gly Glu Glu Leu Asp Gln Phe Val Glu Asp Glu Ile Asp Arg	310	315	320	325
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Lys Gln Phe Val Val Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala	20	25	30	

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 35 40 45
 Asn Met Thr Leu Ile Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr
 50 55 60
 Phe Gln Arg Glu Gln Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn
 65 70 75 80
 Asn Ile Gln Val Val Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu
 85 90 95
 Gly Lys Leu Ser Thr Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly
 100 105 110
 Thr Gly His Ile Ala Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile
 115 120 125
 Gln Asp Val Thr Pro Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile
 130 135 140
 Thr Val Pro Ala Asp Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu
 145 150 155 160
 Gly Trp Lys Ala Asp Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser
 165 170 175
 Phe Asp Gln Leu Val Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp
 180 185 190
 Pro Lys Gln Thr Thr Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile
 195 200 205
 Gln Ala Leu Leu Asn Gly Thr Ala Lys Ala Ser Thr Gly Gly Phe Ala
 210 215 220
 Asp Met Tyr Pro Gln Val Glu Ala Gly Arg Leu Lys Val Leu Gly Ile
 225 230 235 240
 Ala Ala Glu Glu Arg Leu Pro Gly Ser Asp Ile Pro Thr Leu Val Glu
 245 250 255
 Gln Gly Tyr Asp Val Thr Leu Thr Asn Trp Arg Ala Met Phe Ala Pro
 260 265 270
 Pro Gly Leu Ser Asp Asp Gln Ile Ala Glu Leu Arg Ala Ile Val Ala
 275 280 285
 Glu Ser Val Glu Thr Ala Glu Trp Gln Ser Ala Val Glu Arg Asn Tyr
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<211> 775

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(775)

<223> FRXA02564

<400> 1223

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 Met Ala Glu Val Gly
 1 5

gca gaa ccc gca ggg tct gca caa tcc aaa act aaa caa ttt gtt gta 163
 Ala Glu Pro Ala Gly Ser Ala Gln Ser Lys Thr Lys Gln Phe Val Val
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ggc acc gca gcg gtg gtc atc act gca atc gct gcg ttt ttc tcc atc 211
 Gly Thr Ala Ala Val Val Ile Thr Ala Ile Ala Ala Phe Phe Ser Ile
 25 30 35

cag tct gca tcc ggt ggc gag gat att cgt tcc aac atg acg ctg att 259
 Gln Ser Ala Ser Gly Gly Glu Asp Ile Arg Ser Asn Met Thr Leu Ile
 40 45 50

gct cct gca gct gca ggt gga ggt tgg gat act ttc caa cgt gag cag 307
 Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr Phe Gln Arg Glu Gln
 55 60 65

cag cag tct atg cgc gtg aat aag atc gtg aac aat att cag gtg gtc 355
 Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn Asn Ile Gln Val Val
 70 75 80 85

aac atc cct gga gct ggt gga acc att gca ctt ggc aaa ctg tct acc 403
 Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu Gly Lys Leu Ser Thr
 90 95 100

atg act gca ccg aac acc ttg atg gtg ggt gga acg ggg cat atc gca 451
 Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly Thr Gly His Ile Ala
 105 110 115

gca caa att caa ttc gat acc cct gcg aaa atc cag gat gtc acc cca 499
 Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile Gln Asp Val Thr Pro
 120 125 130

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 Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile Thr Val Pro Ala Asp
 135 140 145

tct cca tac aac acc ctt gaa gag ctc att gaa ggt tgg aag gca gat 595
 Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu Gly Trp Lys Ala Asp
 150 155 160 165

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 Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser Phe Asp Gln Leu Val
 170 175 180

atg aca gaa att gca ctg tct gca ggt ata gat cct aag caa acc acc 691
 Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp Pro Lys Gln Thr Thr
 185 190 195

ttt att cct tct gat ggt ggt ggc gaa gcg att cag gcg cta ctg aac 739
 Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile Gln Ala Leu Leu Asn
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<210> 1224

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 1224

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 20 25 30

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 35 40 45

Asn Met Thr Leu Ile Ala Pro Ala Ala Ala Gly Gly Gly Trp Asp Thr
 50 55 60

Phe Gln Arg Glu Gln Gln Gln Ser Met Arg Val Asn Lys Ile Val Asn
 65 70 75 80

Asn Ile Gln Val Val Asn Ile Pro Gly Ala Gly Gly Thr Ile Ala Leu
 85 90 95

Gly Lys Leu Ser Thr Met Thr Ala Pro Asn Thr Leu Met Val Gly Gly
 100 105 110

Thr Gly His Ile Ala Ala Gln Ile Gln Phe Asp Thr Pro Ala Lys Ile
 115 120 125

Gln Asp Val Thr Pro Ile Ala Arg Val Val Glu Glu Phe Asp Ile Ile
 130 135 140

Thr Val Pro Ala Asp Ser Pro Tyr Asn Thr Leu Glu Glu Leu Ile Glu
 145 150 155 160

Gly Trp Lys Ala Asp Pro Ala Gly Val Ser Trp Thr Gly Gly Gly Ser
 165 170 175

Phe Asp Gln Leu Val Met Thr Glu Ile Ala Leu Ser Ala Gly Ile Asp
 180 185 190

Pro Lys Gln Thr Thr Phe Ile Pro Ser Asp Gly Gly Gly Glu Ala Ile
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 225

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 <223> RXN02568

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                                     Met Asp Gly Thr Ser
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cca cag aac aaa att tcc acc act ccc cca gcg cca gga aat gct att    163
Pro Gln Asn Lys Ile Ser Thr Thr Pro Pro Ala Pro Gly Asn Ala Ile
                10                15                20

cct gca cct gga ggc gcc att cct aca cca gcg aaa act gag cag gac    211
Pro Ala Pro Gly Gly Ala Ile Pro Thr Pro Ala Lys Thr Glu Gln Asp
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gca gta cct cca act gtg gcg gcg aaa cta ccc gta cct gga agt tct    259
Ala Val Pro Pro Thr Val Ala Ala Lys Leu Pro Val Pro Gly Ser Ser
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att cca gca ccc ggt aga gca ttg cca act cca gtg gct ccg gga ggt    307
Ile Pro Ala Pro Gly Arg Ala Leu Pro Thr Pro Val Ala Pro Gly Gly
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tcc gtc cca gct ccg aga gcg tcc gca cct gcg gtt cct aac gtt cct    355
Ser Val Pro Ala Pro Arg Ala Ser Ala Pro Ala Val Pro Asn Val Pro
                70                75                80                85

gca gct ccc ggc gct gct gtt cca gct ccg gga atc tcg atc ccg gca    403
Ala Ala Pro Gly Ala Ala Val Pro Ala Pro Gly Ile Ser Ile Pro Ala
                90                95                100

gca cct agt gcc cca ggc agt gca att cca aca cca ggc aca gca atc    451
Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly Thr Ala Ile
                105                110                115

cct gtg cct gga agt gca act cct gtc cca gca cct ggg gtt agt gca    499
Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly Val Ser Ala
                120                125                130

cct ggc gca agc gtt cca agc att cca gta cca gga tct gtc acc cca    547
Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser Val Thr Pro
                135                140                145

cct gca cca gga att tcc gca cct ggc ggt gca ctt ccg act cct ggc    595
Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro Thr Pro Gly
                150                155                160                165

agt gcg ccc cca aca cct ggc ggt gcc ctt ccg act cca ggt gag gca    643
Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro Gly Glu Ala
                170                175                180
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ctt ccc gtt ccc gga gca cct ggt gca ccc gga gca tcc gga atc cca Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser Gly Ile Pro 185 190 195	691
agt cct ggc ctt cca acc cca ggt gtc cca act ccc gga gct tcc tta Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly Ala Ser Leu 200 205 210	739
cca gtc cca gga gca cca gac gca cct gga acc cca agc att ccc gca Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser Ile Pro Ala 215 220 225	787
gct ccc ggc att caa gca cca gga att cca gca gca cca gga gcc cct Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro Gly Ala Pro 230 235 240 245	835
gcc caa gct gct gct cac gca aag cca gta ttc caa gat gca gag aaa Ala Gln Ala Ala His Ala Lys Pro Val Phe Gln Asp Ala Glu Lys 250 255 260	883
cga cct cgc aca gat gaa gct gga aat gcg aag aag gaa ctg ccg ctg Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu Leu Pro Leu 265 270 275	931
aga gtt cgg ttg gcg cag cca att aca cgt aag cag tgg gca atg act Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp Ala Met Thr 280 285 290	979
ctt ggt gtc ctg gtt ctc gga gca att gtc gtg gct gca atc gcg gtg Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala Ile Ala Val 295 300 305	1027
gtc ctt gcc aaa tgg gcg ttt acc acg gag tgg ttg cag gac ttc gtc Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln Asp Phe Val 310 315 320 325	1075
gag aag tat ccg ggt aaa tat gac aac ccc gaa ggt gcg cca gta gga Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala Pro Val Gly 330 335 340	1123
att cca acg tgg ctg agt tgg cag cac ttc ttc aac atg ttc ttc atg Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met Phe Phe Met 345 350 355	1171
gtg ttg att atc aag acg ggc att gag atc aat aga acc cgc agg cca Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr Arg Arg Pro 360 365 370	1219
aag ggt tat tgg acg ccg aaa aag ggt ggc aag aag atc tcc ttg acg Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile Ser Leu Thr 375 380 385	1267
ttg tgg atc cac ctg gtt ttg gat ttg ttg tgg atc atc aac ggt gcg Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile Asn Gly Ala 390 395 400 405	1315
gtg ttc atc att ttg ttg ttc gcg acg ggt cag tgg atg cgc att gtt Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met Arg Ile Val 410 415 420	1363

cca acc agt tgg gat gtg ttc ccg aac gcg ctg agt gct ggt ttg cag 1411
 Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala Gly Leu Gln
 425 430 435

tat gtg tcg ttg gat tgg ccg act gag aat ggt tgg gcg aat tac aac 1459
 Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala Asn Tyr Asn
 440 445 450

agt ttg cag gag ctg acg tac ttc ttc act gtc ttt att gcg gca ccg 1507
 Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile Ala Ala Pro
 455 460 465

ttg tcg att gtg tct ggt ttc cgg atg tcg agt tac tgg cct aag aac 1555
 Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp Pro Lys Asn
 470 475 480 485

aat gcg acg atg aat aag ttg atc ccc atc ggg ttt gct cgt gcg ctg 1603
 Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala Arg Ala Leu
 490 495 500

cac atg cca gtg atg gtg tat tac atc gtg ttc att tgt atc cac gtg 1651
 His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys Ile His Val
 505 510 515

ttc ttg gtg ttg gcg acc ggc gcg ttg cgc aat ttc aac cat atg tat 1699
 Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn His Met Tyr
 520 525 530

gca ggt caa gac gtt gtg aac tgg gtt ggt ttt ggt tgg ttc gtg gcg 1747
 Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp Phe Val Ala
 535 540 545

tcg ttg 1753
 Ser Leu
 550

<210> 1226
 <211> 551
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1226
 Met Asp Gly Thr Ser Pro Gln Asn Lys Ile Ser Thr Thr Pro Pro Ala
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 Pro Gly Asn Ala Ile Pro Ala Pro Gly Gly Ala Ile Pro Thr Pro Ala
 20 25 30
 Lys Thr Glu Gln Asp Ala Val Pro Thr Val Ala Ala Lys Leu Pro
 35 40 45
 Val Pro Gly Ser Ser Ile Pro Ala Pro Gly Arg Ala Leu Pro Thr Pro
 50 55 60
 Val Ala Pro Gly Gly Ser Val Pro Ala Pro Arg Ala Ser Ala Pro Ala
 65 70 75 80
 Val Pro Asn Val Pro Ala Ala Pro Gly Ala Ala Val Pro Ala Pro Gly
 85 90 95

Ile Ser Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr
 100 105 110
 Pro Gly Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala
 115 120 125
 Pro Gly Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro
 130 135 140
 Gly Ser Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala
 145 150 155 160
 Leu Pro Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro
 165 170 175
 Thr Pro Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly
 180 185 190
 Ala Ser Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr
 195 200 205
 Pro Gly Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr
 210 215 220
 Pro Ser Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala
 225 230 235 240
 Ala Pro Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe
 245 250 255
 Gln Asp Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys
 260 265 270
 Lys Glu Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys
 275 280 285
 Gln Trp Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val
 290 295 300
 Ala Ala Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp
 305 310 315 320
 Leu Gln Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu
 325 330 335
 Gly Ala Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe
 340 345 350
 Asn Met Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn
 355 360 365
 Arg Thr Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys
 370 375 380
 Lys Ile Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp
 385 390 395 400
 Ile Ile Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln
 405 410 415
 Trp Met Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu

420	425	430
Ser Ala Gly Leu Gln Tyr Val	Ser Leu Asp Trp Pro	Thr Glu Asn Gly
435	440	445
Trp Ala Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val		
450	455	460
Phe Ile Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser		
465	470	475 480
Tyr Trp Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly		
485	490	495
Phe Ala Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe		
500	505	510
Ile Cys Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn		
515	520	525
Phe Asn His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe		
530	535	540
Gly Trp Phe Val Ala Ser Leu		
545	550	

<210> 1227

<211> 1359

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1359)

<223> FRXA02568

<400> 1227

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Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly	
1 5 10 15	
aca gca atc cct gtg cct gga agt gca act cct gtc cca gca cct ggc	96
Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly	
20 25 30	
gtt agt gca cct ggc gca agc gtt cca agc att cca gta cca gga tct	144
Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser	
35 40 45	
gtc acc cca cct gca cca gga att tcc gca cct ggc ggt gca ctt ccg	192
Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro	
50 55 60	
act cct ggc agt gcg ccc cca aca cct ggc ggt gcc ctt ccg act cca	240
Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro	
65 70 75 80	
ggt gag gca ctt ccc gtt ccc gga gca cct ggt gca ccc gga gca tcc	288
Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser	
85 90 95	

gga atc cca agt cct ggc ctt cca acc cca ggt gtc cca act ccc gga Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly 100 105 110	336
gct tcc tta cca gtc cca gga gca cca gac gca cct gga acc cca agc Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser 115 120 125	384
att ccc gca gct ccc ggc att caa gca cca gga att cca gca gca cca Ile Pro Ala Ala Pro Gly Ile Gln Ala Pro Gly Ile Pro Ala Ala Pro 130 135 140	432
gga gcc cct gcc caa gct gct gct cac gca aag cca gta ttc caa gat Gly Ala Pro Ala Gln Ala Ala Ala His Ala Lys Pro Val Phe Gln Asp 145 150 155 160	480
gca gag aaa cga cct cgc aca gat gaa gct gga aat gcg aag aag gaa Ala Glu Lys Arg Pro Arg Thr Asp Glu Ala Gly Asn Ala Lys Lys Glu 165 170 175	528
ctg ccg ctg aga gtt cgg ttg gcg cag cca att aca cgt aag cag tgg Leu Pro Leu Arg Val Arg Leu Ala Gln Pro Ile Thr Arg Lys Gln Trp 180 185 190	576
gca atg act ctt ggt gtc ctg gtt ctc gga gca att gtc gtg gct gca Ala Met Thr Leu Gly Val Leu Val Leu Gly Ala Ile Val Val Ala Ala 195 200 205	624
atc gcg gtg gtc ctt gcc aaa tgg gcg ttt acc acg gag tgg ttg cag Ile Ala Val Val Leu Ala Lys Trp Ala Phe Thr Thr Glu Trp Leu Gln 210 215 220	672
gac ttc gtc gag aag tat ccg ggt aaa tat gac aac ccc gaa ggt gcg Asp Phe Val Glu Lys Tyr Pro Gly Lys Tyr Asp Asn Pro Glu Gly Ala 225 230 235 240	720
cca gta gga att cca acg tgg ctg agt tgg cag cac ttc ttc aac atg Pro Val Gly Ile Pro Thr Trp Leu Ser Trp Gln His Phe Phe Asn Met 245 250 255	768
ttc ttc atg gtg ttg att atc aag acg ggc att gag atc aat aga acc Phe Phe Met Val Leu Ile Ile Lys Thr Gly Ile Glu Ile Asn Arg Thr 260 265 270	816
cgc agg cca aag ggt tat tgg acg ccg aaa aag ggt ggc aag aag atc Arg Arg Pro Lys Gly Tyr Trp Thr Pro Lys Lys Gly Gly Lys Lys Ile 275 280 285	864
tcc ttg acg ttg tgg atc cac ctg gtt ttg gat ttg ttg tgg atc atc Ser Leu Thr Leu Trp Ile His Leu Val Leu Asp Leu Leu Trp Ile Ile 290 295 300	912
aac ggt gcg gtg ttc atc att ttg ttg ttc gcg acg ggt cag tgg atg Asn Gly Ala Val Phe Ile Ile Leu Leu Phe Ala Thr Gly Gln Trp Met 305 310 315 320	960
cgc att gtt cca acc agt tgg gat gtg ttc ccg aac gcg ctg agt gct Arg Ile Val Pro Thr Ser Trp Asp Val Phe Pro Asn Ala Leu Ser Ala 325 330 335	1008

ggt ttg cag tat gtg tcg ttg gat tgg ccg act gag aat ggt tgg gcg 1056
 Gly Leu Gln Tyr Val Ser Leu Asp Trp Pro Thr Glu Asn Gly Trp Ala
 340 345 350

aat tac aac agt ttg cag gag ctg acg tac ttc ttc act gtc ttt att 1104
 Asn Tyr Asn Ser Leu Gln Glu Leu Thr Tyr Phe Phe Thr Val Phe Ile
 355 360 365

gcg gca ccg ttg tcg att gtg tct ggt ttc cgg atg tcg agt tac tgg 1152
 Ala Ala Pro Leu Ser Ile Val Ser Gly Phe Arg Met Ser Ser Tyr Trp
 370 375 380

cct aag aac aat gcg acg atg aat aag ttg atc ccc atc ggg ttt gct 1200
 Pro Lys Asn Asn Ala Thr Met Asn Lys Leu Ile Pro Ile Gly Phe Ala
 385 390 395 400

cgt gcg ctg cac atg cca gtg atg gtg tat tac atc gtg ttc att tgt 1248
 Arg Ala Leu His Met Pro Val Met Val Tyr Tyr Ile Val Phe Ile Cys
 405 410 415

atc cac gtg ttc ttg gtg ttg gcg acc ggc gcg ttg cgc aat ttc aac 1296
 Ile His Val Phe Leu Val Leu Ala Thr Gly Ala Leu Arg Asn Phe Asn
 420 425 430

cat atg tat gca ggt caa gac gtt gtg aac tgg gtt ggt ttt ggt tgg 1344
 His Met Tyr Ala Gly Gln Asp Val Val Asn Trp Val Gly Phe Gly Trp
 435 440 445

ttc gtg gcg tcg ttg 1359
 Phe Val Ala Ser Leu
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<210> 1228

<211> 453

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1228

Ile Pro Ala Ala Pro Ser Ala Pro Gly Ser Ala Ile Pro Thr Pro Gly
 1 5 10 15

Thr Ala Ile Pro Val Pro Gly Ser Ala Thr Pro Val Pro Ala Pro Gly
 20 25 30

Val Ser Ala Pro Gly Ala Ser Val Pro Ser Ile Pro Val Pro Gly Ser
 35 40 45

Val Thr Pro Pro Ala Pro Gly Ile Ser Ala Pro Gly Gly Ala Leu Pro
 50 55 60

Thr Pro Gly Ser Ala Pro Pro Thr Pro Gly Gly Ala Leu Pro Thr Pro
 65 70 75 80

Gly Glu Ala Leu Pro Val Pro Gly Ala Pro Gly Ala Pro Gly Ala Ser
 85 90 95

Gly Ile Pro Ser Pro Gly Leu Pro Thr Pro Gly Val Pro Thr Pro Gly
 100 105 110

Ala Ser Leu Pro Val Pro Gly Ala Pro Asp Ala Pro Gly Thr Pro Ser

115					120					125					
Ile	Pro	Ala	Ala	Pro	Gly	Ile	Gln	Ala	Pro	Gly	Ile	Pro	Ala	Ala	Pro
130						135					140				
Gly	Ala	Pro	Ala	Gln	Ala	Ala	Ala	His	Ala	Lys	Pro	Val	Phe	Gln	Asp
145				150						155					160
Ala	Glu	Lys	Arg	Pro	Arg	Thr	Asp	Glu	Ala	Gly	Asn	Ala	Lys	Lys	Glu
				165				170						175	
Leu	Pro	Leu	Arg	Val	Arg	Leu	Ala	Gln	Pro	Ile	Thr	Arg	Lys	Gln	Trp
			180					185					190		
Ala	Met	Thr	Leu	Gly	Val	Leu	Val	Leu	Gly	Ala	Ile	Val	Val	Ala	Ala
			195					200					205		
Ile	Ala	Val	Val	Leu	Ala	Lys	Trp	Ala	Phe	Thr	Thr	Glu	Trp	Leu	Gln
						210		215					220		
Asp	Phe	Val	Glu	Lys	Tyr	Pro	Gly	Lys	Tyr	Asp	Asn	Pro	Glu	Gly	Ala
225					230					235					240
Pro	Val	Gly	Ile	Pro	Thr	Trp	Leu	Ser	Trp	Gln	His	Phe	Phe	Asn	Met
				245					250					255	
Phe	Phe	Met	Val	Leu	Ile	Ile	Lys	Thr	Gly	Ile	Glu	Ile	Asn	Arg	Thr
			260					265					270		
Arg	Arg	Pro	Lys	Gly	Tyr	Trp	Thr	Pro	Lys	Lys	Gly	Gly	Lys	Lys	Ile
		275					280					285			
Ser	Leu	Thr	Leu	Trp	Ile	His	Leu	Val	Leu	Asp	Leu	Leu	Trp	Ile	Ile
		290					295					300			
Asn	Gly	Ala	Val	Phe	Ile	Ile	Leu	Leu	Phe	Ala	Thr	Gly	Gln	Trp	Met
305					310					315					320
Arg	Ile	Val	Pro	Thr	Ser	Trp	Asp	Val	Phe	Pro	Asn	Ala	Leu	Ser	Ala
				325					330				335		
Gly	Leu	Gln	Tyr	Val	Ser	Leu	Asp	Trp	Pro	Thr	Glu	Asn	Gly	Trp	Ala
			340					345					350		
Asn	Tyr	Asn	Ser	Leu	Gln	Glu	Leu	Thr	Tyr	Phe	Phe	Thr	Val	Phe	Ile
		355					360					365			
Ala	Ala	Pro	Leu	Ser	Ile	Val	Ser	Gly	Phe	Arg	Met	Ser	Ser	Tyr	Trp
		370					375					380			
Pro	Lys	Asn	Asn	Ala	Thr	Met	Asn	Lys	Leu	Ile	Pro	Ile	Gly	Phe	Ala
385					390					395					400
Arg	Ala	Leu	His	Met	Pro	Val	Met	Val	Tyr	Tyr	Ile	Val	Phe	Ile	Cys
				405					410					415	
Ile	His	Val	Phe	Leu	Val	Leu	Ala	Thr	Gly	Ala	Leu	Arg	Asn	Phe	Asn
			420					425					430		
His	Met	Tyr	Ala	Gly	Gln	Asp	Val	Val	Asn	Trp	Val	Gly	Phe	Gly	Trp
		435					440					445			

Phe Val Ala Ser Leu
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<210> 1229
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(697)
<223> RXN02593

<400> 1229
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cataggggta ttcagtctag ctgcttttaa acaagccata atg gaa gcc atg gcc 115
Met Glu Ala Met Ala
1 5
aca acg atc acc gtt ttc tct ccc acc cac tcc ccc gca caa atc cgc 163
Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser Pro Ala Gln Ile Arg
10 15 20
gaa acc atc ctc agc gcc gcg aaa gaa gac gac gtg gac ttc ctc gga 211
Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp Val Asp Phe Leu Gly
25 30 35
gtc ccc ttt acc cac ccc aga aac gtc acc atc gaa gtc gac gac gaa 259
Val Pro Phe Thr His Pro Arg Asn Val Thr Ile Glu Val Asp Asp Glu
40 45 50
ctg atc aac gac tgc tta ggc tgg ctc gac gac gtg gca ctc gcc tcc 307
Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp Val Ala Leu Ala Ser
55 60 65
ggc ctg ggc atc caa tac aac gac gaa gtg ctc cgc tac ggc gac gaa 355
Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu Arg Tyr Gly Asp Glu
70 75 80 85
gac att tcc ttt acc gtc caa acc aaa aat gac gat gac gcc cgc atc 403
Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp Asp Asp Ala Arg Ile
90 95 100
ggc gcc tcc cgc ctt gga ctc gag cac cag ttg aac gtc att gcc ggg 451
Gly Ala Ser Arg Leu Gly Leu Glu His Gln Leu Asn Val Ile Ala Gly
105 110 115
ggc tct gga gat tcc ggg gat tcc ggg gat tat ttg aag att gca cac 499
Gly Ser Gly Asp Ser Gly Asp Ser Gly Asp Tyr Leu Lys Ile Ala His
120 125 130
ttc gac cta gac aac ccc gcc gac gag tcc tcc tac atc ttc gcg cgc 547
Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser Tyr Ile Phe Ala Arg
135 140 145
agc ctc gca gaa gta gac ggc tgg acc cta gaa ttc ggc gtc gca gga 595
Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu Phe Gly Val Ala Gly
150 155 160 165

gta aaa aac acc acc att gtt tcc tcc atc gac gat gcc atc acc acc 643
 Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp Asp Ala Ile Thr Thr
 170 175 180

att ttg cga tgg atg aac ggc gaa gac atc cgc gac ctc aac tgg acc 691
 Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg Asp Leu Asn Trp Thr
 185 190 195

cgc gca taaatggcct catttccgga gct 720
 Arg Ala

<210> 1230

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 1230

Met Glu Ala Met Ala Thr Thr Ile Thr Val Phe Ser Pro Thr His Ser
 1 5 10 15

Pro Ala Gln Ile Arg Glu Thr Ile Leu Ser Ala Ala Lys Glu Asp Asp
 20 25 30

Val Asp Phe Leu Gly Val Pro Phe Thr His Pro Arg Asn Val Thr Ile
 35 40 45

Glu Val Asp Asp Glu Leu Ile Asn Asp Cys Leu Gly Trp Leu Asp Asp
 50 55 60

Val Ala Leu Ala Ser Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu
 65 70 75 80

Arg Tyr Gly Asp Glu Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp
 85 90 95

Asp Asp Ala Arg Ile Gly Ala Ser Arg Leu Gly Leu Glu His Gln Leu
 100 105 110

Asn Val Ile Ala Gly Gly Ser Gly Asp Ser Gly Asp Ser Gly Asp Tyr
 115 120 125

Leu Lys Ile Ala His Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser
 130 135 140

Tyr Ile Phe Ala Arg Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu
 145 150 155 160

Phe Gly Val Ala Gly Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp
 165 170 175

Asp Ala Ile Thr Thr Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg
 180 185 190

Asp Leu Asn Trp Thr Arg Ala
 195

<210> 1231

<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA02593

<400> 1231
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tgccggggggc tctggagatt ccgggggattc cggggattat ttg aag att gca cac 115
Leu Lys Ile Ala His
1 5
ttc gac cta gac aac ccc gcc gac gag tcc tcc tac atc ttc gcg cgc 163
Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser Tyr Ile Phe Ala Arg
10 15 20
agc ctc gca gaa gta gac ggc tgg acc cta gaa ttc ggc gtc gca gga 211
Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu Phe Gly Val Ala Gly
25 30 35
gta aaa aac acc acc att gtt tcc tcc atc gac gat gcc atc acc acc 259
Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp Asp Ala Ile Thr Thr
40 45 50
att ttg cga tgg atg aac ggc gaa gac atc cgc gac ctc aac tgg acc 307
Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg Asp Leu Asn Trp Thr
55 60 65
cgc gca taaatggcct catttccgga gct 336
Arg Ala
70

<210> 1232
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 1232
Leu Lys Ile Ala His Phe Asp Leu Asp Asn Pro Ala Asp Glu Ser Ser
1 5 10 15
Tyr Ile Phe Ala Arg Ser Leu Ala Glu Val Asp Gly Trp Thr Leu Glu
20 25 30
Phe Gly Val Ala Gly Val Lys Asn Thr Thr Ile Val Ser Ser Ile Asp
35 40 45
Asp Ala Ile Thr Thr Ile Leu Arg Trp Met Asn Gly Glu Asp Ile Arg
50 55 60
Asp Leu Asn Trp Thr Arg Ala
65 70

<210> 1233
<211> 447

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> FRXA02594

<400> 1233

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cataggggta	ttcagttctag	ctgcttttta	acaagccata	atg	gaa	gcc	atg	gcc	115
				Met	Glu	Ala	Met	Ala	
				. 1				5	

aca	acg	atc	acc	gtt	ttc	tct	ccc	acc	cac	tcc	ccc	gca	caa	atc	cgc	163
Thr	Thr	Ile	Thr	Val	Phe	Ser	Pro	Thr	His	Ser	Pro	Ala	Gln	Ile	Arg	
			10					15						20		

gaa	acc	atc	ctc	agc	gcc	gcg	aaa	gaa	gac	gac	gtg	gac	ttc	ctc	gga	211
Glu	Thr	Ile	Leu	Ser	Ala	Ala	Lys	Glu	Asp	Asp	Val	Asp	Phe	Leu	Gly	
			25					30					35			

gtc	ccc	ttt	acc	cac	ccc	aga	aac	gtc	acc	atc	gaa	gtc	gac	gac	gaa	259
Val	Pro	Phe	Thr	His	Pro	Arg	Asn	Val	Thr	Ile	Glu	Val	Asp	Asp	Glu	
		40					45					50				

ctg	atc	aac	gac	tgc	tta	ggc	tgg	ctc	gac	gac	gtg	gca	ctc	gcc	tcc	307
Leu	Ile	Asn	Asp	Cys	Leu	Gly	Trp	Leu	Asp	Asp	Val	Ala	Leu	Ala	Ser	
		55				60					65					

ggc	ctg	ggc	atc	caa	tac	aac	gac	gaa	gtg	ctc	cgc	tac	ggc	gac	gaa	355
Gly	Leu	Gly	Ile	Gln	Tyr	Asn	Asp	Glu	Val	Leu	Arg	Tyr	Gly	Asp	Glu	
	70			75					80					85		

gac	att	tcc	ttt	acc	gtc	caa	acc	aaa	aat	gac	gat	gac	gcc	cgc	atc	403
Asp	Ile	Ser	Phe	Thr	Val	Gln	Thr	Lys	Asn	Asp	Asp	Asp	Ala	Arg	Ile	
			90					95						100		

ggc	gcc	tcc	cgc	ctt	gga	ctc	tagcaccagt	tgaacgtcat	tgc	447
Gly	Ala	Ser	Arg	Leu	Gly	Leu				
			105							

<210> 1234

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1234

Met	Glu	Ala	Met	Ala	Thr	Thr	Ile	Thr	Val	Phe	Ser	Pro	Thr	His	Ser
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Pro	Ala	Gln	Ile	Arg	Glu	Thr	Ile	Leu	Ser	Ala	Ala	Lys	Glu	Asp	Asp
			20					25					30		

Val	Asp	Phe	Leu	Gly	Val	Pro	Phe	Thr	His	Pro	Arg	Asn	Val	Thr	Ile
		35					40					45			

Glu	Val	Asp	Asp	Glu	Leu	Ile	Asn	Asp	Cys	Leu	Gly	Trp	Leu	Asp	Asp
	50					55					60				

Val Ala Leu Ala Ser Gly Leu Gly Ile Gln Tyr Asn Asp Glu Val Leu
 65 70 75 80
 Arg Tyr Gly Asp Glu Asp Ile Ser Phe Thr Val Gln Thr Lys Asn Asp
 85 90 95
 Asp Asp Ala Arg Ile Gly Ala Ser Arg Leu Gly Leu
 100 105

<210> 1235
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 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1471)
 <223> RXN02606

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 cttcggttgt gtggaaaaca gaaaaggagg ggaaaacaaa atg caa gaa atc cac 115
 Met Gln Glu Ile His
 1 5
 acc atc atg aaa cac atg gac gcg ctc atc gcc gac ccg tcc gcc gcc 163
 Thr Ile Met Lys His Met Asp Ala Leu Ile Ala Asp Pro Ser Ala Ala
 10 15 20
 gca ttc aaa gca aca ctc ccc ttc gcc gaa ctc ctc gaa aag ctc cac 211
 Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu Leu Glu Lys Leu His
 25 30 35
 aac aaa aaa gcg ctt ttc gac gcc gcc ctc gcc aaa tcc gcc gag cgc 259
 Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala Lys Ser Ala Glu Arg
 40 45 50
 gcc gat gcc gga cgc atc atc gga aaa acc tcc cac atc gat gcc ctc 307
 Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser His Ile Asp Ala Leu
 55 60 65
 gcg tac ctt ctc gac atc tcc aaa tcc gaa gca ttc cga cgc aca aaa 355
 Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala Phe Arg Arg Thr Lys
 70 75 80 85
 cgc gcc gaa gaa cac tac ggc aac cca agc ccg gaa ccc agt tca gaa 403
 Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro Glu Pro Ser Ser Glu
 90 95 100
 gaa ctc gcg aaa gaa acc ccc gaa gag aag cta gcc aga gaa gaa aaa 451
 Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu Ala Arg Glu Glu Lys
 105 110 115
 gag aaa caa gac cta gcc gaa caa gca gaa gcc aac cgc atc gcc cgc 499
 Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala Asn Arg Ile Ala Arg
 120 125 130
 gaa cac ggc atc tcc gcc gaa aaa caa gac acc atc cgc tac gaa cta 547

Glu	His	Gly	Ile	Ser	Ala	Glu	Lys	Gln	Asp	Thr	Ile	Arg	Tyr	Glu	Leu		
135						140					145						
595																	
gaa	aaa	ctc	aac	gac	aac	aca	tcc	cta	tcc	cga	gcc	tca	ctc	cgc	aaa		
Glu	Lys	Leu	Asn	Asp	Asn	Thr	Ser	Leu	Ser	Arg	Ala	Ser	Leu	Arg	Lys		
150					155					160					165		
643																	
cta	gca	atg	cag	gaa	gcc	acc	agc	cga	acc	ccc	gaa	gac	cta	cgc	aac		
Leu	Ala	Met	Gln	Glu	Ala	Thr	Ser	Arg	Thr	Pro	Glu	Asp	Leu	Arg	Asn		
				170					175					180			
691																	
tgg	acc	cgc	aac	aaa	gtt	atc	cgc	ata	aac	ccc	acc	gcc	aaa	gac	cca		
Trp	Thr	Arg	Asn	Lys	Val	Ile	Arg	Ile	Asn	Pro	Thr	Ala	Lys	Asp	Pro		
			185					190						195			
739																	
ctc	gcc	gca	gta	aag	aaa	cgc	tcc	tta	agc	atc	gga	cgc	caa	gac	cac		
Leu	Ala	Ala	Val	Lys	Lys	Arg	Ser	Leu	Ser	Ile	Gly	Arg	Gln	Asp	His		
		200					205					210					
787																	
gac	ggc	gga	gcc	aaa	gca	tcc	ctc	tat	tta	gat	gcc	aaa	ggt	cta	gcc		
Asp	Gly	Gly	Ala	Lys	Ala	Ser	Leu	Tyr	Leu	Asp	Ala	Lys	Gly	Leu	Ala		
	215					220					225						
835																	
ctg	ctc	aaa	tca	ctg	atg	tct	aaa	gcc	aag	ccg	ggg	cat	ttg	ctt	gaa		
Leu	Leu	Lys	Ser	Leu	Met	Ser	Lys	Ala	Lys	Pro	Gly	His	Leu	Leu	Glu		
230					235					240					245		
883																	
gac	tct	ttg	gcg	gag	gat	aaa	cgt	acg	aaa	ccg	caa	cgc	caa	tac	gat		
Asp	Ser	Leu	Ala	Glu	Asp	Lys	Arg	Thr	Lys	Pro	Gln	Arg	Gln	Tyr	Asp		
				250					255					260			
931																	
gcc	ttc	gcc	gac	atc	ctc	cac	cgc	gca	cac	agc	gat	ctc	ctc	ccc	gca		
Ala	Phe	Ala	Asp	Ile	Leu	His	Arg	Ala	His	Ser	Asp	Leu	Leu	Pro	Ala		
			265					270					275				
979																	
cga	tcc	gga	gtg	ggc	acc	atc	ctc	gtc	tcc	ctc	tcc	gcc	aaa	gac	gta		
Arg	Ser	Gly	Val	Gly	Thr	Ile	Leu	Val	Ser	Leu	Ser	Ala	Lys	Asp	Val		
		280					285					290					
1027																	
aca	aac	ctc	aaa	gca	tcg	ggc	ccc	gac	cac	cgc	tac	ccc	acc	agc	acc		
Thr	Asn	Leu	Lys	Ala	Ser	Gly	Pro	Asp	His	Arg	Tyr	Pro	Thr	Ser	Thr		
	295					300					305						
1075																	
ggc	ata	aaa	ctc	aca	ccg	ctt	gag	atc	ctg	cga	ctc	ggt	gca	gcc	aaa		
Gly	Ile	Lys	Leu	Thr	Pro	Leu	Glu	Ile	Leu	Arg	Leu	Gly	Ala	Ala	Lys		
310					315					320					325		
1123																	
tat	gac	ttc	gtg	acc	gtc	ctc	gac	tcc	gaa	tcc	ggc	cgt	ccg	ctg	cac		
Tyr	Asp	Phe	Val	Thr	Val	Leu	Asp	Ser	Glu	Ser	Gly	Arg	Pro	Leu	His		
				330					335					340			
1171																	
ctg	gca	cgc	act	caa	cgc	acc	gcc	agc	ctg	tat	caa	cgc	cta	gcc	ctc		
Leu	Ala	Arg	Thr	Gln	Arg	Thr	Ala	Ser	Leu	Tyr	Gln	Arg	Leu	Ala	Leu		
			345					350					355				
1219																	
ttc	gcc	tcc	gaa	ctc	gtc	tgc	acc	cgc	gaa	ggc	tgc	gac	tcc	ccc	ttc		
Phe	Ala	Ser	Glu	Leu	Val	Cys	Thr	Arg	Glu	Gly	Cys	Asp	Ser	Pro	Phe		
		360					365					370					
1267																	
gaa	gac	aac	gaa	ata	cac	cac	atc	aga	tcc	tgg	cta	gac	ggc	ggc	ccc		
Glu	Asp	Asn	Glu	Ile	His	His	Ile	Arg	Ser	Trp	Leu	Asp	Gly	Gly	Pro		

375 380 385
 aca gac ata gaa aac atc acc aac atc tgc ccc cac gac cac gga aac 1315
 Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro His Asp His Gly Asn
 390 395 400 405
 aac aac gac caa cgc gac ggc aaa gac aac atg ggg cac atg aac ata 1363
 Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met Gly His Met Asn Ile
 410 415 420
 gat ccc aca acc ggg cgc gtc gga tat caa ccc gcc gac cgc cga aaa 1411
 Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro Ala Asp Arg Arg Lys
 425 430 435
 ccc atg cgg ttt aac aac acc gca gcc gca gca gaa tca gga gga gca 1459
 Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala Glu Ser Gly Gly Ala
 440 445 450
 cag gcc agg acc taagttttta gcgcgccaaa aag 1494
 Gln Ala Arg Thr
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<210> 1236

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 1236

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 Asp Pro Ser Ala Ala Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu
 20 25 30
 Leu Glu Lys Leu His Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala
 35 40 45
 Lys Ser Ala Glu Arg Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser
 50 55 60
 His Ile Asp Ala Leu Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala
 65 70 75 80
 Phe Arg Arg Thr Lys Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro
 85 90 95
 Glu Pro Ser Ser Glu Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu
 100 105 110
 Ala Arg Glu Glu Lys Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala
 115 120 125
 Asn Arg Ile Ala Arg Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr
 130 135 140
 Ile Arg Tyr Glu Leu Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg
 145 150 155 160
 Ala Ser Leu Arg Lys Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro
 165 170 175

Glu Asp Leu Arg Asn Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro
 180 185 190
 Thr Ala Lys Asp Pro Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile
 195 200 205
 Gly Arg Gln Asp His Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp
 210 215 220
 Ala Lys Gly Leu Ala Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro
 225 230 235 240
 Gly His Leu Leu Glu Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro
 245 250 255
 Gln Arg Gln Tyr Asp Ala Phe Ala Asp Ile Leu His Arg Ala His Ser
 260 265 270
 Asp Leu Leu Pro Ala Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu
 275 280 285
 Ser Ala Lys Asp Val Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg
 290 295 300
 Tyr Pro Thr Ser Thr Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg
 305 310 315 320
 Leu Gly Ala Ala Lys Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser
 325 330 335
 Gly Arg Pro Leu His Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr
 340 345 350
 Gln Arg Leu Ala Leu Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly
 355 360 365
 Cys Asp Ser Pro Phe Glu Asp Asn Glu Ile His His Ile Arg Ser Trp
 370 375 380
 Leu Asp Gly Gly Pro Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro
 385 390 395 400
 His Asp His Gly Asn Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met
 405 410 415
 Gly His Met Asn Ile Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro
 420 425 430
 Ala Asp Arg Arg Lys Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala
 435 440 445
 Glu Ser Gly Gly Ala Gln Ala Arg Thr
 450 455

<210> 1237

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> FRXA02606

<400> 1237

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cttcggttgt gtggaaaaca gaaaaggagg ggaaaacaaa atg caa gaa atc cac 115
Met Gln Glu Ile His
1 5

acc atc atg aaa cac atg gac gcg ctc atc gcc gac ccg tcc gcc gcc 163
Thr Ile Met Lys His Met Asp Ala Leu Ile Ala Asp Pro Ser Ala Ala
10 15 20

gca ttc aaa gca aca ctc ccc ttc gcc gaa ctc ctc gaa aag ctc cac 211
Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu Leu Glu Lys Leu His
25 30 35

aac aaa aaa gcg ctt ttc gac gcc gcc ctc gcc aaa tcc gcc gag cgc 259
Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala Lys Ser Ala Glu Arg
40 45 50

gcc gat gcc gga cgc atc atc gga aaa acc tcc cac atc gat gcc ctc 307
Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser His Ile Asp Ala Leu
55 60 65

gcg tac ctt ctc gac atc tcc aaa tcc gaa gca ttc cga cgc aca aaa 355
Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala Phe Arg Arg Thr Lys
70 75 80 85

cgc gcc gaa gaa cac tac ggc aac cca agc ccg gaa ccc agt tca gaa 403
Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro Glu Pro Ser Ser Glu
90 95 100

gaa ctc gcg aaa gaa acc ccc gaa gag aag cta gcc aga gaa gaa aaa 451
Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu Ala Arg Glu Glu Lys
105 110 115

gag aaa caa gac cta gcc gaa caa gca gaa gcc aac cgc atc gcc cgc 499
Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala Asn Arg Ile Ala Arg
120 125 130

gaa cac ggc atc tcc gcc gaa aaa caa gac acc atc cgc tac gaa cta 547
Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr Ile Arg Tyr Glu Leu
135 140 145

gaa aaa ctc aac gac aac aca tcc cta tcc cga gcc tca ctc cgc aaa 595
Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg Ala Ser Leu Arg Lys
150 155 160 165

cta gca atg cag gaa gcc acc agc cga acc ccc gaa gac cta cgc aac 643
Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro Glu Asp Leu Arg Asn
170 175 180

tgg acc cgc aac aaa gtt atc cgc ata aac ccc acc gcc aaa gac cca 691
Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro Thr Ala Lys Asp Pro
185 190 195

ctc gcc gca gta aag aaa cgc tcc tta agc atc gga cgc caa gac cac 739

Leu	Ala	Ala	Val	Lys	Lys	Arg	Ser	Leu	Ser	Ile	Gly	Arg	Gln	Asp	His		
	200						205					210					
gac	ggc	gga	gcc	aaa	gca	tcc	ctc	tat	tta	gat	gcc	aaa	ggt	cta	gcc	787	
Asp	Gly	Gly	Ala	Lys	Ala	Ser	Leu	Tyr	Leu	Asp	Ala	Lys	Gly	Leu	Ala		
	215					220					225						
ctg	ctc	aaa	tca	ctg	atg	tct	aaa	gcc	aag	ccg	ggg	cat	ttg	ctt	gaa	835	
Leu	Leu	Lys	Ser	Leu	Met	Ser	Lys	Ala	Lys	Pro	Gly	His	Leu	Leu	Glu		
230					235					240					245		
gac	tct	ttg	gcg	gag	gat	aaa	cgt	acg	aaa	ccg	caa	cgc	caa	tac	gat	883	
Asp	Ser	Leu	Ala	Glu	Asp	Lys	Arg	Thr	Lys	Pro	Gln	Arg	Gln	Tyr	Asp		
				250					255					260			
gcc	ttc	gcc	gac	atc	ctc	cac	cgc	gca	cac	agc	gat	ctc	ctc	ccc	gca	931	
Ala	Phe	Ala	Asp	Ile	Leu	His	Arg	Ala	His	Ser	Asp	Leu	Leu	Pro	Ala		
			265					270					275				
cga	tcc	gga	gtg	ggc	acc	atc	ctc	gtc	tcc	ctc	tcc	gcc	aaa	gac	gta	979	
Arg	Ser	Gly	Val	Gly	Thr	Ile	Leu	Val	Ser	Leu	Ser	Ala	Lys	Asp	Val		
		280					285					290					
aca	aac	ctc	aaa	gca	tcg	ggc	ccc	gac	cac	cgc	tac	ccc	acc	agc	acc	1027	
Thr	Asn	Leu	Lys	Ala	Ser	Gly	Pro	Asp	His	Arg	Tyr	Pro	Thr	Ser	Thr		
	295					300					305						
ggc	ata	aaa	ctc	aca	ccg	ctt	gag	atc	ctg	cga	ctc	ggt	gca	gcc	aaa	1075	
Gly	Ile	Lys	Leu	Thr	Pro	Leu	Glu	Ile	Leu	Arg	Leu	Gly	Ala	Ala	Lys		
310					315					320					325		
tat	gac	ttc	gtg	acc	gtc	ctc	gac	tcc	gaa	tcc	ggc	cgt	ccg	ctg	cac	1123	
Tyr	Asp	Phe	Val	Thr	Val	Leu	Asp	Ser	Glu	Ser	Gly	Arg	Pro	Leu	His		
				330					335					340			
ctg	gca	cgc	act	caa	cgc	acc	gcc	agc	ctg	tat	caa	cgc	cta	gcc	ctc	1171	
Leu	Ala	Arg	Thr	Gln	Arg	Thr	Ala	Ser	Leu	Tyr	Gln	Arg	Leu	Ala	Leu		
			345					350					355				
ttc	gcc	tcc	gaa	ctc	gtc	tgc	acc	cgc	gaa	ggc	tgc	gac	tcc	ccc	ttc	1219	
Phe	Ala	Ser	Glu	Leu	Val	Cys	Thr	Arg	Glu	Gly	Cys	Asp	Ser	Pro	Phe		
		360					365					370					
gaa	gac	aac	gaa	ata	cac	cac	atc	aga	tcc	tgg	cta	gac	ggc	ggc	ccc	1267	
Glu	Asp	Asn	Glu	Ile	His	His	Ile	Arg	Ser	Trp	Leu	Asp	Gly	Gly	Pro		
	375					380					385						
aca	gac	ata	gaa	aac	atc	acc	aac	atc	tgc	ccc	cac	gac	cac	gga	aac	1315	
Thr	Asp	Ile	Glu	Asn	Ile	Thr	Asn	Ile	Cys	Pro	His	Asp	His	Gly	Asn		
	390				395				400						405		
aac	aac	gac	caa	cgc	gac	ggc	aaa	gac	aac	atg	ggg	cac	atg	aac	ata	1363	
Asn	Asn	Asp	Gln	Arg	Asp	Gly	Lys	Asp	Asn	Met	Gly	His	Met	Asn	Ile		
			410					415						420			
gat	ccc	aca	acc	ggg	cgc	gtc	gga	tat	caa	ccc	gcc	gac	cgc	cga	aaa	1411	
Asp	Pro	Thr	Thr	Gly	Arg	Val	Gly	Tyr	Gln	Pro	Ala	Asp	Arg	Arg	Lys		
			425				430					435					
ccc	atg	cgg	ttt	aac	aac	acc	gca	gcc	gca	gca	gaa	tca	gga	gga	gca	1459	
Pro	Met	Arg	Phe	Asn	Asn	Thr	Ala	Ala	Ala	Ala	Glu	Ser	Gly	Gly	Ala		

440

445

450

cag gcc agg acc taagttttta gcgcgcctaaa aag
Gln Ala Arg Thr
455

1494

<210> 1238

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 1238

Met Gln Glu Ile His Thr Ile Met Lys His Met Asp Ala Leu Ile Ala
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Asp Pro Ser Ala Ala Ala Phe Lys Ala Thr Leu Pro Phe Ala Glu Leu
20 25 30
Leu Glu Lys Leu His Asn Lys Lys Ala Leu Phe Asp Ala Ala Leu Ala
35 40 45
Lys Ser Ala Glu Arg Ala Asp Ala Gly Arg Ile Ile Gly Lys Thr Ser
50 55 60
His Ile Asp Ala Leu Ala Tyr Leu Leu Asp Ile Ser Lys Ser Glu Ala
65 70 75 80
Phe Arg Arg Thr Lys Arg Ala Glu Glu His Tyr Gly Asn Pro Ser Pro
85 90 95
Glu Pro Ser Ser Glu Glu Leu Ala Lys Glu Thr Pro Glu Glu Lys Leu
100 105 110
Ala Arg Glu Glu Lys Glu Lys Gln Asp Leu Ala Glu Gln Ala Glu Ala
115 120 125
Asn Arg Ile Ala Arg Glu His Gly Ile Ser Ala Glu Lys Gln Asp Thr
130 135 140
Ile Arg Tyr Glu Leu Glu Lys Leu Asn Asp Asn Thr Ser Leu Ser Arg
145 150 155 160
Ala Ser Leu Arg Lys Leu Ala Met Gln Glu Ala Thr Ser Arg Thr Pro
165 170 175
Glu Asp Leu Arg Asn Trp Thr Arg Asn Lys Val Ile Arg Ile Asn Pro
180 185 190
Thr Ala Lys Asp Pro Leu Ala Ala Val Lys Lys Arg Ser Leu Ser Ile
195 200 205
Gly Arg Gln Asp His Asp Gly Gly Ala Lys Ala Ser Leu Tyr Leu Asp
210 215 220
Ala Lys Gly Leu Ala Leu Leu Lys Ser Leu Met Ser Lys Ala Lys Pro
225 230 235 240
Gly His Leu Leu Glu Asp Ser Leu Ala Glu Asp Lys Arg Thr Lys Pro
245 250 255

Gln Arg Gln Tyr Asp Ala Phe Ala Asp Ile Leu His Arg Ala His Ser
 260 265 270
 Asp Leu Leu Pro Ala Arg Ser Gly Val Gly Thr Ile Leu Val Ser Leu
 275 280 285
 Ser Ala Lys Asp Val Thr Asn Leu Lys Ala Ser Gly Pro Asp His Arg
 290 295 300
 Tyr Pro Thr Ser Thr Gly Ile Lys Leu Thr Pro Leu Glu Ile Leu Arg
 305 310 315 320
 Leu Gly Ala Ala Lys Tyr Asp Phe Val Thr Val Leu Asp Ser Glu Ser
 325 330 335
 Gly Arg Pro Leu His Leu Ala Arg Thr Gln Arg Thr Ala Ser Leu Tyr
 340 345 350
 Gln Arg Leu Ala Leu Phe Ala Ser Glu Leu Val Cys Thr Arg Glu Gly
 355 360 365
 Cys Asp Ser Pro Phe Glu Asp Asn Glu Ile His His Ile Arg Ser Trp
 370 375 380
 Leu Asp Gly Gly Pro Thr Asp Ile Glu Asn Ile Thr Asn Ile Cys Pro
 385 390 395 400
 His Asp His Gly Asn Asn Asn Asp Gln Arg Asp Gly Lys Asp Asn Met
 405 410 415
 Gly His Met Asn Ile Asp Pro Thr Thr Gly Arg Val Gly Tyr Gln Pro
 420 425 430
 Ala Asp Arg Arg Lys Pro Met Arg Phe Asn Asn Thr Ala Ala Ala Ala
 435 440 445
 Glu Ser Gly Gly Ala Gln Ala Arg Thr
 450 455

<210> 1239

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1027)

<223> RXN02610

<400> 1239

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gctgctgaag gaatctgcgg atcggacgta ttgttaaccg atg agg aaa acc atc 115
 Met Arg Lys Thr Ile
 1 5

acc gtt att gct gta ttg atc gtc ctc gcc tta atc ggc gtg ggc atc 163
 Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu Ile Gly Val Gly Ile
 10 15 20

gtg cag tat	gtg aac aca tcc gat	gac tca gat ttc att	ggc cag cct	211
Val Gln Tyr	Val Asn Thr Ser Asp	Asp Ser Asp Phe Ile	Gly Gln Pro	
	25	30	35	
ggc gag cca acc ggt acc	gaa acc acg gaa cca ccg	gtt caa cct gat	259	
Gly Glu Pro Thr	Gly Thr Glu Thr Thr	Glu Pro Pro Val	Gln Pro Asp	
	40	45	50	
tgg tgc cct gcg gta gaa gtc	att gcc gcg ccg ggt acg	tgg gag tcg	307	
Trp Cys Pro Ala Val	Glu Val Ile Ala Ala Pro	Gly Thr Trp Glu Ser		
	55	60	65	
gct gct aat gat gat ccg atc	aac ccg acc gct aat ccg	ctg tca ttc	355	
Ala Ala Asn Asp Asp	Pro Ile Asn Pro Thr Ala	Asn Pro Leu Ser Phe		
	70	75	80	85
atg ttg agc atc act cag cca	ctg cag gag cgt tat tct	gcg gat gac	403	
Met Leu Ser Ile Thr	Gln Pro Leu Gln Glu Arg	Tyr Ser Ala Asp		
	90	95	100	
gtc aag gtg tgg acg ctg ccg	tac act gcg cag ttc cgc	aac atc aac	451	
Val Lys Val Trp Thr	Leu Pro Tyr Thr Ala Gln	Phe Arg Asn Ile Asn		
	105	110	115	
tcg caa aat gag atg tcc tat	gat gat tcg cgc aat gaa	ggc acc gcg	499	
Ser Gln Asn Glu Met Ser	Tyr Asp Asp Ser Arg Asn	Glu Gly Thr Ala		
	120	125	130	
aag atg aat gag gaa ctg atc	aac act cac aat gag tgc	cct gcc acg	547	
Lys Met Asn Glu Glu Leu	Ile Asn Thr His Asn Glu	Cys Pro Ala Thr		
	135	140	145	
gag ttc atc atc gtt ggt ttc	tcc cag ggt gcg gtc att	gcg ggc gat	595	
Glu Phe Ile Ile Val	Gly Phe Ser Gln Gly Ala	Val Ile Ala Gly Asp		
	150	155	160	165
gtg gct gct cag atc ggt tca	gag caa ggt gtt att cca	gct gac agc	643	
Val Ala Ala Gln Ile Gly	Ser Glu Gln Gly Val Ile	Pro Ala Asp Ser		
	170	175	180	
gtc agg ggt gtc gcc ctg atc	gct gac ggt cgc ccg gag	cct ggt gtg	691	
Val Arg Gly Val Ala Leu	Ile Ala Asp Gly Arg Arg	Glu Pro Gly Val		
	185	190	195	
ggc cag ttc cca ggc acg ttt	gtg gat ggc atc ggc gcg	gag gtt act	739	
Gly Gln Phe Pro Gly Thr	Phe Val Asp Gly Ile Gly	Ala Glu Val Thr		
	200	205	210	
ctg cag cct ttg aac ttg ctg	gtg cag ccg att gtt ccg	ggc gca acc	787	
Leu Gln Pro Leu Asn Leu	Leu Val Gln Pro Ile Val	Pro Gly Ala Thr		
	215	220	225	
atg cgt ggc ggg cgc gcg ggc	ggt ttc ggt gtg ctc aac	gac cgg gtg	835	
Met Arg Gly Gly Arg Ala	Gly Gly Phe Gly Val Leu	Asn Asp Arg Val		
	230	235	240	245
cag gat att tgt gct cca aat	gat gcg atc tgt gat gct	ccg gtg aat	883	
Gln Asp Ile Cys Ala Pro	Asn Asp Ala Ile Cys Asp	Ala Pro Val Asn		
	250	255	260	
gtc ggc aac gcc ctt gat cgt	gcg ttg gcc atg gtc tcc	gcc aac ggt	931	

Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met Val Ser Ala Asn Gly
 265 270 275

gtg cac gcg ctc tac gcc acc aat ccg gat gtt ttc cca ggc aca acc 979
 Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val Phe Pro Gly Thr Thr
 280 285 290

acc aat gcg tgg gtt gtg gat tgg gcg acc aac ctc atc gac aac gga 1027
 Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn Leu Ile Asp Asn Gly
 295 300 305

taaagctttt tcgcttttcg acg 1050

<210> 1240

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 1240

Met Arg Lys Thr Ile Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu
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Ile Gly Val Gly Ile Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp
 20 25 30

Phe Ile Gly Gln Pro Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro
 35 40 45

Pro Val Gln Pro Asp Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro
 50 55 60

Gly Thr Trp Glu Ser Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala
 65 70 75 80

Asn Pro Leu Ser Phe Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg
 85 90 95

Tyr Ser Ala Asp Asp Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln
 100 105 110

Phe Arg Asn Ile Asn Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg
 115 120 125

Asn Glu Gly Thr Ala Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn
 130 135 140

Glu Cys Pro Ala Thr Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala
 145 150 155 160

Val Ile Ala Gly Asp Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val
 165 170 175

Ile Pro Ala Asp Ser Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg
 180 185 190

Arg Glu Pro Gly Val Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile
 195 200 205

Gly Ala Glu Val Thr Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile
 210 215 220

Val Pro Gly Ala Thr Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val
 225 230 235 240

Leu Asn Asp Arg Val Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys
 245 250 255

Asp Ala Pro Val Asn Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met
 260 265 270

Val Ser Ala Asn Gly Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val
 275 280 285

Phe Pro Gly Thr Thr Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn
 290 295 300

Leu Ile Asp Asn Gly
 305

<210> 1241
 <211> 1050
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1027)
 <223> FRXA02610

<400> 1241
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gctgctgaag gaatctgcgg atcggacgta ttgttaaccg atg agg aaa acc atc 115
 Met Arg Lys Thr Ile
 1 5

acc gtt att gct gta ttg atc gtc ctc gcc tta atc ggc gtg ggc atc 163
 Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu Ile Gly Val Gly Ile
 10 15 20

gtg cag tat gtg aac aca tcc gat gac tca gat ttc att ggc cag cct 211
 Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp Phe Ile Gly Gln Pro
 25 30 35

ggc gag cca acc ggt acc gaa acc acg gaa cca ccg gtt caa cct gat 259
 Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro Pro Val Gln Pro Asp
 40 45 50

tgg tgc cct gcg gta gaa gtc att gcc gcg ccg ggt acg tgg gag tcg 307
 Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro Gly Thr Trp Glu Ser
 55 60 65

gct gct aat gat gat ccg atc aac ccg acc gct aat ccg ctg tca ttc 355
 Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala Asn Pro Leu Ser Phe
 70 75 80 85

atg ttg agc atc act cag cca ctg cag gag cgt tat tct gcg gat gac 403
 Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg Tyr Ser Ala Asp Asp
 90 95 100

gtc aag gtg tgg acg ctg ccg tac act gcg cag ttc cgc aac atc aac 451
 Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln Phe Arg Asn Ile Asn
 105 110 115

tcg caa aat gag atg tcc tat gat gat tcg cgc aat gaa ggc acc gcg 499
 Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg Asn Glu Gly Thr Ala
 120 125 130

aag atg aat gag gaa ctg atc aac act cac aat gag tgc cct gcc acg 547
 Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn Glu Cys Pro Ala Thr
 135 140 145

gag ttc atc atc gtt ggt ttc tcc cag ggt gcg gtc att gcg ggc gat 595
 Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala Val Ile Ala Gly Asp
 150 155 160 165

gtg gct gct cag atc ggt tca gag caa ggt gtt att cca gct gac agc 643
 Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val Ile Pro Ala Asp Ser
 170 175 180

gtc agg ggt gtc gcc ctg atc gct gac ggt cgc cgg gag cct ggt gtg 691
 Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg Arg Glu Pro Gly Val
 185 190 195

ggc cag ttc cca ggc acg ttt gtg gat ggc atc ggc gcg gag gtt act 739
 Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile Gly Ala Glu Val Thr
 200 205 210

ctg cag cct ttg aac ttg ctg gtg cag ccg att gtt ccg ggc gca acc 787
 Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile Val Pro Gly Ala Thr
 215 220 225

atg cgt ggc ggg cgc gcg ggc ggt ttc ggt gtg ctc aac gac cgg gtg 835
 Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val Leu Asn Asp Arg Val
 230 235 240 245

cag gat att tgt gct cca aat gat gcg atc tgt gat gct ccg gtg aat 883
 Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys Asp Ala Pro Val Asn
 250 255 260

gtc ggc aac gcc ctt gat cgt gcg ttg gcc atg gtc tcc gcc aac ggt 931
 Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met Val Ser Ala Asn Gly
 265 270 275

gtg cac gcg ctc tac gcc acc aat ccg gat gtt ttc cca ggc aca acc 979
 Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val Phe Pro Gly Thr Thr
 280 285 290

acc aat gcg tgg gtt gtg gat tgg gcg acc aac ctc atc gac aac gga 1027
 Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn Leu Ile Asp Asn Gly
 295 300 305

taaagctttt tcgcttttcg acg 1050

<210> 1242

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 1242

Met Arg Lys Thr Ile Thr Val Ile Ala Val Leu Ile Val Leu Ala Leu
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Ile Gly Val Gly Ile Val Gln Tyr Val Asn Thr Ser Asp Asp Ser Asp
20 25 30
Phe Ile Gly Gln Pro Gly Glu Pro Thr Gly Thr Glu Thr Thr Glu Pro
35 40 45
Pro Val Gln Pro Asp Trp Cys Pro Ala Val Glu Val Ile Ala Ala Pro
50 55 60
Gly Thr Trp Glu Ser Ala Ala Asn Asp Asp Pro Ile Asn Pro Thr Ala
65 70 75 80
Asn Pro Leu Ser Phe Met Leu Ser Ile Thr Gln Pro Leu Gln Glu Arg
85 90 95
Tyr Ser Ala Asp Asp Val Lys Val Trp Thr Leu Pro Tyr Thr Ala Gln
100 105 110
Phe Arg Asn Ile Asn Ser Gln Asn Glu Met Ser Tyr Asp Asp Ser Arg
115 120 125
Asn Glu Gly Thr Ala Lys Met Asn Glu Glu Leu Ile Asn Thr His Asn
130 135 140
Glu Cys Pro Ala Thr Glu Phe Ile Ile Val Gly Phe Ser Gln Gly Ala
145 150 155 160
Val Ile Ala Gly Asp Val Ala Ala Gln Ile Gly Ser Glu Gln Gly Val
165 170 175
Ile Pro Ala Asp Ser Val Arg Gly Val Ala Leu Ile Ala Asp Gly Arg
180 185 190
Arg Glu Pro Gly Val Gly Gln Phe Pro Gly Thr Phe Val Asp Gly Ile
195 200 205
Gly Ala Glu Val Thr Leu Gln Pro Leu Asn Leu Leu Val Gln Pro Ile
210 215 220
Val Pro Gly Ala Thr Met Arg Gly Gly Arg Ala Gly Gly Phe Gly Val
225 230 235 240
Leu Asn Asp Arg Val Gln Asp Ile Cys Ala Pro Asn Asp Ala Ile Cys
245 250 255
Asp Ala Pro Val Asn Val Gly Asn Ala Leu Asp Arg Ala Leu Ala Met
260 265 270
Val Ser Ala Asn Gly Val His Ala Leu Tyr Ala Thr Asn Pro Asp Val
275 280 285
Phe Pro Gly Thr Thr Thr Asn Ala Trp Val Val Asp Trp Ala Thr Asn
290 295 300
Leu Ile Asp Asn Gly
305

<400> 1243																
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ggcagctcag caatcaaagt tgctgcgttt ctttccaacc gtg ctg att ccg cat 115																
Val Leu Ile Pro His 1 5																
ggc gtg gcg gtg ctt ttg gtt att att ctc gcc gta gcc tcc cta atg 163																
Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala Val Ala Ser Leu Met 10 15 20																
ttc acc aat tct tca atg gtg aat ctt tcg gca acg att gca cag ctg 211																
Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala Thr Ile Ala Gln Leu 25 30 35																
tgg ctt tcc cta aat ctc ggt gcg gtg gac ggc agt ggg gaa gtg atc 259																
Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly Ser Gly Glu Val Ile 40 45 50																
tca gta ctg ccc acg ctt ccc ggc ttt ata ttc ctc tgg gcc atc gcc 307																
Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe Leu Trp Ala Ile Ala 55 60 65																
gcg cgc atc cac cgc gca gtc aaa gat cgt gtc agc atc gcc gac tta 355																
Ala Arg Ile His Arg Ala Val Lys Asp Arg Val Ser Ile Ala Asp Leu 70 75 80 85																
ggc gtc ctc gca gca ctc gtc ctc ggc atc ccg ctt gcg ctc acc gcc 403																
Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro Leu Ala Leu Thr Ala 90 95 100																
atc gca gcg ttc atg ctt ttc gac gcc tcc agc gtc ctc aac gtc gag 451																
Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser Val Leu Asn Val Glu 105 110 115																
gtc ccg cca atc acg cgc ctc cta cgc gtg atg ttg ttc cac ctc agc 499																
Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met Leu Phe His Leu Ser 120 125 130																
gcc ctc ttc ctc ggc atg ggg cca cgc ctg tgg cag gcg ttg gcg cgc 547																
Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp Gln Ala Leu Ala Arg 135 140 145																
cgc tac ggt gct cca gaa tgg ctt atc gac gcc atc acc caa gct ttc 595																
Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala Ile Thr Gln Ala Phe 150 155 160 165																
cgc ttc ctc atc gca ttt gga aca gtc tcc ttg gtt tcc gtg ctc gtg 643																
Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu Val Ser Val Leu Val 170 175 180																

atg acc gcg atc aac cac agt gca ttc acc gcg acc atg cag ggt tac	691
Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala Thr Met Gln Gly Tyr	
185 190 195	
gac gac tcc gcc tct gtt gtg gcc ttg atc gtc ctg agc att ctg tat	739
Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser Ile Leu Tyr	
200 205 210	
ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc ggc tca ccc	787
Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile Gly Ser Pro	
215 220 225	
ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg cat tcc gtt	835
Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val His Ser Val	
230 235 240 245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc	883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu	
250 255 260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg	931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp	
265 270 275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca	979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala	
280 285 290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga	1027
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly	
295 300 305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt	1075
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val	
310 315 320 325	
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga	1123
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly	
330 335 340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg	1171
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val	
345 350 355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag	1219
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu	
360 365 370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg	1267
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly	
375 380 385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct	1315
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro	
390 395 400 405	
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa	1363
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu	
410 415 420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt	1416

Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
425 430

ctg

1419

<210> 1244

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 1244

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala
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Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp
130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala
145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu
165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala
180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val
195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn
210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe
225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu
245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala

260	265	270
Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val 275 280 285		
Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala 290 295 300		
Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn 305 310 315 320		
Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly 325 330 335		
Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys 340 345 350		
Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu 355 360 365		
Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu 370 375 380		
Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp 385 390 395 400		
Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr 405 410 415		
Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg 420 425 430		

<210> 1245

<211> 737

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(714)

<223> FRXA02624

<400> 1245

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att ctg tat ctg ccc aac atg atg atc ttt gcg atg ggc aat ctg atc Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile 20 25 30	96
ggc tca ccc ctt tac ttc ggt gac gcc tcc atc agc gtc ttc agc gtg Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val 35 40 45	144
cat tcc gtt cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser 50 55 60	192
gaa gcc ctc tca tgg gca gtg gcc tta ctg gtc atc cct gca att att	240

Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile
 65 70 75 80
 gcc acc tgg gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca 288
 Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr
 85 90 95
 aca gca gca gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc 336
 Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe
 100 105 110
 gcc ggc gga acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg 384
 Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu
 115 120 125
 gcg tca gtt ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc 432
 Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu
 130 135 140
 atc gcc gga atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt 480
 Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val
 145 150 155 160
 aag gct gtg gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac 528
 Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp
 165 170 175
 gaa gag gag cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt 576
 Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val
 180 185 190
 gag gaa ggg gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa 624
 Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu
 195 200 205
 gag aat cct gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act 672
 Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr
 210 215 220
 gag gct gaa gaa acc aat gat ggt tcc gag gcc gaa gac cgt 714
 Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
 225 230 235
 taacatatct gttgtgaatt ctg 737

<210> 1246

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 1246

Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val Leu Ser
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Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn Leu Ile
 20 25 30

Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe Ser Val
 35 40 45

gcc tcg gat gtt gtg ctc aat att tct tcg tgg gtc aat cct ttg ctg	259
Ala Ser Asp Val Val Leu Asn Ile Ser Ser Trp Val Asn Pro Leu Leu	
40 45 50	
ggc atc atc atg ttc tcc atg ggc ctg acc ttg aag cca gtt gac ttc	307
Gly Ile Ile Met Phe Ser Met Gly Leu Thr Leu Lys Pro Val Asp Phe	
55 60 65	
gcc ctt gtt gct aaa cgc cca ctc cca gtt ctt atc ggc gtg atc gcc	355
Ala Leu Val Ala Lys Arg Pro Leu Pro Val Leu Ile Gly Val Ile Ala	
70 75 80 85	
cag ttt gtc atc atg ccc ctg atc gca ttg ctg gtg gtc tgg gtt ttg	403
Gln Phe Val Ile Met Pro Leu Ile Ala Leu Leu Val Val Trp Val Leu	
90 95 100	
cag ctg cct gcg gaa att gcg gcc ggt gtc atc ttg gtt ggt tgt gca	451
Gln Leu Pro Ala Glu Ile Ala Ala Gly Val Ile Leu Val Gly Cys Ala	
105 110 115	
cct ggc gga act tcc tcc aac gtg gtg tct tac ctg tcc cgt ggt gat	499
Pro Gly Gly Thr Ser Ser Asn Val Val Ser Tyr Leu Ser Arg Gly Asp	
120 125 130	
gtt gcg ctg tct gtc acc atg act tcc atc tcc acg ctg ctt gct cca	547
Val Ala Leu Ser Val Thr Met Thr Ser Ile Ser Thr Leu Leu Ala Pro	
135 140 145	
att ttc act cca ctg ctt acc ctg tgg ctg gcg ggg caa tac atg cca	595
Ile Phe Thr Pro Leu Leu Thr Leu Trp Leu Ala Gly Gln Tyr Met Pro	
150 155 160 165	
ctt aat gcc gct gat atg gct gta tcc atc gtc caa gtt gtg ctg atc	643
Leu Asn Ala Ala Asp Met Ala Val Ser Ile Val Gln Val Val Leu Ile	
170 175 180	
cca gtc gtg ggc gga ctt gtt gtg cgg ttg atc ttc ccg aca ctc att	691
Pro Val Val Gly Gly Leu Val Val Arg Leu Ile Phe Pro Thr Leu Ile	
185 190 195	
ggc aag gtt ttg cct ctt ttg cca tgg att tca gtc att gcg att tca	739
Gly Lys Val Leu Pro Leu Leu Pro Trp Ile Ser Val Ile Ala Ile Ser	
200 205 210	
ttg atc gtt gcc atc gtg gtc gct ggt tca agg gat aaa atc ctc gaa	787
Leu Ile Val Ala Ile Val Val Ala Gly Ser Arg Asp Lys Ile Leu Glu	
215 220 225	
gca gga ctg ctc gtg ctg gct gcc gtg att att cac aac acc ctc ggc	835
Ala Gly Leu Leu Val Leu Ala Ala Val Ile Ile His Asn Thr Leu Gly	
230 235 240 245	
tac tcc ctg gga tac ctc gct gcg aaa ttc act ggg cag cct gct gca	883
Tyr Ser Leu Gly Tyr Leu Ala Ala Lys Phe Thr Gly Gln Pro Ala Ala	
250 255 260	
gct cga cgc act acc gcg att gag gtc ggt atg caa aac tcc ggc ctc	931
Ala Arg Arg Thr Thr Ala Ile Glu Val Gly Met Gln Asn Ser Gly Leu	
265 270 275	

gca gat gga ctc gca tcc cag tac atg tca cca atg tct gct ctg cca 979
 Ala Asp Gly Leu Ala Ser Gln Tyr Met Ser Pro Met Ser Ala Leu Pro
 280 285 290
 ggc gct atc ttc tct gtc tgg cac aac ctt tcc gga gca ctt ctt gct 1027
 Gly Ala Ile Phe Ser Val Trp His Asn Leu Ser Gly Ala Leu Leu Ala
 295 300 305
 gca ttg tgc agg gcg tcc gat aag agg gct gcg gag aag gtg gct tca 1075
 Ala Leu Cys Arg Ala Ser Asp Lys Arg Ala Ala Glu Lys Val Ala Ser
 310 315 320 325
 gaa aag gct gcc tcg gag aag gcc gct tcc taaaaggcctt cgctcctaaa 1125
 Glu Lys Ala Ala Ser Glu Lys Ala Ala Ser
 330 335
 act 1128

<210> 1248
 <211> 335
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1248
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 Ile Ile Gly Phe Thr Ala Ser Asp Val Val Leu Asn Ile Ser Ser Trp
 35 40 45
 Val Asn Pro Leu Leu Gly Ile Ile Met Phe Ser Met Gly Leu Thr Leu
 50 55 60
 Lys Pro Val Asp Phe Ala Leu Val Ala Lys Arg Pro Leu Pro Val Leu
 65 70 75 80
 Ile Gly Val Ile Ala Gln Phe Val Ile Met Pro Leu Ile Ala Leu Leu
 85 90 95
 Val Val Trp Val Leu Gln Leu Pro Ala Glu Ile Ala Ala Gly Val Ile
 100 105 110
 Leu Val Gly Cys Ala Pro Gly Gly Thr Ser Ser Asn Val Val Ser Tyr
 115 120 125
 Leu Ser Arg Gly Asp Val Ala Leu Ser Val Thr Met Thr Ser Ile Ser
 130 135 140
 Thr Leu Leu Ala Pro Ile Phe Thr Pro Leu Leu Thr Leu Trp Leu Ala
 145 150 155 160
 Gly Gln Tyr Met Pro Leu Asn Ala Ala Asp Met Ala Val Ser Ile Val
 165 170 175
 Gln Val Val Leu Ile Pro Val Val Gly Gly Leu Val Val Arg Leu Ile
 180 185 190

Phe Pro Thr Leu Ile Gly Lys Val Leu Pro Leu Leu Pro Trp Ile Ser
 195 200 205
 Val Ile Ala Ile Ser Leu Ile Val Ala Ile Val Val Ala Gly Ser Arg
 210 215 220
 Asp Lys Ile Leu Glu Ala Gly Leu Leu Val Leu Ala Ala Val Ile Ile
 225 230 235 240
 His Asn Thr Leu Gly Tyr Ser Leu Gly Tyr Leu Ala Ala Lys Phe Thr
 245 250 255
 Gly Gln Pro Ala Ala Ala Arg Arg Thr Thr Ala Ile Glu Val Gly Met
 260 265 270
 Gln Asn Ser Gly Leu Ala Asp Gly Leu Ala Ser Gln Tyr Met Ser Pro
 275 280 285
 Met Ser Ala Leu Pro Gly Ala Ile Phe Ser Val Trp His Asn Leu Ser
 290 295 300
 Gly Ala Leu Leu Ala Ala Leu Cys Arg Ala Ser Asp Lys Arg Ala Ala
 305 310 315 320
 Glu Lys Val Ala Ser Glu Lys Ala Ala Ser Glu Lys Ala Ala Ser
 325 330 335

<210> 1249

<211> 963

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(940)

<223> RXN02656

<400> 1249

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 Met Ile Phe Gly Val
 1 5

ctc gca tac ttg gga tgg ggc atg ttc ccg gcc ttt ttc cca cta ctt 163
 Leu Ala Tyr Leu Gly Trp Gly Met Phe Pro Ala Phe Phe Pro Leu Leu
 10 15 20

ctt ccg gca gga ccg ttc gaa att tta gcg cat ccg atc cta tgg act 211
 Leu Pro Ala Gly Pro Phe Glu Ile Leu Ala His Arg Ile Leu Trp Thr
 25 30 35

gct gta tta atg atg att atc att agt ttc acg tcg gga tgg aaa gag 259
 Ala Val Leu Met Met Ile Ile Ile Ser Phe Thr Ser Gly Trp Lys Glu
 40 45 50

ctt aag tcc gct gat cgc ggt aca tgg tta cgc att ata ttg tca tcg 307
 Leu Lys Ser Ala Asp Arg Gly Thr Trp Leu Arg Ile Ile Leu Ser Ser
 55 60 65

ttg ttt att gcc ggg aac tgg ctg atc tat gtc atc gct gtc aat tct 355
 Leu Phe Ile Ala Gly Asn Trp Leu Ile Tyr Val Ile Ala Val Asn Ser
 70 75 80 85

ggg caa gtt act gaa gcc gct ctc gga tac ttt att aac ccc ctg tta 403
 Gly Gln Val Thr Glu Ala Ala Leu Gly Tyr Phe Ile Asn Pro Leu Leu
 90 95 100

agt gtc gtg ctt ggc att gtg ttc ttc aaa gaa cag tta cga aaa ctg 451
 Ser Val Val Leu Gly Ile Val Phe Lys Glu Gln Leu Arg Lys Leu
 105 110 115

caa att agt gcg gtg gtt att gct gct gcg ggg gtt ttg gta cta aca 499
 Gln Ile Ser Ala Val Val Ile Ala Ala Ala Gly Val Leu Val Leu Thr
 120 125 130

ttt cta ggt gat aag cca ccg tat tta gcg ata aca cta gca ttt aca 547
 Phe Leu Gly Asp Lys Pro Tyr Leu Ala Ile Thr Leu Ala Phe Thr
 135 140 145

ttc ggc atc tat gga gcg ttg aaa aaa caa gtc aag atg tct gct gct 595
 Phe Gly Ile Tyr Gly Ala Leu Lys Lys Gln Val Lys Met Ser Ala Ala
 150 155 160 165

agt tct ttg tgc gct gaa act tta gta ctg ctg ccc atc gca gtc ata 643
 Ser Ser Leu Cys Ala Glu Thr Leu Val Leu Leu Pro Ile Ala Val Ile
 170 175 180

tac ctg att ggg ctc gaa gct tcc ggt cac agt acc ttt ttc aac aat 691
 Tyr Leu Ile Gly Leu Glu Ala Ser Gly His Ser Thr Phe Phe Asn Asn
 185 190 195

ggc agt ggg cac atg gcg tta tta atc tgc tgc ggt ttg gtc aca gcc 739
 Gly Ser Gly His Met Ala Leu Leu Ile Cys Ser Gly Leu Val Thr Ala
 200 205 210

gtc ccg ctg ttg atg ttt gca ttg gcc gcc aag gca ata cct ctt tcc 787
 Val Pro Leu Leu Met Phe Ala Leu Ala Ala Lys Ala Ile Pro Leu Ser
 215 220 225

act gtc ggc atg ctg caa tat ctg acc cca acg atg cag atg ctg tgg 835
 Thr Val Gly Met Leu Gln Tyr Leu Thr Pro Thr Met Gln Met Leu Trp
 230 235 240 245

gca ttg ttt gtg gtc aac gaa tca gta gaa cca atg cgt tgg ttc gga 883
 Ala Leu Phe Val Val Asn Glu Ser Val Glu Pro Met Arg Trp Phe Gly
 250 255 260

ttc gtt ttc att tgg atc gca gtt act att tac atc aca gat agc cta 931
 Phe Val Phe Ile Trp Ile Ala Val Thr Ile Tyr Ile Thr Asp Ser Leu
 265 270 275

ctt aag aag taggtaatag cagtattgat atg 963
 Leu Lys Lys
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<210> 1250

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 1250

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Phe Phe Pro Leu Leu Leu Pro Ala Gly Pro Phe Glu Ile Leu Ala His
20 25 30
Arg Ile Leu Trp Thr Ala Val Leu Met Met Ile Ile Ile Ser Phe Thr
35 40 45
Ser Gly Trp Lys Glu Leu Lys Ser Ala Asp Arg Gly Thr Trp Leu Arg
50 55 60
Ile Ile Leu Ser Ser Leu Phe Ile Ala Gly Asn Trp Leu Ile Tyr Val
65 70 75 80
Ile Ala Val Asn Ser Gly Gln Val Thr Glu Ala Ala Leu Gly Tyr Phe
85 90 95
Ile Asn Pro Leu Leu Ser Val Val Leu Gly Ile Val Phe Phe Lys Glu
100 105 110
Gln Leu Arg Lys Leu Gln Ile Ser Ala Val Val Ile Ala Ala Ala Gly
115 120 125
Val Leu Val Leu Thr Phe Leu Gly Asp Lys Pro Pro Tyr Leu Ala Ile
130 135 140
Thr Leu Ala Phe Thr Phe Gly Ile Tyr Gly Ala Leu Lys Lys Gln Val
145 150 155 160
Lys Met Ser Ala Ala Ser Ser Leu Cys Ala Glu Thr Leu Val Leu Leu
165 170 175
Pro Ile Ala Val Ile Tyr Leu Ile Gly Leu Glu Ala Ser Gly His Ser
180 185 190
Thr Phe Phe Asn Asn Gly Ser Gly His Met Ala Leu Leu Ile Cys Ser
195 200 205
Gly Leu Val Thr Ala Val Pro Leu Leu Met Phe Ala Leu Ala Ala Lys
210 215 220
Ala Ile Pro Leu Ser Thr Val Gly Met Leu Gln Tyr Leu Thr Pro Thr
225 230 235 240
Met Gln Met Leu Trp Ala Leu Phe Val Val Asn Glu Ser Val Glu Pro
245 250 255
Met Arg Trp Phe Gly Phe Val Phe Ile Trp Ile Ala Val Thr Ile Tyr
260 265 270
Ile Thr Asp Ser Leu Leu Lys Lys
275 280

<210> 1251

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXN02673

<400> 1251

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				Met	Ala	Ala	Leu	Leu	
				1				5	

ggt	ctg	ctc	gtc	gtg	att	gcc	ttg	att	atc	tgg	gca	gtc	gtc	gcg	ctt	163
Val	Leu	Leu	Val	Val	Ile	Ala	Leu	Ile	Ile	Trp	Ala	Val	Val	Ala	Leu	
			10					15						20		

cga	ggt	gga	tca	tcg	gag	cct	gag	gaa	gag	cag	cca	aat	aat	gct	gta	211
Arg	Gly	Gly	Ser	Ser	Glu	Pro	Glu	Glu	Glu	Gln	Pro	Asn	Asn	Ala	Val	
			25					30					35			

gtg	acc	tcc	tca	atg	gaa	tct	tcc	gcg	acg	tct	agt	tct	tct	tct	aaa	259
Val	Thr	Ser	Ser	Met	Glu	Ser	Ser	Ala	Thr	Ser	Ser	Ser	Ser	Ser	Lys	
		40					45					50				

gaa	tcc	acg	act	gaa	gcc	acc	aca	gaa	gaa	gag	act	tcc	agt	gct	gaa	307
Glu	Ser	Thr	Thr	Glu	Ala	Thr	Thr	Glu	Glu	Glu	Thr	Ser	Ser	Ala	Glu	
	55					60					65					

cca	acc	gca	aca	tcc	tcc	ggt	gca	gca	gat	gca	aaa	aag	acc	tgt	gag	355
Pro	Thr	Ala	Thr	Ser	Ser	Val	Ala	Ala	Asp	Ala	Lys	Lys	Thr	Cys	Glu	
	70					75				80					85	

ctt	agt	gac	ttg	gtg	att	tcc	gca	agc	act	aat	cag	ccg	act	ttc	tca	403
Leu	Ser	Asp	Leu	Val	Ile	Ser	Ala	Ser	Thr	Asn	Gln	Pro	Thr	Phe	Ser	
			90						95					100		

ggt	tct	gcg	cag	cca	gaa	tta	ttt	atg	gct	gtg	cat	aat	ccg	act	gct	451
Gly	Ser	Ala	Gln	Pro	Glu	Leu	Phe	Met	Ala	Val	His	Asn	Pro	Thr	Ala	
			105					110					115			

ggt	gat	tgc	gaa	att	gac	ctc	gag	gag	aac	aaa	ctc	cgt	ttc	gag	gta	499
Val	Asp	Cys	Glu	Ile	Asp	Leu	Glu	Glu	Asn	Lys	Leu	Arg	Phe	Glu	Val	
		120					125					130				

tac	aat	ctc	gcg	acc	aac	gca	cga	atc	tgg	tct	gat	gtc	gac	tgc	aac	547
Tyr	Asn	Leu	Ala	Thr	Asn	Ala	Arg	Ile	Trp	Ser	Asp	Val	Asp	Cys	Asn	
	135					140					145					

cct	gca	ggt	gaa	gac	ggc	acg	agc	gtg	ttc	cct	gcc	ggc	gag	gat	cgc	595
Pro	Ala	Val	Glu	Asp	Gly	Thr	Ser	Val	Phe	Pro	Ala	Gly	Glu	Asp	Arg	
	150				155					160					165	

tac	ttc	cag	gca	aca	tgg	tct	cgt	acc	act	tca	gcg	cca	aac	cag	tgc	643
Tyr	Phe	Gln	Ala	Thr	Trp	Ser	Arg	Thr	Thr	Ser	Ala	Pro	Asn	Gln	Cys	
			170					175						180		

aac	aac	cg	act	gat	gtc	ccc	gcc	ggt	ggc	tac	tac	ttg	cac	act	gtg	691
Asn	Asn	Arg	Thr	Asp	Val	Pro	Ala	Gly	Gly	Tyr	Tyr	Leu	His	Thr	Val	
			185					190					195			

gtc ggt aat aac cct tca cca gcg gtg acc ttt aac cta act
 Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe Asn Leu Thr
 200 205 210

733

taaacggcca agtccgtcgg tga

756

<210> 1252

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 1252

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 20 25 30

Pro Asn Asn Ala Val Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser
 35 40 45

Ser Ser Ser Ser Lys Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu
 50 55 60

Thr Ser Ser Ala Glu Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala
 65 70 75 80

Lys Lys Thr Cys Glu Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn
 85 90 95

Gln Pro Thr Phe Ser Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val
 100 105 110

His Asn Pro Thr Ala Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys
 115 120 125

Leu Arg Phe Glu Val Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser
 130 135 140

Asp Val Asp Cys Asn Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro
 145 150 155 160

Ala Gly Glu Asp Arg Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser
 165 170 175

Ala Pro Asn Gln Cys Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr
 180 185 190

Tyr Leu His Thr Val Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe
 195 200 205

Asn Leu Thr
 210

<210> 1253

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> FRXA02673

<400> 1253

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aacgccgaga cataatgaag tcatttacaa ggcgcgcgcgc atg gca gcg ctc cta 115
                                         Met Ala Ala Leu Leu
                                         1           5

gtt ctg ctc gtc gtg att gcc ttg att atc tgg gca gtc gtc gcg ctt 163
Val Leu Leu Val Val Ile Ala Leu Ile Ile Trp Ala Val Val Ala Leu
                        10                        15                        20

cga ggt gga tca tcg gag cct gag gaa gag cag cca aat aat gct gta 211
Arg Gly Gly Ser Ser Glu Pro Glu Glu Glu Gln Pro Asn Asn Ala Val
                        25                        30                        35

gtg acc tcc tca atg gaa tct tcc gcg acg tct agt tct tct tct aaa 259
Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser Ser Ser Ser Ser Lys
                        40                        45                        50

gaa tcc acg act gaa gcc acc aca gaa gaa gag act tcc agt gct gaa 307
Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu Thr Ser Ser Ala Glu
                        55                        60                        65

cca acc gca aca tcc tcc gtt gca gca gat gca aaa aag acc tgt gag 355
Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala Lys Lys Thr Cys Glu
                        70                        75                        80                        85

ctt agt gac ttg gtg att tcc gca agc act aat cag ccg act ttc tca 403
Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn Gln Pro Thr Phe Ser
                        90                        95                        100

ggg tct gcg cag cca gaa tta ttt atg gct gtg cat aat ccg act gct 451
Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val His Asn Pro Thr Ala
                        105                        110                        115

gtt gat tgc gaa att gac ctc gag gag aac aaa ctc cgt ttc gag gta 499
Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys Leu Arg Phe Glu Val
                        120                        125                        130

tac aat ctc gcg acc aac gca cga atc tgg tct gat gtc gac tgc aac 547
Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser Asp Val Asp Cys Asn
                        135                        140                        145

cct gca gtt gaa gac ggc acg agc gtg ttc cct gcc ggc gag gat cgc 595
Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro Ala Gly Glu Asp Arg
150                        155                        160                        165

tac ttc cag gca aca tgg tct cgt acc act tca gcg cca aac cag tgc 643
Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser Ala Pro Asn Gln Cys
                        170                        175                        180

aac aac cgc act gat gtc ccc gcc ggt ggc tac tac ttg cac act gtg 691
Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr Tyr Leu His Thr Val
                        185                        190                        195

gtc ggt aat aac cct tca cca gcg gtg acc ttt aac cta act 733

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Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe Asn Leu Thr
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756

<210> 1254

<211> 211

<212> PRT

<213> Corynebacterium glutamicum .

<400> 1254

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20 25 30

Pro Asn Asn Ala Val Val Thr Ser Ser Met Glu Ser Ser Ala Thr Ser
35 40 45

Ser Ser Ser Ser Lys Glu Ser Thr Thr Glu Ala Thr Thr Glu Glu Glu
50 55 60

Thr Ser Ser Ala Glu Pro Thr Ala Thr Ser Ser Val Ala Ala Asp Ala
65 70 75 80

Lys Lys Thr Cys Glu Leu Ser Asp Leu Val Ile Ser Ala Ser Thr Asn
85 90 95

Gln Pro Thr Phe Ser Gly Ser Ala Gln Pro Glu Leu Phe Met Ala Val
100 105 110

His Asn Pro Thr Ala Val Asp Cys Glu Ile Asp Leu Glu Glu Asn Lys
115 120 125

Leu Arg Phe Glu Val Tyr Asn Leu Ala Thr Asn Ala Arg Ile Trp Ser
130 135 140

Asp Val Asp Cys Asn Pro Ala Val Glu Asp Gly Thr Ser Val Phe Pro
145 150 155 160

Ala Gly Glu Asp Arg Tyr Phe Gln Ala Thr Trp Ser Arg Thr Thr Ser
165 170 175

Ala Pro Asn Gln Cys Asn Asn Arg Thr Asp Val Pro Ala Gly Gly Tyr
180 185 190

Tyr Leu His Thr Val Val Gly Asn Asn Pro Ser Pro Ala Val Thr Phe
195 200 205

Asn Leu Thr
210

<210> 1255

<211> 1407

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1384)

<223> RXN02680

<400> 1255

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tttcactttt ttgagaagtt ttacttttat attagttctc atg cgc ctc aac aaa 115
                                         Met Arg Leu Asn Lys
                                         1           5

cga ctc cca gcg gca ctc tcc gga ctg ctg ctc tct gct gcc ctt ctt 163
Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu Ser Ala Ala Leu Leu
              10              15              20

gcc gga tgc tcc act tct gga acc gcc gag acc acg aca aca acc gtt 211
Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr Thr Thr Thr Thr Val
              25              30              35

tca tct gct gcg gca tca aca acc act tcc acc tcc tct gct tcg tct 259
Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr Ser Ser Ala Ser Ser
              40              45              50

tcc tct tcc tcc tcc tct tcc tcc tct tcc tcc gac tca agc acc acc 307
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Thr
              55              60              65

gcc gaa acc atc tcc aac acc gcg gaa gct gcc caa gct ttc ttg tcc 355
Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala Gln Ala Phe Leu Ser
              70              75              80              85

acc ctg tcc acc gaa gaa caa gac gcc gta ctc tac gac tac gac gcc 403
Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu Tyr Asp Tyr Asp Ala
              90              95              100

gaa gaa aag tcc acc ggc tgg tct aac ttc cca gtc acc ttc gtg cag 451
Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro Val Thr Phe Val Gln
              105              110              115

cgt tcc ggc gtg aac ctc acc gac ctc act gag gaa cag caa gca gct 499
Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu Glu Gln Gln Ala Ala
              120              125              130

gcc ctc aac gtg ctg aag aac ctg ctc aac gac gac gcc tac caa atg 547
Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp Asp Ala Tyr Gln Met
              135              140              145

atc gaa gac atc atg gct agc gat cag tac ctc aac gac gaa agc aac 595
Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu Asn Asp Glu Ser Asn
              150              155              160              165

acc acc gag gat tcc ctc ggc cag tac tac atc gca ttc ttc ggc gat 643
Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile Ala Phe Phe Gly Asp
              170              175              180

cca agc agc gac tcc gac tgg tcc atc caa ttc ggc gga cac cac atc 691
Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe Gly Gly His His Ile
              185              190              195

ggc atc aac acc acc ttc tcc gac ggt gcc atc acc ttc gcc cca acc 739
Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile Thr Phe Ala Pro Thr

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200	205	210	
cac ctt ggc acc cag cct tcc gag tgg acc aac gag gac ggc gaa acc His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn Glu Asp Gly Glu Thr 215 220 225			787
ggt gca gca cta agc aac atg tac gaa acc gcc ttc gcc ttc tac gac Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala Phe Ala Phe Tyr Asp 230 235 240 245			835
agc ctc gcc gaa gag cag caa gca cag ctc tac cag ggt gaa gag ttg Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr Gln Gly Glu Glu Leu 250 255 260			883
gat tcc atg gtg tgc gca ccg ggc agc acg tgc gac tac cca acc ggc Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys Asp Tyr Pro Thr Gly 265 270 275			931
acc ggc ttg aaa ggc tct gac ctc acc gat gag caa aaa gaa ttg ctc Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu Gln Lys Glu Leu Leu 280 285 290			979
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gaa act gaa ctc gat gcc atc cgc gaa acc ctg gat gac acc tac atc Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu Asp Asp Thr Tyr Ile 310 315 320 325			1075
aac tgg tcc ggc gcc acc gag tac gac acc tcc acc ggc gac ggc atc Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser Thr Gly Asp Gly Ile 330 335 340			1123
tac ttc cag atc agt ggc cca aag gtc tac att gag ttc gct aac cag Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile Glu Phe Ala Asn Gln 345 350 355			1171
caa ggt tct gca ggt gcc gac atc gac ggt gtc atc acc gct gga tgg Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val Ile Thr Ala Gly Trp 360 365 370			1219
ggc cac att cac acc atc tac cgc gac cca acc aat gac tac gct aac Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr Asn Asp Tyr Ala Asn 375 380 385			1267
tcc gta act cag gaa gca gcc agc gga atg atg ggc ggc ggc cct ggt Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met Gly Gly Gly Pro Gly 390 395 400 405			1315
ggt aat ggt ggc gag atg cct agc ggt gac atg cct act ggt gag atg Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met Pro Thr Gly Glu Met 410 415 420			1363
cct tct ggc gct cca tca aac taacgccatt taagaggccg aac Pro Ser Gly Ala Pro Ser Asn 425			1407

<210> 1256

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 1256

Met Arg Leu Asn Lys Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu
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20 25 30

Thr Thr Thr Thr Val Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr
35 40 45

Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
50 55 60

Asp Ser Ser Thr Thr Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala
65 70 75 80

Gln Ala Phe Leu Ser Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu
85 90 95

Tyr Asp Tyr Asp Ala Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro
100 105 110

Val Thr Phe Val Gln Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu
115 120 125

Glu Gln Gln Ala Ala Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp
130 135 140

Asp Ala Tyr Gln Met Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu
145 150 155 160

Asn Asp Glu Ser Asn Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile
165 170 175

Ala Phe Phe Gly Asp Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe
180 185 190

Gly Gly His His Ile Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile
195 200 205

Thr Phe Ala Pro Thr His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn
210 215 220

Glu Asp Gly Glu Thr Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala
225 230 235 240

Phe Ala Phe Tyr Asp Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr
245 250 255

Gln Gly Glu Glu Leu Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys
260 265 270

Asp Tyr Pro Thr Gly Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu
275 280 285

Gln Lys Glu Leu Leu Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala
290 295 300

Asp Glu Glu Thr Thr Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu
305 310 315 320

Asp Asp Thr Tyr Ile Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser
325 330 335

Thr Gly Asp Gly Ile Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile
340 345 350

Glu Phe Ala Asn Gln Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val
355 360 365

Ile Thr Ala Gly Trp Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr
370 375 380

Asn Asp Tyr Ala Asn Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met
385 390 395 400

Gly Gly Gly Pro Gly Gly Asn Gly Gly Glu Met Pro Ser Gly Asp Met
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Pro Thr Gly Glu Met Pro Ser Gly Ala Pro Ser Asn
420 425

<210> 1257

<211> 1407

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1384)

<223> FRXA02680

<400> 1257

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tttcactttt ttgagaagtt ttacttttat attagttctc atg cgc ctc aac aaa 115
Met Arg Leu Asn Lys
1 5

cga ctc cca gcg gca ctc tcc gga ctg ctg ctc tct gct gcc ctt ctt 163
Arg Leu Pro Ala Ala Leu Ser Gly Leu Leu Leu Ser Ala Ala Leu Leu
10 15 20

gcc gga tgc tcc act tct gga acc gcc gag acc acg aca aca acc gtt 211
Ala Gly Cys Ser Thr Ser Gly Thr Ala Glu Thr Thr Thr Thr Thr Val
25 30 35

tca tct gct gcg gca tca aca acc act tcc acc tcc tct gct tcg tct 259
Ser Ser Ala Ala Ala Ser Thr Thr Thr Ser Thr Ser Ser Ala Ser Ser
40 45 50

tcc tct tcc tcc tcc tct tcc tcc tct tcc tcc gac tca agc acc acc 307
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Thr
55 60 65

gcc gaa acc atc tcc aac acc gcg gaa gct gcc caa gct ttc ttg tcc 355
Ala Glu Thr Ile Ser Asn Thr Ala Glu Ala Ala Gln Ala Phe Leu Ser
70 75 80 85

acc ctg tcc acc gaa gaa caa gac gcc gta ctc tac gac tac gac gcc	403
Thr Leu Ser Thr Glu Glu Gln Asp Ala Val Leu Tyr Asp Tyr Asp Ala	
90 95 100	
gaa gaa aag tcc acc ggc tgg tct aac ttc cca gtc acc ttc gtg cag	451
Glu Glu Lys Ser Thr Gly Trp Ser Asn Phe Pro Val Thr Phe Val Gln	
105 110 115	
cgt tcc ggc gtg aac ctc acc gac ctc act gag gaa cag caa gca gct	499
Arg Ser Gly Val Asn Leu Thr Asp Leu Thr Glu Glu Gln Gln Ala Ala	
120 125 130	
gcc ctc aac gtg ctg aag aac ctg ctc aac gac gac gcc tac caa atg	547
Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp Asp Ala Tyr Gln Met	
135 140 145	
atc gaa gac atc atg gct agc gat cag tac ctc aac gac gaa agc aac	595
Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu Asn Asp Glu Ser Asn	
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Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile Ala Phe Phe Gly Asp	
170 175 180	
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Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe Gly Gly His His Ile	
185 190 195	
ggc atc aac acc acc ttc tcc gac ggt gcc atc acc ttc gcc cca acc	739
Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile Thr Phe Ala Pro Thr	
200 205 210	
cac ctt ggc acc cag cct tcc gag tgg acc aac gag gac ggc gaa acc	787
His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn Glu Asp Gly Glu Thr	
215 220 225	
gtt gca gca cta agc aac atg tac gaa acc gcc ttc gcc ttc tac gac	835
Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala Phe Ala Phe Tyr Asp	
230 235 240 245	
agc ctc gcc gaa gag cag caa gca cag ctc tac cag ggt gaa gag ttg	883
Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr Gln Gly Glu Glu Leu	
250 255 260	
gat tcc atg gtg tgc gca ccg ggc agc acg tgc gac tac cca acc ggc	931
Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys Asp Tyr Pro Thr Gly	
265 270 275	
acc ggc ttg aaa ggc tct gac ctc acc gat gag caa aaa gaa ttg ctc	979
Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu Gln Lys Glu Leu Leu	
280 285 290	
atc gat gtc atc gca aac tgg gtt ggc ctc gcc gat gag gaa acc acc	1027
Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala Asp Glu Glu Thr Thr	
295 300 305	
gaa act gaa ctc gat gcc atc cgc gaa acc ctg gat gac acc tac atc	1075
Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu Asp Asp Thr Tyr Ile	
310 315 320 325	

Glu Gln Gln Ala Ala Ala Leu Asn Val Leu Lys Asn Leu Leu Asn Asp
130 135 140

Asp Ala Tyr Gln Met Ile Glu Asp Ile Met Ala Ser Asp Gln Tyr Leu
145 150 155 160

Asn Asp Glu Ser Asn Thr Thr Glu Asp Ser Leu Gly Gln Tyr Tyr Ile
165 170 175

Ala Phe Phe Gly Asp Pro Ser Ser Asp Ser Asp Trp Ser Ile Gln Phe
180 185 190

Gly Gly His His Ile Gly Ile Asn Thr Thr Phe Ser Asp Gly Ala Ile
195 200 205

Thr Phe Ala Pro Thr His Leu Gly Thr Gln Pro Ser Glu Trp Thr Asn
210 215 220

Glu Asp Gly Glu Thr Val Ala Ala Leu Ser Asn Met Tyr Glu Thr Ala
225 230 235 240

Phe Ala Phe Tyr Asp Ser Leu Ala Glu Glu Gln Gln Ala Gln Leu Tyr
245 250 255

Gln Gly Glu Glu Leu Asp Ser Met Val Cys Ala Pro Gly Ser Thr Cys
260 265 270

Asp Tyr Pro Thr Gly Thr Gly Leu Lys Gly Ser Asp Leu Thr Asp Glu
275 280 285

Gln Lys Glu Leu Leu Ile Asp Val Ile Ala Asn Trp Val Gly Leu Ala
290 295 300

Asp Glu Glu Thr Thr Glu Thr Glu Leu Asp Ala Ile Arg Glu Thr Leu
305 310 315 320

Asp Asp Thr Tyr Ile Asn Trp Ser Gly Ala Thr Glu Tyr Asp Thr Ser
325 330 335

Thr Gly Asp Gly Ile Tyr Phe Gln Ile Ser Gly Pro Lys Val Tyr Ile
340 345 350

Glu Phe Ala Asn Gln Gln Gly Ser Ala Gly Ala Asp Ile Asp Gly Val
355 360 365

Ile Thr Ala Gly Trp Gly His Ile His Thr Ile Tyr Arg Asp Pro Thr
370 375 380

Asn Asp Tyr Ala Asn Ser Val Thr Gln Glu Ala Ala Ser Gly Met Met
385 390 395 400

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Pro Thr Gly Glu Met Pro Ser Gly Ala Pro Ser Asn
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<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> FRXA02679

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tagcgtagtc attggttggg tcgcggtaga tggtgtgaat gtg gcc cca tcc agc 115
Val Ala Pro Ser Ser
1 5

ggt gat gac acc gtc gat gtc ggc acc tgc aga acc ttg ctg gtt agc 163
Gly Asp Asp Thr Val Asp Val Gly Thr Cys Arg Thr Leu Leu Val Ser
10 15 20

gaa ctc aat gta gac ctt tgg gcc act gat ctg gaa gta gat gcc gtc 211
Glu Leu Asn Val Asp Leu Trp Ala Thr Asp Leu Glu Val Asp Ala Val
25 30 35

gcc ggt gga ggt gtc gta ctc ggt ggc gcc gga cca gtt gat gta ggt 259
Ala Gly Gly Gly Val Val Leu Gly Gly Ala Gly Pro Val Asp Val Gly
40 45 50

gtc atc cag ggt ttc gcg gat ggc atc gag ttc agt ttc ggt ggt ttc 307
Val Ile Gln Gly Phe Ala Asp Gly Ile Glu Phe Ser Phe Gly Gly Phe
55 60 65

ctc atc ggc gag gcc aac cca gtt tgc gat gac atc gat gag caa ttc 355
Leu Ile Gly Glu Ala Asn Pro Val Cys Asp Asp Ile Asp Glu Gln Phe
70 75 80 85

ttt ttg ctc atc ggt gag gtc aga gcc ttt caa gcc ggt gcc ggt tgg 403
Phe Leu Leu Ile Gly Glu Val Arg Ala Phe Gln Ala Gly Ala Gly Trp
90 95 100

gta gtc gca cgt gct gcc cgg tgc gca cac cat gga atc caa ctc ttc 451
Val Val Ala Arg Ala Ala Arg Cys Ala His His Gly Ile Gln Leu Phe
105 110 115

acc ctg gta gag ctg tgc ttg ctg ctc ttc ggc gag gct gtc gta gaa 499
Thr Leu Val Glu Leu Cys Leu Leu Leu Phe Gly Glu Ala Val Val Glu
120 125 130

ggc gaa ggc ggt ttc gta cat gtt gct tagtgctgca acggtttcgc 546
Gly Glu Gly Gly Phe Val His Val Ala
135 140

cgt 549

<210> 1260

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 1260

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20										25										30																																		
Glu	Val	Asp	Ala	Val	Ala	Gly	Gly	Gly	Val	Val	Leu	Gly	Gly	Ala	Gly																																							
		35					40					45																																										
Pro	Val	Asp	Val	Gly	Val	Ile	Gln	Gly	Phe	Ala	Asp	Gly	Ile	Glu	Phe																																							
		50				55					60																																											
Ser	Phe	Gly	Gly	Phe	Leu	Ile	Gly	Glu	Ala	Asn	Pro	Val	Cys	Asp	Asp																																							
		65			70					75					80																																							
Ile	Asp	Glu	Gln	Phe	Phe	Leu	Leu	Ile	Gly	Glu	Val	Arg	Ala	Phe	Gln																																							
				85					90					95																																								
Ala	Gly	Ala	Gly	Trp	Val	Val	Ala	Arg	Ala	Ala	Arg	Cys	Ala	His	His																																							
			100					105					110																																									
Gly	Ile	Gln	Leu	Phe	Thr	Leu	Val	Glu	Leu	Cys	Leu	Leu	Leu	Phe	Gly																																							
		115					120					125																																										
Glu	Ala	Val	Val	Glu	Gly	Glu	Gly	Gly	Phe	Val	His	Val	Ala																																									
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<211> 567

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(544)

<223> FRXA02681

<400> 1261

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				Val	Gly	Trp	Gly	Glu		
					1			5		

ggt	gat	ggc	acc	gtc	gga	gaa	ggt	ggt	gtt	gat	gcc	gat	gtg	gtg	tcc		163
Gly	Asp	Gly	Thr	Val	Gly	Glu	Gly	Gly	Val	Asp	Ala	Asp	Val	Val	Ser		
			10					15						20			

gcc	gaa	ttg	gat	gga	cca	gtc	gga	gtc	gct	gct	tgg	atc	gcc	gaa	gaa		211
Ala	Glu	Leu	Asp	Gly	Pro	Val	Gly	Val	Ala	Ala	Trp	Ile	Ala	Glu	Glu		
			25					30					35				

tgc	gat	gta	gta	ctg	gcc	gag	gga	atc	ctc	ggt	ggt	gtt	gct	ttc	gtc		259
Cys	Asp	Val	Val	Leu	Ala	Glu	Gly	Ile	Leu	Gly	Gly	Val	Ala	Phe	Val		
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gtt	gag	gta	ctg	atc	gct	agc	cat	gat	gtc	ttc	gat	cat	ttg	gta	ggc		307
Val	Glu	Val	Leu	Ile	Ala	Ser	His	Asp	Val	Phe	Asp	His	Leu	Val	Gly		
		55				60					65						

gtc	gtc	gtt	gag	cag	gtt	ctt	cag	cac	gtt	gag	ggc	agc	tgc	ttg	ctg		355
Val	Val	Val	Glu	Gln	Val	Leu	Gln	His	Val	Glu	Gly	Ser	Cys	Leu	Leu		
		70				75				80					85		

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 Phe Leu Ser Glu Val Gly Glu Val His Ala Gly Thr Leu His Glu Gly
 90 95 100

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 Asp Trp Glu Val Arg Pro Ala Gly Gly Leu Phe Phe Gly Val Val Val
 105 110 115

gta gag tac ggc gtc ttg ttc ttc ggt gga cag ggt gga caa gaa agc 499
 Val Glu Tyr Gly Val Leu Phe Phe Gly Gly Gln Gly Gly Gln Glu Ser
 120 125 130

ttg ggc agc ttc cgc ggt gtt gga gat ggt ttc ggc ggt ggt gct 544
 Leu Gly Ser Phe Arg Gly Val Gly Asp Gly Phe Gly Gly Gly Ala
 135 140 145

tgagtcggag gaagaggagg aag 567

<210> 1262

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 1262

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Trp Ile Ala Glu Glu Cys Asp Val Val Leu Ala Glu Gly Ile Leu Gly
 35 40 45

Gly Val Ala Phe Val Val Glu Val Leu Ile Ala Ser His Asp Val Phe
 50 55 60

Asp His Leu Val Gly Val Val Val Glu Gln Val Leu Gln His Val Glu
 65 70 75 80

Gly Ser Cys Leu Leu Phe Leu Ser Glu Val Gly Glu Val His Ala Gly
 85 90 95

Thr Leu His Glu Gly Asp Trp Glu Val Arg Pro Ala Gly Gly Leu Phe
 100 105 110

Phe Gly Val Val Val Val Glu Tyr Gly Val Leu Phe Phe Gly Gly Gln
 115 120 125

Gly Gly Gln Glu Ser Leu Gly Ser Phe Arg Gly Val Gly Asp Gly Phe
 130 135 140

Gly Gly Gly Ala
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<210> 1263

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1876)

<223> RXN02693

<400> 1263

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                                         Met Val Ser Leu Pro
                                         1           5

aga cta gcg tct ctg ctc acc act cgc ctg gca acg ctt aaa ccc gca 163
Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala Thr Leu Lys Pro Ala
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Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly Ala Gln Val Ile Ala
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gag cta gtt ccg ggg atc cga atg tcg cca aac cgc agg cga atc ctc 259
Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn Arg Arg Arg Ile Leu
                        40                        45                        50

cct gca aat atg ggc gct ggc ttt atc gga gcg gaa atc gca atg tgg 307
Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala Glu Ile Ala Met Trp
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tgg gct ctc tcg ccg tca ttg ttg ccg aaa ccg tgg tgg gtt acg gct 355
Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro Trp Trp Val Thr Ala
                        70                        75                        80                        85

gct aac ctg gct gtt tta caa gcg gtg ggg cat gcg gca gcg acg gga 403
Ala Asn Leu Ala Val Leu Gln Ala Val Gly His Ala Ala Ala Thr Gly
                        90                        95                        100

atc cac tcg atc ctc ccc aga acc aac cgg cgg gta tcc agg aaa att 451
Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg Val Ser Arg Lys Ile
                        105                        110                        115

tac aac gcc acc cac atc gca act ggt gcc atc acg ttg acc acc acg 499
Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile Thr Leu Thr Thr Thr
                        120                        125                        130

gtt gtg gga ttg atc agg cat cgc acc caa atc cgg ctg att ggg cag 547
Val Val Gly Leu Ile Arg His Arg Thr Gln Ile Arg Leu Ile Gly Gln
                        135                        140                        145

aag aat ttt gga ccg aag gag acg atc gcg ggc att agt gtc ggc acc 595
Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly Ile Ser Val Gly Thr
                        150                        155                        160                        165

ttg ggg tac ggc gcg ctg ctg atc acc ggc gaa tta acc cag cac agt 643
Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu Leu Thr Gln His Ser
                        170                        175                        180

att aat gag gtc aag ctc cta att gag agg ttt tta ccg ccg tgg ata 691
Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe Leu Pro Pro Trp Ile
                        185                        190                        195

agt ttc atc gca gcg gtt tcg gtc att aca ttg acc act ttg acc ttg 739

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Ala	Asp	Arg	Val	Leu	Leu	Arg	Arg	Ile	Leu	His	Asn	Ser	Ala	Ile	Gln		
	215					220					225						
gca	gcg	cac	ctt	aat	cgc	atg	gtg	ttc	cca	gga	act	gag	cag	ccg	tgg	835	
Ala	Ala	His	Leu	Asn	Arg	Met	Val	Phe	Pro	Gly	Thr	Glu	Gln	Pro	Trp		
	230				235					240					245		
gag	ccg	gag	cgt	tcg	ggg	agc	ccg	tgg	tcg	tat	gaa	aaa	tgg	ggg	gcg	883	
Glu	Pro	Glu	Arg	Ser	Gly	Ser	Pro	Trp	Ser	Tyr	Glu	Lys	Trp	Gly	Ala		
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gtg	ggg	tcg	cag	ggc	cgt	gca	gtg	ttg	tcg	gga	ggc	cca	cgc	aaa	gat	931	
Val	Gly	Ser	Gln	Gly	Arg	Ala	Val	Leu	Ser	Gly	Gly	Pro	Arg	Lys	Asp		
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Asp	Ile	Ile	Thr	Val	Thr	Arg	Leu	Ser	Asp	Thr	Glu	Thr	His	Glu	Pro		
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Ile	Arg	Ile	Phe	Ile	Gly	Met	Val	Pro	Gly	Arg	Ser	Leu	Ser	Asp	Gln		
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gtg	gat	ctt	gtc	att	cat	gaa	atg	cgc	cgc	acg	gga	gcc	ctg	cgc	cgc	1075	
Val	Asp	Leu	Val	Ile	His	Glu	Met	Arg	Arg	Thr	Gly	Ala	Leu	Arg	Arg		
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gac	cac	atc	gtg	atc	aac	aat	tcc	acg	ggc	acc	ggc	tgg	atc	acc	gat	1123	
Asp	His	Ile	Val	Ile	Asn	Asn	Ser	Thr	Gly	Thr	Gly	Trp	Ile	Thr	Asp		
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Trp	Ser	Ala	His	Thr	Phe	Glu	Phe	Leu	Thr	Gly	Gly	Asn	Cys	Val	Thr		
			345					350					355				
att	tcc	atg	caa	tat	tct	tat	ctt	ccc	agt	gca	ctg	agc	tgg	tac	aag	1219	
Ile	Ser	Met	Gln	Tyr	Ser	Tyr	Leu	Pro	Ser	Ala	Leu	Ser	Trp	Tyr	Lys		
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gac	aac	gac	ggc	ccc	att	aat	gcg	gcg	aga	atg	ctt	atc	gac	gcc	gtc	1267	
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Leu	His	Glu	Leu	Asp	Gln	Leu	Pro	Thr	Gly	Ser	Arg	Pro	Lys	Leu	Phe		
	390				395				400						405		
ctc	gcg	gga	gag	tca	ctg	ggg	gcg	tat	ggg	ttg	gct	gag	gtg	tgg	gga	1363	
Leu	Ala	Gly	Glu	Ser	Leu	Gly	Ala	Tyr	Gly	Leu	Ala	Glu	Val	Trp	Gly		
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gac	gtc	gaa	aag	ctt	ctt	gga	acc	gct	gac	ggc	gtg	ctg	ctc	agt	ggg	1411	
Asp	Val	Glu	Lys	Leu	Leu	Gly	Thr	Ala	Asp	Gly	Val	Leu	Leu	Ser	Gly		
			425					430					435				
gcg	ccg	cgt	ttt	tcg	gac	gcc	atg	aat	gcg	ttg	cgc	acc	cgg	cgc	gat	1459	
Ala	Pro	Arg	Phe	Ser	Asp	Ala	Met	Asn	Ala	Leu	Arg	Thr	Arg	Arg	Asp		

440	445	450	
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cgt ttt gcg ggc gag cct gag cac ctt gat atg ccg gct acc tgg cag Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met Pro Ala Thr Trp Gln 470 475 480 485			1555
ttt ccg cgc atg atc gtg gcg cag cac gcc tct gat cca att gtg tgg Phe Pro Arg Met Ile Val Ala Gln His Ala Ser Asp Pro Ile Val Trp 490 495 500			1603
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aag caa gac cac caa gat gtc ttt ccc cgc ttg cga tgg atg ccg ttt Lys Gln Asp His Gln Asp Val Phe Pro Arg Leu Arg Trp Met Pro Phe 520 525 530			1699
gta acc ggc tgg cag gtg gct ttg gat ttg ttc act tca acc tcc gtt Val Thr Gly Trp Gln Val Ala Leu Asp Leu Phe Thr Ser Thr Ser Val 535 540 545			1747
ccc ggc ggg cac ggg cac aat tat cac gag gag ttt att gat tat tgg Pro Gly Gly His Gly His Asn Tyr His Glu Glu Phe Ile Asp Tyr Trp 550 555 560 565			1795
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<211> 592

<212> PRT

<213> Corynebacterium glutamicum

<400> 1264

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Ala Gln Val Ile Ala Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn	
35 40 45	

Arg Arg Arg Ile Leu Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala	
50 55 60	

Glu Ile Ala Met Trp Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro	
65 70 75 80	

Arg Pro Lys Leu Phe Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu
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 Ala Glu Val Trp Gly Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly
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 Val Leu Leu Ser Gly Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu
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 Arg Thr Arg Arg Asp Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp
 450 455 460
 Ser Gly Arg His Ile Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met
 465 470 475 480
 Pro Ala Thr Trp Gln Phe Pro Arg Met Ile Val Ala Gln His Ala Ser
 485 490 495
 Asp Pro Ile Val Trp Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu
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 Trp Leu Lys Thr Pro Lys Gln Asp His Gln Asp Val Phe Pro Arg Leu
 515 520 525
 Arg Trp Met Pro Phe Val Thr Gly Trp Gln Val Ala Leu Asp Leu Phe
 530 535 540
 Thr Ser Thr Ser Val Pro Gly Gly His Gly His Asn Tyr His Glu Glu
 545 550 555 560
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<212> DNA

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<220>

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<222> (101)..(1747)

<223> FRXA02693

<400> 1265

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 Met Val Ser Leu Pro
 1 5

aga cta gcg tct ctg ctc acc act cgc ctg gca acg ctt aaa ccc gca 163
 Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala Thr Leu Lys Pro Ala
 10 15 20

cta aaa cct gcc acc cac ctc gcc tcc ctc ggc gcg cag gtc att gca 211
 Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly Ala Gln Val Ile Ala
 25 30 35

gag cta gtt ccg ggg atc cga atg tcg cca aac cgc agg cga atc ctc Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn Arg Arg Arg Ile Leu 40 45 50	259
cct gca aat atg ggc gct ggc ttt atc gga gcg gaa atc gca atg tgg Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala Glu Ile Ala Met Trp 55 60 65	307
tgg gct ctc tcg ccg tca ttg ttg ccg aaa ccg tgg tgg gtt acg gct Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro Trp Trp Val Thr Ala 70 75 80 85	355
gct aac ctg gct gtt tta caa gcg gtg ggg cat gcg gca gcg acg gga Ala Asn Leu Ala Val Leu Gln Ala Val Gly His Ala Ala Ala Thr Gly 90 95 100	403
atc cac tcg atc ctc ccc aga acc aac cgg cgg gta tcc agg aaa att Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg Val Ser Arg Lys Ile 105 110 115	451
tac aac gcc acc cac atc gca act ggt gcc atc acg ttg acc acc acg Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile Thr Leu Thr Thr Thr 120 125 130	499
gtt gtg gga ttg atc agg cat cgc acc caa atc cgg ctg att ggg cag Val Val Gly Leu Ile Arg His Arg Thr Gln Ile Arg Leu Ile Gly Gln 135 140 145	547
aag aat ttt gga ccg aag gag acg atc gcg ggc att agt gtc ggc acc Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly Ile Ser Val Gly Thr 150 155 160 165	595
ttg ggg tac ggc gcg ctg ctg atc acc ggc gaa tta acc cag cac agt Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu Leu Thr Gln His Ser 170 175 180	643
att aat gag gtc aag ctc cta att gag agg ttt tta ccg ccg tgg ata Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe Leu Pro Pro Trp Ile 185 190 195	691
agt ttc atc gca gcg gtt tcg gtc att aca ttg acc act ttg acc ttg Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu Thr Thr Leu Thr Leu 200 205 210	739
gcc gat cgc gtt ttg ttg ccg cgc atc ttg cat aat tct gca att caa Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His Asn Ser Ala Ile Gln 215 220 225	787
gca gcg cac ctt aat cgc atg gtg ttc cca gga act gag cag ccg tgg Ala Ala His Leu Asn Arg Met Val Phe Pro Gly Thr Glu Gln Pro Trp 230 235 240 245	835
gag ccg gag cgt tcg ggt agc ccg tgg tcg tat gaa aaa tgg ggt gcg Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr Glu Lys Trp Gly Ala 250 255 260	883
gtg ggt tcg cag ggc cgt gca gtg ttg tcg gga ggc cca cgc aaa gat Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly Gly Pro Arg Lys Asp 265 270 275	931

gac atc atc acg gta acc agg ctt tct gac acg gaa aca cat gaa ccg	979
Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr Glu Thr His Glu Pro	
280 285 290	
att cgt att ttt atc ggt atg gtt ccg gga cga tcc tta agc gat cag	1027
Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg Ser Leu Ser Asp Gln	
295 300 305	
gtg gat ctt gtc att cat gaa atg cgc cgc acg gga gcc ctg cgc cgc	1075
Val Asp Leu Val Ile His Glu Met Arg Arg Thr Gly Ala Leu Arg Arg	
310 315 320 325	
gac cac atc gtg atc aac aat tcc acg ggc acc ggc tgg atc acc gat	1123
Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr Gly Trp Ile Thr Asp	
330 335 340	
tgg tcc gcc cac acc ttt gag ttc ctc acc ggc gga aac tgc gtg aca	1171
Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly Gly Asn Cys Val Thr	
345 350 355	
att tcc atg caa tat tct tat ctt ccc agt gca ctg agc tgg tac aag	1219
Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala Leu Ser Trp Tyr Lys	
360 365 370	
gac aac gac ggc ccc att aat gcg gcg aga atg ctt atc gac gcc gtc	1267
Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met Leu Ile Asp Ala Val	
375 380 385	
ctc cac gag cta gac cag ctt ccc acc ggg agt cgc cca aag ctg ttc	1315
Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser Arg Pro Lys Leu Phe	
390 395 400 405	
ctc gcg gga gag tca ctg ggg gcg tat ggg ttg gct gag gtg tgg gga	1363
Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu Ala Glu Val Trp Gly	
410 415 420	
gac gtc gaa aag ctt ctt gga acc gct gac ggc gtg ctg ctc agt ggg	1411
Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly Val Leu Leu Ser Gly	
425 430 435	
gcg ccg cgt ttt tcg gac gcc atg aat gcg ttg cgc acc cgg cgc gat	1459
Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu Arg Thr Arg Arg Asp	
440 445 450	
gcg agc agc tcc gag cgg ctg ccc gtg att gat agc ggg cgg cac atc	1507
Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp Ser Gly Arg His Ile	
455 460 465	
cgt ttt gcg ggc gag cct gag cac ctt gat atg ccg gct acc tgg cag	1555
Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met Pro Ala Thr Trp Gln	
470 475 480 485	
ttt ccg cgc atg atc gtg gcg cag cac gcc tct gat cca att gtg tgg	1603
Phe Pro Arg Met Ile Val Ala Gln His Ala Ser Asp Pro Ile Val Trp	
490 495 500	
tgg aac gcg gag ctg ttt att cgg cgg ccg gaa tgg ttg aaa act ccc	1651
Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu Trp Leu Lys Thr Pro	
505 510 515	
aag caa gac cac caa gat gtc ttt aac cgc ttg cga tgg atg ccg ttt	1699

Lys Gln Asp His Gln Asp Val Phe Asn Arg Leu Arg Trp Met Pro Phe
 520 525 530

gtt gcc ggc tgg cag gtg gct ttg gat ttg ttc act tca acc tcc gtt 1747
 Val Ala Gly Trp Gln Val Ala Leu Asp Leu Phe Thr Ser Thr Ser Val
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<210> 1266

<211> 549

<212> PRT

<213> Corynebacterium glutamicum

<400> 1266

Met Val Ser Leu Pro Arg Leu Ala Ser Leu Leu Thr Thr Arg Leu Ala
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Thr Leu Lys Pro Ala Leu Lys Pro Ala Thr His Leu Ala Ser Leu Gly
 20 25 30

Ala Gln Val Ile Ala Glu Leu Val Pro Gly Ile Arg Met Ser Pro Asn
 35 40 45

Arg Arg Arg Ile Leu Pro Ala Asn Met Gly Ala Gly Phe Ile Gly Ala
 50 55 60

Glu Ile Ala Met Trp Trp Ala Leu Ser Pro Ser Leu Leu Pro Lys Pro
 65 70 75 80

Trp Trp Val Thr Ala Ala Asn Leu Ala Val Leu Gln Ala Val Gly His
 85 90 95

Ala Ala Ala Thr Gly Ile His Ser Ile Leu Pro Arg Thr Asn Arg Arg
 100 105 110

Val Ser Arg Lys Ile Tyr Asn Ala Thr His Ile Ala Thr Gly Ala Ile
 115 120 125

Thr Leu Thr Thr Thr Val Val Gly Leu Ile Arg His Arg Thr Gln Ile
 130 135 140

Arg Leu Ile Gly Gln Lys Asn Phe Gly Pro Lys Glu Thr Ile Ala Gly
 145 150 155 160

Ile Ser Val Gly Thr Leu Gly Tyr Gly Ala Leu Leu Ile Thr Gly Glu
 165 170 175

Leu Thr Gln His Ser Ile Asn Glu Val Lys Leu Leu Ile Glu Arg Phe
 180 185 190

Leu Pro Pro Trp Ile Ser Phe Ile Ala Ala Val Ser Val Ile Thr Leu
 195 200 205

Thr Thr Leu Thr Leu Ala Asp Arg Val Leu Leu Arg Arg Ile Leu His
 210 215 220

Asn Ser Ala Ile Gln Ala Ala His Leu Asn Arg Met Val Phe Pro Gly
 225 230 235 240

Thr Glu Gln Pro Trp Glu Pro Glu Arg Ser Gly Ser Pro Trp Ser Tyr
 245 250 255

Glu Lys Trp Gly Ala Val Gly Ser Gln Gly Arg Ala Val Leu Ser Gly
260 265 270

Gly Pro Arg Lys Asp Asp Ile Ile Thr Val Thr Arg Leu Ser Asp Thr
275 280 285

Glu Thr His Glu Pro Ile Arg Ile Phe Ile Gly Met Val Pro Gly Arg
290 295 300

Ser Leu Ser Asp Gln Val Asp Leu Val Ile His Glu Met Arg Arg Thr
305 310 315 320

Gly Ala Leu Arg Arg Asp His Ile Val Ile Asn Asn Ser Thr Gly Thr
325 330 335

Gly Trp Ile Thr Asp Trp Ser Ala His Thr Phe Glu Phe Leu Thr Gly
340 345 350

Gly Asn Cys Val Thr Ile Ser Met Gln Tyr Ser Tyr Leu Pro Ser Ala
355 360 365

Leu Ser Trp Tyr Lys Asp Asn Asp Gly Pro Ile Asn Ala Ala Arg Met
370 375 380

Leu Ile Asp Ala Val Leu His Glu Leu Asp Gln Leu Pro Thr Gly Ser
385 390 395 400

Arg Pro Lys Leu Phe Leu Ala Gly Glu Ser Leu Gly Ala Tyr Gly Leu
405 410 415

Ala Glu Val Trp Gly Asp Val Glu Lys Leu Leu Gly Thr Ala Asp Gly
420 425 430

Val Leu Leu Ser Gly Ala Pro Arg Phe Ser Asp Ala Met Asn Ala Leu
435 440 445

Arg Thr Arg Arg Asp Ala Ser Ser Ser Glu Arg Leu Pro Val Ile Asp
450 455 460

Ser Gly Arg His Ile Arg Phe Ala Gly Glu Pro Glu His Leu Asp Met
465 470 475 480

Pro Ala Thr Trp Gln Phe Pro Arg Met Ile Val Ala Gln His Ala Ser
485 490 495

Asp Pro Ile Val Trp Trp Asn Ala Glu Leu Phe Ile Arg Arg Pro Glu
500 505 510

Trp Leu Lys Thr Pro Lys Gln Asp His Gln Asp Val Phe Asn Arg Leu
515 520 525

Arg Trp Met Pro Phe Val Ala Gly Trp Gln Val Ala Leu Asp Leu Phe
530 535 540

Thr Ser Thr Ser Val
545

<210> 1267

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXN02696

<400> 1267

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cacatgaaat ttaagacatt ccaggtgaag ggaaactgcc atg tcc atg ctc aag 115
                                         Met Ser Met Leu Lys
                                         1 5
aag act aaa gaa ttc ttc gga ctc gct cca tac gaa gcg gag cac gag 163
Lys Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr Glu Ala Glu His Glu
                        10 15 20
gat gct tac tat gca gat gaa cca cgt tac gag ggc acc gct gcg tac 211
Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu Gly Thr Ala Ala Tyr
                        25 30 35
gca cct gaa tac cgt gag cgt gac tac ggc tat gca cca gag gca cca 259
Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr Ala Pro Glu Ala Pro
                        40 45 50
gcc cct gtt gct cca tcg cca gca cct cgc tct tac cag tcc acc atc 307
Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser Tyr Gln Ser Thr Ile
                        55 60 65
gtt cca gta gag ctt cat tcc ttt gaa gac gct cag gtt att ggt gga 355
Val Pro Val Glu Leu His Ser Phe Glu Asp Ala Gln Val Ile Gly Gly
                        70 75 80 85
gca ttt cgc gac ggc gac gca gtt gtt ttc gac atg agc ttg ctt tcc 403
Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp Met Ser Leu Leu Ser
                        90 95 100
cgt gag gaa gca cgc cgc att gtg gac ttc gct gca ggc ctg tgc ttc 451
Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala Ala Gly Leu Cys Phe
                        105 110 115
gca ttg cgt ggc aag atg cag aag att gac agc gtc acc ttc gct gtc 499
Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser Val Thr Phe Ala Val
                        120 125 130
gtt cca gag ctg tcc aac atc agc act tcc gag ctc gag cgc gcc gca 547
Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu Leu Glu Arg Ala Ala
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Arg Ile Arg
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<210> 1268

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1268

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Glu Ala Glu His Glu Asp Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu
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Gly Thr Ala Ala Tyr Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr
          35              40              45

Ala Pro Glu Ala Pro Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser
          50              55              60

Tyr Gln Ser Thr Ile Val Pro Val Glu Leu His Ser Phe Glu Asp Ala
65              70              75              80

Gln Val Ile Gly Gly Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp
                85              90              95

Met Ser Leu Leu Ser Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala
                100              105              110

Ala Gly Leu Cys Phe Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser
          115              120              125

Val Thr Phe Ala Val Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu
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Leu Glu Arg Ala Ala Arg Ile Arg
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<210> 1269

<211> 578

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (100)..(555)

<223> FRXA02696

<220>

<221> misc_feature

<222> 1, 6, 22, 32, 37, 39, 70, 80, 87, 94

<223> n = a, t, c, or g

<400> 1269

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gctgtacatn taagtcattn ctgggttnagg tganctgcc atg tcc atg ctc aag aag 117
                               Met Ser Met Leu Lys Lys
                               1              5

act aaa gaa ttc ttc gga ctc gct cca tac gaa gcg gag cac gag gat 165
Thr Lys Glu Phe Phe Gly Leu Ala Pro Tyr Glu Ala Glu His Glu Asp
          10              15              20

gct tac tat gca gat gaa cca cgt tac gag ggc acc gct gcg tac gca 213
Ala Tyr Tyr Ala Asp Glu Pro Arg Tyr Glu Gly Thr Ala Ala Tyr Ala
          25              30              35

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cct gaa tac cgt gag cgt gac tac ggc tat gca cca gag gca cca gcc 261
 Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr Ala Pro Glu Ala Pro Ala
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 cct gtt gct cca tcg cca gca cct cgc tct tac cag tcc acc atc gtt 309
 Pro Val Ala Pro Ser Pro Ala Pro Arg Ser Tyr Gln Ser Thr Ile Val
 55 60 65 70
 cca gta gag ctt cat tcc ttt gaa gac gct cag gtt att ggt gga gca 357
 Pro Val Glu Leu His Ser Phe Glu Asp Ala Gln Val Ile Gly Gly Ala
 75 80 85
 ttt cgc gac ggc gac gca gtt gtt ttc gac atg agc ttg ctt tcc cgt 405
 Phe Arg Asp Gly Asp Ala Val Val Phe Asp Met Ser Leu Leu Ser Arg
 90 95 100
 gag gaa gca cgc cgc att gtg gac ttc gct gca ggc ctg tgc ttc gca 453
 Glu Glu Ala Arg Arg Ile Val Asp Phe Ala Ala Gly Leu Cys Phe Ala
 105 110 115
 ttg cgt ggc aag atg cag aag att gac agc gtc acc ttc gct gtc gtt 501
 Leu Arg Gly Lys Met Gln Lys Ile Asp Ser Val Thr Phe Ala Val Val
 120 125 130
 cca gag ctg tcc aac atc agc act tcc gag ctc gag cgc gcc gca cgc 549
 Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu Leu Glu Arg Ala Ala Arg
 135 140 145 150
 atc cgc taaacacacc ctggtggtgt gga 578
 Ile Arg

<210> 1270

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1270

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 20 25 30
 Gly Thr Ala Ala Tyr Ala Pro Glu Tyr Arg Glu Arg Asp Tyr Gly Tyr
 35 40 45
 Ala Pro Glu Ala Pro Ala Pro Val Ala Pro Ser Pro Ala Pro Arg Ser
 50 55 60
 Tyr Gln Ser Thr Ile Val Pro Val Glu Leu His Ser Phe Glu Asp Ala
 65 70 75 80
 Gln Val Ile Gly Gly Ala Phe Arg Asp Gly Asp Ala Val Val Phe Asp
 85 90 95
 Met Ser Leu Leu Ser Arg Glu Glu Ala Arg Arg Ile Val Asp Phe Ala
 100 105 110

Ala Gly Leu Cys Phe Ala Leu Arg Gly Lys Met Gln Lys Ile Asp Ser
 115 120 125

Val Thr Phe Ala Val Val Pro Glu Leu Ser Asn Ile Ser Thr Ser Glu
 130 135 140

Leu Glu Arg Ala Ala Arg Ile Arg
 145 150

<210> 1271
 <211> 1650
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1627)
 <223> RXN02697

<400> 1271
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ggctatccgc tcaaccgaac gtcggatgta gtagacgcgt atg aca ctt ttt caa 115
 Met Thr Leu Phe Gln
 1 5

cgt tta acc aac cct gta gtg ctc ggc ggc cta gca ggt gtt ttg ctt 163
 Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu Ala Gly Val Leu Leu
 10 15 20

ctg ctc ggc tct ttc ggt ggc ggt gcc att cgg tac cgt ggc gga gtg 211
 Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg Tyr Arg Gly Gly Val
 25 30 35

ctc gat gcg ttg ggg ctt aac ttc ctt gct ttt ggc cac gcg cag ggt 259
 Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe Gly His Ala Gln Gly
 40 45 50

att tcc aat acc gtg ttg tgg gtt ggg cag ctg ctg ctg att ggc gcg 307
 Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu Leu Leu Ile Gly Ala
 55 60 65

tgg gtt cac ctt gga cgt cgg ttg ttc aag aaa aaa gtc gct gat gac 355
 Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys Lys Val Ala Asp Asp
 70 75 80 85

acc gca gac gct gct gac tta ggt ctt gta aag cgc acg ttg tat gcc 403
 Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys Arg Thr Leu Tyr Ala
 90 95 100

atg gtg gtg ccc ctc att ttt gcg gca cca atg atg tcg cgt gat gtt 451
 Met Val Val Pro Leu Ile Phe Ala Ala Pro Met Met Ser Arg Asp Val
 105 110 115

tat tcc tat ctc atg cag ggc gcg atg ctg cgt gat ggc ttc gat ccc 499
 Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg Asp Gly Phe Asp Pro
 120 125 130

tac act gag ggc gct gcg gta aac cct ggc ccc atg ttg ctt gag gtc 547
 Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro Met Leu Leu Glu Val

135	140	145	
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tgg att gga gac atg atc acc acg gtt gtg ggc gat aat gtc acc ttg Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly Asp Asn Val Thr Leu 170 175 180			643
ggc gtc gtc gct tac aag atc ttg tcg atc att ggc ctt gct gtg aca Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr 185 190 195			691
ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala 200 205 210			739
att gca ttg tgg att ggt gtg gcc aat cct gtg atg atc atc cac atg Ile Ala Leu Trp Ile Gly Val Ala Asn Pro Val Met Ile Ile His Met 215 220 225			787
atc ggc ggc atg cac aat gaa tcc ctc atg gtg gga ttg gtc agc gtc Ile Gly Gly Met His Asn Glu Ser Leu Met Val Gly Leu Val Ser Val 230 235 240 245			835
ggc ttg ttg cta gca ctg aag aag cgt ttc gtg gca ggt gtg gca ctc Gly Leu Leu Leu Ala Leu Lys Lys Arg Phe Val Ala Gly Val Ala Leu 250 255 260			883
att gca gtg gct gtg tcg ctg aaa gct aca gcg gcg att gca ctt cct Ile Ala Val Ala Val Ser Leu Lys Ala Thr Ala Ala Ile Ala Leu Pro 265 270 275			931
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aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg ttc Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala Phe 295 300 305			1027
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agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg gtg Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu Val 345 350 355			1171
gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc gac Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe Asp 360 365 370			1219
tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc atg Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile Met 375 380 385			1267

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 Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu Arg
 390 395 400 405
 agg gcg gtc act ggt aca gca gcg gct tat gcc gtg gct ttt gtg ttc 1363
 Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val Phe
 410 415 420
 aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg ctc 1411
 Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu Leu
 425 430 435
 ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt gct 1459
 Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly Ala
 440 445 450
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 Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln Leu
 455 460 465
 tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt gcc 1555
 Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu Ala
 470 475 480 485
 acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg gag 1603
 Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr Glu
 490 495 500
 aaa ccc tcc ccg cat acc gtt tcc tagttgcata aggtaaaccg cca 1650
 Lys Pro Ser Pro His Thr Val Ser
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<210> 1272

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 1272

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 20 25 30
 Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe
 35 40 45
 Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu
 50 55 60
 Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys
 65 70 75 80
 Lys Val Ala Asp Asp Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys
 85 90 95
 Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met
 100 105 110

Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg
 115 120 125
 Asp Gly Phe Asp Pro Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro
 130 135 140
 Met Leu Leu Glu Val Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr
 145 150 155 160
 Gly Pro Leu His Leu Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly
 165 170 175
 Asp Asn Val Thr Leu Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile
 180 185 190
 Gly Leu Ala Val Thr Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe
 195 200 205
 Gly Ala Asn Pro Ala Ile Ala Leu Trp Ile Gly Val Ala Asn Pro Val
 210 215 220
 Met Ile Ile His Met Ile Gly Gly Met His Asn Glu Ser Leu Met Val
 225 230 235 240
 Gly Leu Val Ser Val Gly Leu Leu Leu Ala Leu Lys Lys Arg Phe Val
 245 250 255
 Ala Gly Val Ala Leu Ile Ala Val Ala Val Ser Leu Lys Ala Thr Ala
 260 265 270
 Ala Ile Ala Leu Pro Phe Val Val Trp Ile Gly Met His His Phe Ala
 275 280 285
 Gly Phe Leu Ala Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln
 290 295 300
 Gln Val Pro Ala Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr
 305 310 315 320
 Gly Val Val Val Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly
 325 330 335
 Trp Ile Ser Glu Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala
 340 345 350
 Phe Pro Ser Leu Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe
 355 360 365
 Val Asp Asp Phe Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile
 370 375 380
 Ser Met Leu Ile Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe
 385 390 395 400
 Arg Gln Asn Glu Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala
 405 410 415
 Val Ala Phe Val Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser
 420 425 430
 Leu Ile Ser Leu Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg

435	440	445
Phe Ala Ala Gly Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser		
450	455	460
Gly Asn His Gln Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile		
465	470	475
Ile Ala Trp Leu Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala		
485	490	495
Thr Thr Ala Thr Glu Lys Pro Ser Pro His Thr Val Ser		
500	505	

<210> 1273

<211> 722

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(699)

<223> FRXA02697

<400> 1273

cct ttt gtg gtg tgg atc ggc atg cat cat ttc gca gga ttc tta gcc	48
Pro Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala	
1 5 10 15	
acc aaa aag ggc aaa gac tcc cct acc ctt aag caa cag gtc ccc gcg	96
Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala	
20 25 30	
ttc ttt gcc act gga gct gca ggt gtt gct gtc act ggt gtt gtt gtc	144
Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val	
35 40 45	
agt gcg atc act tgg gcg tct ggc gct tcg tgg ggc tgg atc agt gag	192
Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu	
50 55 60	
atc agt ggc aac agc aag gta atc aac ccg ctg gct ttc cct tct ttg	240
Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu	
65 70 75 80	
gtg gcc agt gtg atc acc atg gtg gct gaa gtg ttc gtt gac gat ttc	288
Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe	
85 90 95	
gac tac aac gca gtg gtt aat gtt gtg cgc tca atc tcc atg ctg atc	336
Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile	
100 105 110	
atg ctt ggc ggg ttg gtc gta tgt tgg tgg ctg ttc cgc cag aac gaa	384
Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu	
115 120 125	
cgc agg gcg gtc act ggt aca gcg gcg gct tat gcc gtg gct ttt gtg	432
Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val	
130 135 140	

ttc aat tct gtg acc ttg ccg tgg tac tac gcc agc ttg atc tct ttg 480
 Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu
 145 150 155 160

ctc ggc aca ttt aaa cca ccg atg tgg ttg att cgc ttc gca gcg ggt 528
 Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly
 165 170 175

gct tcg gtg ttt atc gcg ctg atg ttt acc gga agt gga aac cac cag 576
 Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln
 180 185 190

ctg tac aac atc gtt acg gtg atc atc gca gca att atc gcg tgg ctt 624
 Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu
 195 200 205

gcc acc gtg gtg atc ttt gat gac act gac cct gca aca acg gcc acg 672
 Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr
 210 215 220

gag aaa ccc tcc ccg cat acc gtt tcc tagttgcata aggtaaaccg 719
 Glu Lys Pro Ser Pro His Thr Val Ser
 225 230

cca 722

<210> 1274

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 1274

Pro Phe Val Val Trp Ile Gly Met His His Phe Ala Gly Phe Leu Ala
 1 5 10 15

Thr Lys Lys Gly Lys Asp Ser Pro Thr Leu Lys Gln Gln Val Pro Ala
 20 25 30

Phe Phe Ala Thr Gly Ala Ala Gly Val Ala Val Thr Gly Val Val Val
 35 40 45

Ser Ala Ile Thr Trp Ala Ser Gly Ala Ser Trp Gly Trp Ile Ser Glu
 50 55 60

Ile Ser Gly Asn Ser Lys Val Ile Asn Pro Leu Ala Phe Pro Ser Leu
 65 70 75 80

Val Ala Ser Val Ile Thr Met Val Ala Glu Val Phe Val Asp Asp Phe
 85 90 95

Asp Tyr Asn Ala Val Val Asn Val Val Arg Ser Ile Ser Met Leu Ile
 100 105 110

Met Leu Gly Gly Leu Val Val Cys Trp Trp Leu Phe Arg Gln Asn Glu
 115 120 125

Arg Arg Ala Val Thr Gly Thr Ala Ala Ala Tyr Ala Val Ala Phe Val
 130 135 140

Phe Asn Ser Val Thr Leu Pro Trp Tyr Tyr Ala Ser Leu Ile Ser Leu
 145 150 155 160
 Leu Gly Thr Phe Lys Pro Pro Met Trp Leu Ile Arg Phe Ala Ala Gly
 165 170 175
 Ala Ser Val Phe Ile Ala Leu Met Phe Thr Gly Ser Gly Asn His Gln
 180 185 190
 Leu Tyr Asn Ile Val Thr Val Ile Ile Ala Ala Ile Ile Ala Trp Leu
 195 200 205
 Ala Thr Val Val Ile Phe Asp Asp Thr Asp Pro Ala Thr Thr Ala Thr
 210 215 220
 Glu Lys Pro Ser Pro His Thr Val Ser
 225 230

<210> 1275
 <211> 748
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(748)
 <223> FRXA02719

<400> 1275
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 ggctatccgc tcaaccgaac gtcggatgta gtagacgcgt atg aca ctt ttt caa 115
 Met Thr Leu Phe Gln
 1 5
 cgt tta acc aac cct gta gtg ctc ggc ggc cta gca ggt gtt ttg ctt 163
 Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu Ala Gly Val Leu Leu
 10 15 20
 ctg ctc ggc tct ttc ggt ggc ggt gcc att cgg tac cgt ggc gga gtg 211
 Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg Tyr Arg Gly Gly Val
 25 30 35
 ctc gat gcg ttg ggg ctt aac ttc ctt gct ttt ggc cac gcg cag ggt 259
 Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe Gly His Ala Gln Gly
 40 45 50
 att tcc aat acc gtg ttg tgg gtt ggg cag ctg ctg ctg att ggc gcg 307
 Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu Leu Leu Ile Gly Ala
 55 60 65
 tgg gtt cac ctt gga cgt cgg ttg ttc aag aaa aaa gtc gct gat gac 355
 Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys Val Ala Asp Asp
 70 75 80 85
 acc gca gac gct gct gac tta ggt ctt gta aag cgc acg ttg tat gcc 403
 Thr Ala Asp Ala Ala Asp Leu Gly Leu Val Lys Arg Thr Leu Tyr Ala
 90 95 100
 atg gtg gtg ccc ctc att ttt gcg gca cca atg atg tcg cgt gat gtt 451

Met Val Val Pro Leu Ile Phe Ala Ala Pro Met Met Ser Arg Asp Val
 105 110 115

tat tcc tat ctc atg cag ggc gcg atg ctg cgt gat ggc ttc gat ccc 499
 Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg Asp Gly Phe Asp Pro
 120 125 130

tac act gag ggc gct gcg gta aac cct ggc ccc atg ttg ctt gag gtc 547
 Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro Met Leu Leu Glu Val
 135 140 145

tct cat gat tgg cgc aac acc acg acg ccg tat ggt cca cta cac ctg 595
 Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr Gly Pro Leu His Leu
 150 155 160 165

tgg att gga gac atg atc acc acg gtt gtg ggc gat aat gtc acc ttg 643
 Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly Asp Asn Val Thr Leu
 170 175 180

ggc gtc gtc gct tac aag atc ttg tgc atc att ggc ctt gct gtg aca 691
 Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile Gly Leu Ala Val Thr
 185 190 195

ggc tgg agc att gtc cgc att gca caa cat ttt gga gcc aac cca gca 739
 Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe Gly Ala Asn Pro Ala
 200 205 210

att gca ttg 748
 Ile Ala Leu
 215

<210> 1276

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 1276

Met Thr Leu Phe Gln Arg Leu Thr Asn Pro Val Val Leu Gly Gly Leu
 1 5 10 15

Ala Gly Val Leu Leu Leu Gly Ser Phe Gly Gly Gly Ala Ile Arg
 20 25 30

Tyr Arg Gly Gly Val Leu Asp Ala Leu Gly Leu Asn Phe Leu Ala Phe
 35 40 45

Gly His Ala Gln Gly Ile Ser Asn Thr Val Leu Trp Val Gly Gln Leu
 50 55 60

Leu Leu Ile Gly Ala Trp Val His Leu Gly Arg Arg Leu Phe Lys Lys
 65 70 75 80

Lys Val Ala Asp Asp Thr Ala Asp Ala Asp Leu Gly Leu Val Lys
 85 90 95

Arg Thr Leu Tyr Ala Met Val Val Pro Leu Ile Phe Ala Ala Pro Met
 100 105 110

Met Ser Arg Asp Val Tyr Ser Tyr Leu Met Gln Gly Ala Met Leu Arg
 115 120 125

Asp Gly Phe Asp Pro Tyr Thr Glu Gly Ala Ala Val Asn Pro Gly Pro
 130 135 140
 Met Leu Leu Glu Val Ser His Asp Trp Arg Asn Thr Thr Thr Pro Tyr
 145 150 155 160
 Gly Pro Leu His Leu Trp Ile Gly Asp Met Ile Thr Thr Val Val Gly
 165 170 175
 Asp Asn Val Thr Leu Gly Val Val Ala Tyr Lys Ile Leu Ser Ile Ile
 180 185 190
 Gly Leu Ala Val Thr Gly Trp Ser Ile Val Arg Ile Ala Gln His Phe
 195 200 205
 Gly Ala Asn Pro Ala Ile Ala Leu
 210 215

<210> 1277

<211> 825

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(802)

<223> RXN02720

<400> 1277

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 cgccaggccg gcgtggtgtg gctgccaaag gaggcataaa ttg gag cgc cgc gaa 115
 Leu Glu Arg Arg Glu
 1 5
 gag ctg cag gta cga ctg cag cag gtg caa gcg cgt atc gac gcg acc 163
 Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala Arg Ile Asp Ala Thr
 10 15 20
 ctc aac gaa cac aac cgc ccc gag ggc agt gta cgt ctg ttg ccg gtc 211
 Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val Arg Leu Leu Pro Val
 25 30 35
 acc aaa ttc cac ccc gtg gaa gac atc aag atc tta caa gag ttt ggt 259
 Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile Leu Gln Glu Phe Gly
 40 45 50
 gtc acc gca gtg gga gag aac cgc gaa caa gaa gca cgc gcc aaa gca 307
 Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu Ala Arg Ala Lys Ala
 55 60 65
 ctc gaa ctt ccc gac atg gac ttt cat atg att ggc caa atc caa tca 355
 Leu Glu Leu Pro Asp Met Asp Phe His Met Ile Gly Gln Ile Gln Ser
 70 75 80 85
 aag aaa gcc aac tcg atc gcc agg tgg gca gct gca gtg cac tcc gtt 403
 Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala Ala Val His Ser Val
 90 95 100

gat agc gag aaa atc gcc gaa gca ttg ggc agg gga gta gcc ctt gca 451
Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg Gly Val Ala Leu Ala
105 110 115

ttg gat aga ggc gac cgc acc agt gac gag ctt ccg tgt ttt att caa 499
Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu Pro Cys Phe Ile Gln
120 125 130

ctg agt ttg gat ggt gac ccg agc cga ggt gga act cca ttg agc cag 547
Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly Thr Pro Leu Ser Gln
135 140 145

gtc aca caa ctt gcc gat tgc atc agt gac acc aca cat ctg cgt ttt 595
Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr Thr His Leu Arg Phe
150 155 160 165

gag ggc ctc atg tgc gtc cca ccg ctt ggt tgg ggc cct gaa aaa gct 643
Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp Gly Pro Glu Lys Ala
170 175 180

ttt tcc cag gca aga gac gta ctt tca ggt tta gag gaa cac ttt gac 691
Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu Glu Glu His Phe Asp
185 190 195

agg tct ttg gaa ttt tcg gca ggt atg tct gga gac cta gtt gct gcg 739
Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly Asp Leu Val Ala Ala
200 205 210

att aaa cac ggc tca aca atc gtg cgt gtc gga act gaa att ctt ggg 787
Ile Lys His Gly Ser Thr Ile Val Arg Val Gly Thr Glu Ile Leu Gly
215 220 225

aac cga ccg cta gcg tagaaaaatca agttaagggt gtg 825
Asn Arg Pro Leu Ala
230

<210> 1278

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 1278

Leu Glu Arg Arg Glu Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala
1 5 10 15

Arg Ile Asp Ala Thr Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val
20 25 30

Arg Leu Leu Pro Val Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile
35 40 45

Leu Gln Glu Phe Gly Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu
50 55 60

Ala Arg Ala Lys Ala Leu Glu Leu Pro Asp Met Asp Phe His Met Ile
65 70 75 80

Gly Gln Ile Gln Ser Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala
85 90 95

Ala Val His Ser Val Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg
 100 105 110

Gly Val Ala Leu Ala Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu
 115 120 125

Pro Cys Phe Ile Gln Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly
 130 135 140

Thr Pro Leu Ser Gln Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr
 145 150 155 160

Thr His Leu Arg Phe Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp
 165 170 175

Gly Pro Glu Lys Ala Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu
 180 185 190

Glu Glu His Phe Asp Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly
 195 200 205

Asp Leu Val Ala Ala Ile Lys His Gly Ser Thr Ile Val Arg Val Gly
 210 215 220

Thr Glu Ile Leu Gly Asn Arg Pro Leu Ala
 225 230

<210> 1279

<211> 727

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(727)

<223> FRXA02720

<400> 1279

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cgccaggccg gcgtggtgtg gctgccaaag gaggcataaa ttg gag cgc cgc gaa 115
 Leu Glu Arg Arg Glu
 1 5

gag ctg cag gta cga ctg cag cag gtg caa gcg cgt atc gac gcg acc 163
 Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala Arg Ile Asp Ala Thr
 10 15 20

ctc aac gaa cac aac cgc ccc gag ggc agt gta cgt ctg ttg ccg gtc 211
 Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val Arg Leu Leu Pro Val
 25 30 35

acc aaa ttc cac ccc gtg gaa gac atc aag atc tta caa gag ttt ggt 259
 Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile Leu Gln Glu Phe Gly
 40 45 50

gtc acc gca gtg gga gag aac cgc gaa caa gaa gca cgc gcc aaa gca 307
 Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu Ala Arg Ala Lys Ala
 55 60 65

ctc gaa ctt ccc gac atg gac ttt cat atg att ggc caa atc caa tca 355
 Leu Glu Leu Pro Asp Met Asp Phe His Met Ile Gly Gln Ile Gln Ser
 70 75 80 85

aag aaa gcc aac tcg atc gcc agg tgg gca gct gca gtg cac tcc gtt 403
 Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala Ala Val His Ser Val
 90 95 100

gat agc gag aaa atc gcc gaa gca ttg ggc agg gga gta gcc ctt gca 451
 Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg Gly Val Ala Leu Ala
 105 110 115

ttg gat aga ggc gac cgc acc agt gac gag ctt ccg tgt ttt att caa 499
 Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu Pro Cys Phe Ile Gln
 120 125 130

ctg agt ttg gat ggt gac ccg agc cga ggt gga act cca ttg agc cag 547
 Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly Thr Pro Leu Ser Gln
 135 140 145

gtc aca caa ctt gcc gat tgc atc agt gac acc aca cat ctg cgt ttt 595
 Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr Thr His Leu Arg Phe
 150 155 160 165

gag ggc ctc atg tgc gtc cca ccg ctt ggt tgg ggc cct gaa aaa gct 643
 Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp Gly Pro Glu Lys Ala
 170 175 180

ttt tcc cag gca aga gac gta ctt tca ggt tta gag gaa cac ttt gac 691
 Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu Glu Glu His Phe Asp
 185 190 195

agg tct ttg gaa ttt tcg gca ggt atg tct gga gac 727
 Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly Asp
 200 205

<210> 1280
 <211> 209
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1280
 Leu Glu Arg Arg Glu Glu Leu Gln Val Arg Leu Gln Gln Val Gln Ala
 1 5 10 15
 Arg Ile Asp Ala Thr Leu Asn Glu His Asn Arg Pro Glu Gly Ser Val
 20 25 30
 Arg Leu Leu Pro Val Thr Lys Phe His Pro Val Glu Asp Ile Lys Ile
 35 40 45
 Leu Gln Glu Phe Gly Val Thr Ala Val Gly Glu Asn Arg Glu Gln Glu
 50 55 60
 Ala Arg Ala Lys Ala Leu Glu Leu Pro Asp Met Asp Phe His Met Ile
 65 70 75 80
 Gly Gln Ile Gln Ser Lys Lys Ala Asn Ser Ile Ala Arg Trp Ala Ala
 85 90 95

Ala Val His Ser Val Asp Ser Glu Lys Ile Ala Glu Ala Leu Gly Arg
100 105 110

Gly Val Ala Leu Ala Leu Asp Arg Gly Asp Arg Thr Ser Asp Glu Leu
115 120 125

Pro Cys Phe Ile Gln Leu Ser Leu Asp Gly Asp Pro Ser Arg Gly Gly
130 135 140

Thr Pro Leu Ser Gln Val Thr Gln Leu Ala Asp Cys Ile Ser Asp Thr
145 150 155 160

Thr His Leu Arg Phe Glu Gly Leu Met Cys Val Pro Pro Leu Gly Trp
165 170 175

Gly Pro Glu Lys Ala Phe Ser Gln Ala Arg Asp Val Leu Ser Gly Leu
180 185 190

Glu Glu His Phe Asp Arg Ser Leu Glu Phe Ser Ala Gly Met Ser Gly
195 200 205

Asp

<210> 1281
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN02744

<400> 1281
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tggaacatcac cggaaaagaa ctgaggagtt aacgcacacc atg tct aaa cct ttt 115
Met Ser Lys Pro Phe
1 5

gaa aac tct gcg ctc cgc ggt tct tct cga ttc cca gct gga acg ttc 163
Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe Pro Ala Gly Thr Phe
10 15 20

acc cct gct ccc aaa cga gcc acc ccg gca aaa atg ttg gct gct cag 211
Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys Met Leu Ala Ala Gln
25 30 35

ggc aag atg gaa tcc ctg ctg ttt ctt cgc cac ggc gaa cag caa ctg 259
Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His Gly Glu Gln Gln Leu
40 45 50

ctc agc atc atc att ccc ttg gtc gcg ctc atc gca cta gcg aat ttt 307
Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile Ala Leu Ala Asn Phe
55 60 65

gat ttc atc cct ggt gag aac tcc ctc gac aag act ttc ccc ttc gcg 355
Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys Thr Phe Pro Phe Ala
70 75 80 85

ctg gcc aca gca gcc atg agc gct ggt ttt aca ggt caa gcc atc agc 403
 Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr Gly Gln Ala Ile Ser
 90 95 100

cta gct ttt gac cgc cgc tat ggt gcc ctc aag cgc acc ggc gcc agc 451
 Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys Arg Thr Gly Ala Ser
 105 110 115

ggt gtt ccc gcc tgg acg att att ttt ggc aaa gtc atc gca gtc att 499
 Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys Val Ile Ala Val Ile
 120 125 130

gca gtc acc att gtg cag atc atc ttt ctc ggt gtg act gca ctg ctg 547
 Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly Val Thr Ala Leu Leu
 135 140 145

ttg ggc tgg tcc gca cct gtc ggt ggt gtg ctc ttt ggc atc gtg acc 595
 Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu Phe Gly Ile Val Thr
 150 155 160 165

cta ttt gtg ggt gtt tcc agc ttc acc gcg ctc ggc atg ctg atg ggc 643
 Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu Gly Met Leu Met Gly
 170 175 180

gga acg ttg tcc tcc gaa ttg gta ttg gca ctg gct aac ttg att tgg 691
 Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu Ala Asn Leu Ile Trp
 185 190 195

att gta ctg tcc ggc ctt gca gca tgg gcg gtc ttt tcc cct tcc gtc 739
 Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val Phe Ser Pro Ser Val
 200 205 210

aac gct gaa gga gtg ctg tcc atc atc cca tcc gtt gcg ctg tcc caa 787
 Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser Val Ala Leu Ser Gln
 215 220 225

ggt atg gtt gac gca ttc aac ggc gaa ctt ccg tgg ctc cag cta gga 835
 Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro Trp Leu Gln Leu Gly
 230 235 240 245

att ttg gtg ggc tgg cta att atc acc ggc gtg gcc gca aac aag cta 883
 Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val Ala Ala Asn Lys Leu
 250 255 260

ttt aac ttc tct gcg agc cgc tagatataacc cttagtcgga aaa 927
 Phe Asn Phe Ser Ala Ser Arg
 265

<210> 1282
 <211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1282
 Met Ser Lys Pro Phe Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe
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 Pro Ala Gly Thr Phe Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys
 20 25 30

Met Leu Ala Ala Gln Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His
 35 40 45
 Gly Glu Gln Gln Leu Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile
 50 55 60
 Ala Leu Ala Asn Phe Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys
 65 70 75 80
 Thr Phe Pro Phe Ala Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr
 85 90 95
 Gly Gln Ala Ile Ser Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys
 100 105 110
 Arg Thr Gly Ala Ser Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys
 115 120 125
 Val Ile Ala Val Ile Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly
 130 135 140
 Val Thr Ala Leu Leu Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu
 145 150 155 160
 Phe Gly Ile Val Thr Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu
 165 170 175
 Gly Met Leu Met Gly Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu
 180 185 190
 Ala Asn Leu Ile Trp Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val
 195 200 205
 Phe Ser Pro Ser Val Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser
 210 215 220
 Val Ala Leu Ser Gln Gly Met Val Asp Ala Phe Asn Gly Glu Leu Pro
 225 230 235 240
 Trp Leu Gln Leu Gly Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val
 245 250 255
 Ala Ala Asn Lys Leu Phe Asn Phe Ser Ala Ser Arg
 260 265

<210> 1283

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> FRXA02744

<400> 1283

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tggaacatcac cggaagaa ctgaggagtt aacgcacacc atg tct aaa cct ttt 115

	Met	Ser	Lys	Pro	Phe	
	1				5	
gaa aac tct gcg ctc cgc ggt tct tct cga ttc cca gct gga acg ttc						163
Glu Asn Ser Ala Leu Arg Gly Ser Ser Arg Phe Pro Ala Gly Thr Phe						
	10			15	20	
acc cct gct ccc aaa cga gcc acc ccg gca aaa atg ttg gct gct cag						211
Thr Pro Ala Pro Lys Arg Ala Thr Pro Ala Lys Met Leu Ala Ala Gln						
	25			30	35	
ggc aag atg gaa tcc ctg ctg ttt ctt cgc cac ggc gaa cag caa ctg						259
Gly Lys Met Glu Ser Leu Leu Phe Leu Arg His Gly Glu Gln Gln Leu						
	40			45	50	
ctc agc atc atc att ccc ttg gtc gcg ctc atc gca cta gcg aat ttt						307
Leu Ser Ile Ile Ile Pro Leu Val Ala Leu Ile Ala Leu Ala Asn Phe						
	55			60	65	
gat ttc atc cct ggt gag aac tcc ctc gac aag act ttc ccc ttc gcg						355
Asp Phe Ile Pro Gly Glu Asn Ser Leu Asp Lys Thr Phe Pro Phe Ala						
	70			75	80	85
ctg gcc aca gca gcc atg agc gct ggt ttt aca ggt caa gcc atc agc						403
Leu Ala Thr Ala Ala Met Ser Ala Gly Phe Thr Gly Gln Ala Ile Ser						
	90			95	100	
cta gct ttt gac cgc cgc tat ggt gcc ctc aag cgc acc ggc gcc agc						451
Leu Ala Phe Asp Arg Arg Tyr Gly Ala Leu Lys Arg Thr Gly Ala Ser						
	105			110	115	
ggt gtt ccc gcc tgg acg att att ttt ggc aaa gtc atc gca gtc att						499
Gly Val Pro Ala Trp Thr Ile Ile Phe Gly Lys Val Ile Ala Val Ile						
	120			125	130	
gca gtc acc att gtg cag atc atc ttt ctc ggt gtg act gca ctg ctg						547
Ala Val Thr Ile Val Gln Ile Ile Phe Leu Gly Val Thr Ala Leu Leu						
	135			140	145	
ttg ggc tgg tcc gca cct gtc ggt ggt gtg ctc ttt ggc atc gtg acc						595
Leu Gly Trp Ser Ala Pro Val Gly Gly Val Leu Phe Gly Ile Val Thr						
	150			155	160	165
cta ttt gtg ggt gtt tcc agc ttc acc gcg ctc ggc atg ctg atg ggc						643
Leu Phe Val Gly Val Ser Ser Phe Thr Ala Leu Gly Met Leu Met Gly						
	170			175	180	
gga acg ttg tcc tcc gaa ttg gta ttg gca ctg gct aac ttg att tgg						691
Gly Thr Leu Ser Ser Glu Leu Val Leu Ala Leu Ala Asn Leu Ile Trp						
	185			190	195	
att gta ctg tcc ggc ctt gca gca tgg gcg gtc ttt tcc cct tcc gtc						739
Ile Val Leu Ser Gly Leu Ala Ala Trp Ala Val Phe Ser Pro Ser Val						
	200			205	210	
aac gct gaa gga gtg ctg tcc atc atc cca tcc gtt gcg ctg tcc caa						787
Asn Ala Glu Gly Val Leu Ser Ile Ile Pro Ser Val Ala Leu Ser Gln						
	215			220	225	
ggt atg gtt gac gca ttc aac ggc gaa ctt ccg tgg ctc cag cta gga						835
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<400> 1284																
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			20					25					30			
Met	Leu	Ala	Ala	Gln	Gly	Lys	Met	Glu	Ser	Leu	Leu	Phe	Leu	Arg	His	
		35					40					45				
Gly	Glu	Gln	Gln	Leu	Leu	Ser	Ile	Ile	Ile	Pro	Leu	Val	Ala	Leu	Ile	
	50					55					60					
Ala	Leu	Ala	Asn	Phe	Asp	Phe	Ile	Pro	Gly	Glu	Asn	Ser	Leu	Asp	Lys	
65					70					75					80	
Thr	Phe	Pro	Phe	Ala	Leu	Ala	Thr	Ala	Ala	Met	Ser	Ala	Gly	Phe	Thr	
				85					90					95		
Gly	Gln	Ala	Ile	Ser	Leu	Ala	Phe	Asp	Arg	Arg	Tyr	Gly	Ala	Leu	Lys	
			100					105					110			
Arg	Thr	Gly	Ala	Ser	Gly	Val	Pro	Ala	Trp	Thr	Ile	Ile	Phe	Gly	Lys	
		115					120					125				
Val	Ile	Ala	Val	Ile	Ala	Val	Thr	Ile	Val	Gln	Ile	Ile	Phe	Leu	Gly	
	130					135					140					
Val	Thr	Ala	Leu	Leu	Leu	Gly	Trp	Ser	Ala	Pro	Val	Gly	Gly	Val	Leu	
145					150					155					160	
Phe	Gly	Ile	Val	Thr	Leu	Phe	Val	Gly	Val	Ser	Ser	Phe	Thr	Ala	Leu	
				165					170					175		
Gly	Met	Leu	Met	Gly	Gly	Thr	Leu	Ser	Ser	Glu	Leu	Val	Leu	Ala	Leu	
			180					185					190			
Ala	Asn	Leu	Ile	Trp	Ile	Val	Leu	Ser	Gly	Leu	Ala	Ala	Trp	Ala	Val	
		195					200					205				
Phe	Ser	Pro	Ser	Val	Asn	Ala	Glu	Gly	Val	Leu	Ser	Ile	Ile	Pro	Ser	
	210					215					220					
Val	Ala	Leu	Ser	Gln	Gly	Met	Val	Asp	Ala	Phe	Asn	Gly	Glu	Leu	Pro	
225					230					235					240	

Trp Leu Gln Leu Gly Ile Leu Val Gly Trp Leu Ile Ile Thr Gly Val
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Ala Ala Asn Lys Leu Phe Asn Phe Ser Ala Ser Arg
260 265

<210> 1285

<211> 1689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1666)

<223> RXN02770

<400> 1285

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Met Leu Val Ala Ala
1 5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
10 15 20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr
25 30 35

aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259
Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala
40 45 50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307
Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met
55 60 65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355
Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn
70 75 80 85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403
Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly
90 95 100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451
Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln
105 110 115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499
Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu
120 125 130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547
Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys
135 140 145

gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu 150 155 160	595
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu 170 175 180	643
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro 185 190 195	691
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu 200 205 210	739
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ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala 230 235 240 245	835
gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala 250 255 260	883
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu 265 270 275	931
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile 280 285 290	979
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala 295 300 305	1027
ggt gtg ttt tac gct gcg gag gcc ccg cag gcg ttt gcg gcc tgc gtt Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val 310 315 320 325	1075
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp 330 335 340	1123
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val 345 350 355	1171
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn 360 365 370	1219
gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly 375 380 385	1267
ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt	1315

Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys
 390 395 400 405

gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt 1363
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser
 410 415 420

ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag 1411
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln
 425 430 435

tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat 1459
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His
 440 445 450

cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg 1507
 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr
 455 460 465

agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta 1555
 Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu
 470 475 480 485

gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt 1603
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val
 490 495 500

gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg 1651
 Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp
 505 510 515

tcc aga agt gag gaa taagtagtga gcgaacaagc tct 1689
 Ser Arg Ser Glu Glu
 520

<210> 1286

<211> 522

<212> PRT

<213> Corynebacterium glutamicum

<400> 1286

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Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser
 20 25 30

Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp
 35 40 45

Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
 50 55 60

Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
 65 70 75 80

Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala
 85 90 95

Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser

100							105					110			
Ala	Thr	Ala	Gly	Gln	Met	Pro	Glu	Leu	Phe	Gln	Ser	His	Val	Pro	Leu
		115					120				125				
Thr	Ser	Gln	Ile	Glu	Arg	Val	Asp	Cys	Val	Ser	Gly	Ser	Lys	Val	Ala
		130					135				140				
Thr	Val	Val	Phe	Lys	Glu	Asp	Leu	Gly	Glu	Arg	Trp	Arg	Tyr	Leu	Phe
145							150				155				
Glu	Gln	Gly	Asp	Leu	Leu	Pro	Ala	His	Ala	Val	Ala	Ser	Lys	Ala	Gly
						165				170					
Met	Thr	Leu	Glu	Glu	Leu	Asn	Gln	Ala	Leu	Lys	Asp	Lys	Asp	Pro	Glu
						180				185					
Ala	Leu	Thr	Glu	Pro	Ala	Arg	Val	Trp	Ser	Glu	Gly	Phe	Gln	Leu	Ser
						195				200					
Gln	Phe	Asp	Pro	Glu	Leu	Gln	Thr	Ala	Phe	Gly	Pro	Tyr	Lys	Val	Asp
						210				215					
Ser	Val	Gly	Glu	Phe	Gly	Glu	Val	Lys	Leu	Val	Arg	Asn	Glu	Phe	Tyr
225							230				235				
Ser	Gly	Asp	Gln	Ala	Val	Glu	Ala	Glu	Ile	Thr	Met	Trp	Pro	Lys	Gly
						245				250					
Ser	Asp	Leu	Ser	Ala	Ile	Ala	Asp	Asn	Gly	Asn	Leu	Gln	Ile	Ala	His
						260				265					
Val	Val	Ala	Trp	Glu	Ser	Glu	Pro	Trp	Val	Asn	Arg	Asp	Asp	Pro	Leu
						275				280					
Asn	Pro	Tyr	Asp	Ile	Lys	Glu	Glu	Val	Gly	Val	Leu	Thr	Glu	Gln	Leu
						290				295					
Thr	Leu	Ala	Ser	Ala	Gly	Val	Phe	Tyr	Ala	Ala	Glu	Ala	Arg	Gln	Ala
305							310				315				
Phe	Ala	Ala	Cys	Val	Asp	Gln	Glu	Ala	Val	Ala	Ala	Ala	Ser	Ser	Ser
						325				330					
Ile	Ser	Gly	Ile	Asp	Val	Pro	Ala	Val	Gly	Val	His	Ser	Val	Arg	His
						340				345					
Gln	Asn	Pro	Val	Val	His	Gln	Ile	Gly	Asp	Leu	Pro	Ala	Gln	His	Met
						355				360					
Ala	Val	Asp	Ile	Asn	Ala	Ala	Ser	Ala	Leu	Ala	Gly	Gln	Ser	Ile	Arg
						370				375					
Ile	Gly	Tyr	Asp	Gly	Pro	Asp	Glu	Arg	Lys	Ala	Ala	Met	Val	Glu	Ala
385							390				395				
Ile	Arg	Gln	Ser	Cys	Glu	Pro	Ala	Gly	Ile	Thr	Val	Ile	Asp	Ala	Ser
						405				410					
Gln	Glu	Ala	Val	Ser	Leu	Asn	Asp	Leu	Ser	Arg	Thr	Glu	Val	Ser	Glu
						420				425					

Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
 435 440 445
 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
 450 455 460
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
 465 470 475 480
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
 485 490 495
 Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp
 500 505 510
 Asn Met Asp Arg Trp Ser Arg Ser Glu Glu
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<210> 1287

<211> 1343

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1320)

<223> FRXA02770

<400> 1287

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tca gat ggt cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca 96
 Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr
 20 25 30

gct ggg cag atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg 144
 Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser
 35 40 45

cag att gag cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg 192
 Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val
 50 55 60

gtg ttc aag gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag 240
 Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln
 65 70 75 80

ggc gat ttg ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc 288
 Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr
 85 90 95

ttg gag gag ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg 336
 Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu
 100 105 110

act gaa cct gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt 384
 Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe

115	120	125	
gat cca gag ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val 130 135 140			432
ggt gaa ttc ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly 145 150 155 160			480
gac cag gcg gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp 165 170 175			528
ctc agc gcc att gcg gat aat gga aac ctt cag atc gca cat gtt gtg Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val 180 185 190			576
gcg tgg gag agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro 195 200 205			624
tat gac att aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu 210 215 220			672
gcc agt gcc ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala 225 230 235 240			720
gcc tgc gtt gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser 245 250 255			768
gga atc gat gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn 260 265 270			816
ccg gtc gtg cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val 275 280 285			864
gat att aat gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly 290 295 300			912
tac gac gga ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg 305 310 315 320			960
caa agt tgt gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu 325 330 335			1008
gct gtt agt ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly 340 345 350			1056
tat gag cag tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val 355 360 365			1104

gat cca cat cgg gag tat gaa aat gcc aat acc att gga act gat gcg 1152
 Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala
 370 375 380

gag tcg acg agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca 1200
 Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser
 385 390 395 400

att cca cta gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc 1248
 Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val
 405 410 415

ggt aac gtt gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg 1296
 Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met
 420 425 430

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 Asp Arg Trp Ser Arg Ser Glu Glu
 435 440

<210> 1288

<211> 440

<212> PRT

<213> Corynebacterium glutamicum

<400> 1288

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Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr
 20 25 30

Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser
 35 40 45

Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val
 50 55 60

Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln
 65 70 75 80

Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr
 85 90 95

Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu
 100 105 110

Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe
 115 120 125

Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val
 130 135 140

Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly
 145 150 155 160

Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp
 165 170 175

Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val
 180 185 190
 Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro
 195 200 205
 Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu
 210 215 220
 Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala
 225 230 235 240
 Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ser Ser Ser Ile Ser
 245 250 255
 Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn
 260 265 270
 Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val
 275 280 285
 Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly
 290 295 300
 Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg
 305 310 315 320
 Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu
 325 330 335
 Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly
 340 345 350
 Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val
 355 360 365
 Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala
 370 375 380
 Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser
 385 390 395 400
 Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val
 405 410 415
 Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met
 420 425 430
 Asp Arg Trp Ser Arg Ser Glu Glu
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<210> 1289

<211> 1314

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1291)

<223> RXN02781

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ccggtgtgg cgcccttct gggcgatacc ggctgccagc gtg gtc gcg gcc ctg 115
                                   Val Val Ala Ala Leu
                                   1 5

gtt ttc ggt ttc ctg ctt ccc acg tgg gaa cgt ggg ttg tcc gac gcc 163
Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg Gly Leu Ser Asp Ala
              10              15              20

gcg ctc aaa ttc gtt ttt gag ggt ggg cct gat gcc gcc cgc gag gtg 211
Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp Ala Ala Arg Glu Val
              25              30              35

ctg ggc acc atc gcc gcc tcc acg atc tca gtg acc ggt ctc atc ttc 259
Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val Thr Gly Leu Ile Phe
              40              45              50

tcc atc act ctc gtt gtt ctg cag ctg gtg agc agc cag ttc agc ccg 307
Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser Ser Gln Phe Ser Pro
              55              60              65

cga atg ctc aac ggc ttt ctg cgc aac cgc atc gtg cag gcc acc ctg 355
Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile Val Gln Ala Thr Leu
              70              75              80              85

gcg atg ttc ctg ggg acg ttc gtg ttc tcc ctg acg gtc atc cgg tac 403
Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu Thr Val Ile Arg Tyr
              90              95              100

gtg tgg agc gag gac gag gac atc acc gga ttc gtc ccc cgt gct tca 451
Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe Val Pro Arg Ala Ser
              105              110              115

gtg tcg gtt gcc ttc ctg ctg gtg ctc ggg tgt ctg gga ctg ttc ctg 499
Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys Leu Gly Leu Phe Leu
              120              125              130

gcg ttc atc cgg ctc atc acc ttc tcg atg cgg gtg gcc aac gcc atc 547
Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg Val Ala Asn Ala Ile
              135              140              145

tcc gag atc ggg gag gag acg atg gct ctg gcc gca cgt atc tat ccc 595
Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala Ala Arg Ile Tyr Pro
              150              155              160              165

gtg cag agc gac gac gca ggc cca gtc cag ggg ccg ggc tgg tca ccg 643
Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly Pro Gly Trp Ser Pro
              170              175              180

cgg ccc ggt gac ccc cgg gaa gaa atc cgg gtg ggc aac cat ggt tcg 691
Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val Gly Asn His Gly Ser
              185              190              195

ctg gtg tgg atc gac tac cgg aag ctg gtg tcc tgg tcg acg gaa cac 739
Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser Trp Ser Thr Glu His
              200              205              210

cag gcg gtg atc acg gtc gac cgg ccg gtg ggg gac ttc ctc gtc gag 787

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Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly Asp Phe Leu Val Glu
 215 220 225
 ggc cag ccg ctg ctg cgg gtc tgg tgg gac ggg gaa ctc agc gac cgg 835
 Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly Glu Leu Ser Asp Arg
 230 235 240 245
 gac cga cgc gtt ctg cac tcg gcc atc gag gtg cgg acc gag cgg gaa 883
 Asp Arg Arg Val Leu His Ser Ala Ile Glu Val Arg Thr Glu Arg Glu
 250 255 260
 ctt cac cag gat gtg gcg ttc gga ctg cgt caa ctg gtc gac att gcc 931
 Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln Leu Val Asp Ile Ala
 265 270 275
 gat cgt gcg ttg tcc ccg ggc atc aat gat ccg gcc acg gcg gcc cag 979
 Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro Ala Thr Ala Ala Gln
 280 285 290
 tgt gtc cag gag atc cac cgg atc ttc cgc tat ttg gtc acc gtc atc 1027
 Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr Leu Val Thr Val Ile
 295 300 305
 gag ccc agc ccc tac atc gcc gat gac gac ggt cgg gtc cgt gtg gtg 1075
 Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly Arg Val Arg Val Val
 310 315 320 325
 cac cag ccg caa cgt atc gcg gac atg ctc tat gag gtg atc cgt gag 1123
 His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr Glu Val Ile Arg Glu
 330 335 340
 atc cat ctc tac ggg gcg gat tct gcg atg att ccg agg ctg ctg cgc 1171
 Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile Pro Arg Leu Leu Arg
 345 350 355
 acc atg gtc gag gac ctg gtg acg gcc gct gcc gat cat tcc ctg cct 1219
 Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala Asp His Ser Leu Pro
 360 365 370
 gcc gtc gag cgt gcc cgc gcc atc ctg gac gat gag acg gac gag gac 1267
 Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp Glu Thr Asp Glu Asp
 375 380 385
 cgc gac agt gac acc gcg aac gtc tgatccggga tcaggtggcg gtg 1314
 Arg Asp Ser Asp Thr Ala Asn Val
 390 395

<210> 1290

<211> 397

<212> PRT

<213> Corynebacterium glutamicum

<400> 1290

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Gly Leu Ser Asp Ala Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp
 20 25 30

Ala Ala Arg Glu Val Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val

35					40					45					
Thr	Gly	Leu	Ile	Phe	Ser	Ile	Thr	Leu	Val	Val	Leu	Gln	Leu	Val	Ser
	50					55					60				
Ser	Gln	Phe	Ser	Pro	Arg	Met	Leu	Asn	Gly	Phe	Leu	Arg	Asn	Arg	Ile
	65					70					75				80
Val	Gln	Ala	Thr	Leu	Ala	Met	Phe	Leu	Gly	Thr	Phe	Val	Phe	Ser	Leu
				85					90					95	
Thr	Val	Ile	Arg	Tyr	Val	Trp	Ser	Glu	Asp	Glu	Asp	Ile	Thr	Gly	Phe
			100					105					110		
Val	Pro	Arg	Ala	Ser	Val	Ser	Val	Ala	Phe	Leu	Leu	Val	Leu	Gly	Cys
		115					120					125			
Leu	Gly	Leu	Phe	Leu	Ala	Phe	Ile	Arg	Leu	Ile	Thr	Phe	Ser	Met	Arg
	130					135					140				
Val	Ala	Asn	Ala	Ile	Ser	Glu	Ile	Gly	Glu	Glu	Thr	Met	Ala	Leu	Ala
	145					150					155				160
Ala	Arg	Ile	Tyr	Pro	Val	Gln	Ser	Asp	Asp	Ala	Gly	Pro	Val	Gln	Gly
			165					170						175	
Pro	Gly	Trp	Ser	Pro	Arg	Pro	Gly	Asp	Pro	Arg	Glu	Glu	Ile	Arg	Val
			180					185					190		
Gly	Asn	His	Gly	Ser	Leu	Val	Trp	Ile	Asp	Tyr	Arg	Lys	Leu	Val	Ser
		195					200					205			
Trp	Ser	Thr	Glu	His	Gln	Ala	Val	Ile	Thr	Val	Asp	Arg	Pro	Val	Gly
	210					215					220				
Asp	Phe	Leu	Val	Glu	Gly	Gln	Pro	Leu	Leu	Arg	Val	Trp	Trp	Asp	Gly
	225					230					235				240
Glu	Leu	Ser	Asp	Arg	Asp	Arg	Arg	Val	Leu	His	Ser	Ala	Ile	Glu	Val
			245						250					255	
Arg	Thr	Glu	Arg	Glu	Leu	His	Gln	Asp	Val	Ala	Phe	Gly	Leu	Arg	Gln
		260						265					270		
Leu	Val	Asp	Ile	Ala	Asp	Arg	Ala	Leu	Ser	Pro	Gly	Ile	Asn	Asp	Pro
	275						280					285			
Ala	Thr	Ala	Ala	Gln	Cys	Val	Gln	Glu	Ile	His	Arg	Ile	Phe	Arg	Tyr
	290					295					300				
Leu	Val	Thr	Val	Ile	Glu	Pro	Ser	Pro	Tyr	Ile	Ala	Asp	Asp	Asp	Gly
	305					310					315				320
Arg	Val	Arg	Val	Val	His	Gln	Pro	Gln	Arg	Ile	Ala	Asp	Met	Leu	Tyr
			325					330						335	
Glu	Val	Ile	Arg	Glu	Ile	His	Leu	Tyr	Gly	Ala	Asp	Ser	Ala	Met	Ile
		340						345					350		
Pro	Arg	Leu	Leu	Arg	Thr	Met	Val	Glu	Asp	Leu	Val	Thr	Ala	Ala	Ala
	355						360					365			

Asp His Ser Leu Pro Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp
 370 375 380

Glu Thr Asp Glu Asp Arg Asp Ser Asp Thr Ala Asn Val
 385 390 395

<210> .1291

<211> 1314

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1291)

<223> FRXA02781

<400> 1291

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 Val Val Ala Ala Leu
 1 5
 gtt ttc ggt ttc ctg ctt ccc acg tgg gaa cgt ggg ttg tcc gac gcc 163
 Val Phe Gly Phe Leu Leu Pro Thr Trp Glu Arg Gly Leu Ser Asp Ala
 10 15 20
 gcg ctc aaa ttc gtt ttt gag ggt ggg cct gat gcc gcc cgc gag gtg 211
 Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp Ala Ala Arg Glu Val
 25 30 35
 ctg ggc acc atc gcc gcc tcc acg atc tca gtg acc ggt ctc atc ttc 259
 Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val Thr Gly Leu Ile Phe
 40 45 50
 tcc atc act ctc gtt gtt ctg cag ctg gtg agc agc cag ttc agc ccg 307
 Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser Ser Gln Phe Ser Pro
 55 60 65
 cga atg ctc aac ggc ttt ctg cgc aac cgc atc gtg cag gcc acc ctg 355
 Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile Val Gln Ala Thr Leu
 70 75 80 85
 gcg atg ttc ctg ggg acg ttc gtg ttc tcc ctg acg gtc atc cgg tac 403
 Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu Thr Val Ile Arg Tyr
 90 95 100
 gtg tgg agc gag gac gag gac atc acc gga ttc gtc ccc cgt gct tca 451
 Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe Val Pro Arg Ala Ser
 105 110 115
 gtg tcg gtt gcc ttc ctg ctg gtg ctc ggg tgt ctg gga ctg ttc ctg 499
 Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys Leu Gly Leu Phe Leu
 120 125 130
 gcg ttc atc cgg ctc atc acc ttc tcg atg cgg gtg gcc aac gcc atc 547
 Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg Val Ala Asn Ala Ile
 135 140 145

tcc gag atc ggg gag gag acg atg gct ctg gcc gca cgt atc tat ccc Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala Ala Arg Ile Tyr Pro 150 155 160 165	595
gtg cag agc gac gac gca ggc cca gtc cag ggg ccg ggc tgg tca ccg Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly Pro Gly Trp Ser Pro 170 175 180	643
cgg ccc ggt gac ccc cgg gaa gaa atc cgg gtg ggc aac cat ggt tcg Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val Gly Asn His Gly Ser 185 190 195	691
ctg gtg tgg atc gac tac cgg aag ctg gtg tcc tgg tcg acg gaa cac Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser Trp Ser Thr Glu His 200 205 210	739
cag gcg gtg atc acg gtc gac cgg ccg gtg ggg gac ttc ctc gtc gag Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly Asp Phe Leu Val Glu 215 220 225	787
ggc cag ccg ctg ctg cgg gtc tgg tgg gac ggg gaa ctc agc gac cgg Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly Glu Leu Ser Asp Arg 230 235 240 245	835
gac cga cgc gtt ctg cac tcg gcc atc gag gtg cgg acc gag cgg gaa Asp Arg Arg Val Leu His Ser Ala Ile Glu Val Arg Thr Glu Arg Glu 250 255 260	883
ctt cac cag gat gtg gcg ttc gga ctg cgt caa ctg gtc gac att gcc Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln Leu Val Asp Ile Ala 265 270 275	931
gat cgt gcg ttg tcc ccg ggc atc aat gat ccg gcc acg gcg gcc cag Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro Ala Thr Ala Ala Gln 280 285 290	979
tgt gtc cag gag atc cac cgg atc ttc cgc tat ttg gtc acc gtc atc Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr Leu Val Thr Val Ile 295 300 305	1027
gag ccc agc ccc tac atc gcc gat gac gac ggt cgg gtc cgt gtg gtg Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly Arg Val Arg Val Val 310 315 320 325	1075
cac cag ccg caa cgt atc gcg gac atg ctc tat gag gtg atc cgt gag His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr Glu Val Ile Arg Glu 330 335 340	1123
atc cat ctc tac ggg gcg gat tct gcg atg att ccg agg ctg ctg cgc Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile Pro Arg Leu Leu Arg 345 350 355	1171
acc atg gtc gag gac ctg gtg acg gcc gct gcc gat cat tcc ctg cct Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala Asp His Ser Leu Pro 360 365 370	1219
gcc gtc gag cgt gcc cgc ggc atc ctg gac gat gag acg gac gag gac Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp Glu Thr Asp Glu Asp 375 380 385	1267
cgc gac agt gac acc gcg aac gtc tgatccggga tcaggtggcg gtg	1314

Arg Asp Ser Asp Thr Ala Asn Val
390 395

<210> 1292

<211> 397

<212> PRT

<213> Corynebacterium glutamicum

<400> 1292

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Gly Leu Ser Asp Ala Ala Leu Lys Phe Val Phe Glu Gly Gly Pro Asp
20 25 30

Ala Ala Arg Glu Val Leu Gly Thr Ile Ala Ala Ser Thr Ile Ser Val
35 40 45

Thr Gly Leu Ile Phe Ser Ile Thr Leu Val Val Leu Gln Leu Val Ser
50 55 60

Ser Gln Phe Ser Pro Arg Met Leu Asn Gly Phe Leu Arg Asn Arg Ile
65 70 75 80

Val Gln Ala Thr Leu Ala Met Phe Leu Gly Thr Phe Val Phe Ser Leu
85 90 95

Thr Val Ile Arg Tyr Val Trp Ser Glu Asp Glu Asp Ile Thr Gly Phe
100 105 110

Val Pro Arg Ala Ser Val Ser Val Ala Phe Leu Leu Val Leu Gly Cys
115 120 125

Leu Gly Leu Phe Leu Ala Phe Ile Arg Leu Ile Thr Phe Ser Met Arg
130 135 140

Val Ala Asn Ala Ile Ser Glu Ile Gly Glu Glu Thr Met Ala Leu Ala
145 150 155 160

Ala Arg Ile Tyr Pro Val Gln Ser Asp Asp Ala Gly Pro Val Gln Gly
165 170 175

Pro Gly Trp Ser Pro Arg Pro Gly Asp Pro Arg Glu Glu Ile Arg Val
180 185 190

Gly Asn His Gly Ser Leu Val Trp Ile Asp Tyr Arg Lys Leu Val Ser
195 200 205

Trp Ser Thr Glu His Gln Ala Val Ile Thr Val Asp Arg Pro Val Gly
210 215 220

Asp Phe Leu Val Glu Gly Gln Pro Leu Leu Arg Val Trp Trp Asp Gly
225 230 235 240

Glu Leu Ser Asp Arg Asp Arg Arg Val Leu His Ser Ala Ile Glu Val
245 250 255

Arg Thr Glu Arg Glu Leu His Gln Asp Val Ala Phe Gly Leu Arg Gln
260 265 270

Leu Val Asp Ile Ala Asp Arg Ala Leu Ser Pro Gly Ile Asn Asp Pro
 275 280 285
 Ala Thr Ala Ala Gln Cys Val Gln Glu Ile His Arg Ile Phe Arg Tyr
 290 295 300
 Leu Val Thr Val Ile Glu Pro Ser Pro Tyr Ile Ala Asp Asp Asp Gly
 305 310 315 320
 Arg Val Arg Val Val His Gln Pro Gln Arg Ile Ala Asp Met Leu Tyr
 325 330 335
 Glu Val Ile Arg Glu Ile His Leu Tyr Gly Ala Asp Ser Ala Met Ile
 340 345 350
 Pro Arg Leu Leu Arg Thr Met Val Glu Asp Leu Val Thr Ala Ala Ala
 355 360 365
 Asp His Ser Leu Pro Ala Val Glu Arg Ala Arg Gly Ile Leu Asp Asp
 370 375 380
 Glu Thr Asp Glu Asp Arg Asp Ser Asp Thr Ala Asn Val
 385 390 395

<210> 1293

<211> 1422

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1399)

<223> RXN02782

<400> 1293

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caatcacaga agctagttga gcatattgta gaatataact atg cca aca ctg ctt 115
 Met Pro Thr Leu Leu
 1 5

att gac acc cat ccg cat ctt gca gcg caa ctt ctt gac cct ggt tta 163
 Ile Asp Thr His Pro His Leu Ala Ala Gln Leu Leu Asp Pro Gly Leu
 10 15 20

ggt gaa ctt ctt aca gcc ggt tcc aac aaa aaa gtg cag tgg cag tgc 211
 Gly Glu Leu Leu Thr Ala Gly Ser Asn Lys Lys Val Gln Trp Gln Cys
 25 30 35

cct aag cac tcc aat cac atc tgg acg gcc tcg gtt aat aac cgc acc 259
 Pro Lys His Ser Asn His Ile Trp Thr Ala Ser Val Asn Asn Arg Thr
 40 45 50

aat gca aag aac ccg cgc tgc ccc tat tgt gcc gga aca cga gtg ttg 307
 Asn Ala Lys Asn Pro Arg Cys Pro Tyr Cys Ala Gly Thr Arg Val Leu
 55 60 65

gca ggt ttt aat gat ctc gcc acc act cac ccg cat ctt gct gta cag 355
 Ala Gly Phe Asn Asp Leu Ala Thr Thr His Pro His Leu Ala Val Gln
 70 75 80 85

ctg gtt gac caa gat att gcc gtc acc att tcc gct ggt tct ggc aaa	403
Leu Val Asp Gln Asp Ile Ala Val Thr Ile Ser Ala Gly Ser Gly Lys	
90 95 100	
aga caa ctg tgg cag tgt gta gta aac cca aaa cac cag tgg ttg gct	451
Arg Gln Leu Trp Gln Cys Val Val Asn Pro Lys His Gln Trp Leu Ala	
105 110 115	
acg cca aat aat cgc acg agt act aaa tct gcg agt tct ggt tgc ccc	499
Thr Pro Asn Asn Arg Thr Ser Thr Lys Ser Ala Ser Ser Gly Cys Pro	
120 125 130	
tac tgt gcc aac cga gcg gta tta gtc ggt gac aat gac ttt gca aca	547
Tyr Cys Ala Asn Arg Ala Val Leu Val Gly Asp Asn Asp Phe Ala Thr	
135 140 145	
acc tac ccc gaa ctt gca gcg caa tta gta gat caa tct gca gcg aca	595
Thr Tyr Pro Glu Leu Ala Ala Gln Leu Val Asp Gln Ser Ala Ala Thr	
150 155 160 165	
acc ttt aca gcc ggc cac aac aag cct gtt gag tgg atc tgt tgc aag	643
Thr Phe Thr Ala Gly His Asn Lys Pro Val Glu Trp Ile Cys Cys Lys	
170 175 180	
cat gaa cca cca ttt atc tgg aaa acc tca cca att ttg cgt gta cga	691
His Glu Pro Pro Phe Ile Trp Lys Thr Ser Pro Ile Leu Arg Val Arg	
185 190 195	
cag aac acc cag tgc cct gtg tgc tca gag cga act gtg gcg ccg gcg	739
Gln Asn Thr Gln Cys Pro Val Cys Ser Glu Arg Thr Val Ala Pro Ala	
200 205 210	
ctt aat gat ctt gca acc act cac cct aaa ctt gcc gag caa att gca	787
Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu Ala Glu Gln Ile Ala	
215 220 225	
gat cct caa cca agt ggt gtg agc gcc gcg gcc att atc ccc acc att	835
Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala Ile Ile Pro Thr Ile	
230 235 240 245	
agc agg ggt tcc cat acg caa tta aca tgg caa tgt tct aaa aat cat	883
Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys Ser Lys Asn His	
250 255 260	
gac cac caa tgg gtc gcc aca gta aag gat cgt gtt cgc gga aca gac	931
Asp His Gln Trp Val Ala Thr Val Lys Asp Arg Val Arg Gly Thr Asp	
265 270 275	
tgc ccc acc tgc gca aat aca gga act tca cgc aaa gag gct gaa ctt	979
Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys Glu Ala Glu Leu	
280 285 290	
att gag gtc atc cgt gca tta ttc cca aac act gat gtc cag caa ggt	1027
Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp Val Gln Gln Gly	
295 300 305	
gcg ctc att aat gga cgt acc ggt aat caa ggt gca tcg ccg tca acc	1075
Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala Ser Pro Ser Thr	
310 315 320 325	

gat gta ctc ata ccg tcc aaa aat ctc gct atc gag ttc aac ggc ctg 1123
 Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu Phe Asn Gly Leu
 330 335 340

tac tgg cac tct gag ctt ttc atc aaa gat aag cat tat cat gcg aac 1171
 Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys His Tyr His Ala Asn
 345 350 355

aaa tca gct ctc gca gaa caa gcc ggt gtg cag ctc att cat gtg tgg 1219
 Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu Ile His Val Trp
 360 365 370

gag gac gac tgg aat ctt cgc cgc gac att gtg atc cgc atg atc gca 1267
 Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile Arg Met Ile Ala
 375 380 385

cac aag ctt cat gca acc cat aac ctc agt gct gtt ttg cct acc gaa 1315
 His Lys Leu His Ala Thr His Asn Leu Ser Ala Val Leu Pro Thr Glu
 390 395 400 405

act act gac tca cgt gtg gca acc acc gct ttc gcc gta cac tca cac 1363
 Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala Val His Ser His
 410 415 420

tgt cgg tgg tct ctg gtt cac gcg ctg ctg cat tct tgaacagcaa 1409
 Cys Arg Trp Ser Leu Val His Ala Leu Leu His Ser
 425 430

ccatattcag ggt 1422

<210> 1294

<211> 433

<212> PRT

<213> Corynebacterium glutamicum

<400> 1294

Met Pro Thr Leu Leu Ile Asp Thr His Pro His Leu Ala Ala Gln Leu
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Leu Asp Pro Gly Leu Gly Glu Leu Leu Thr Ala Gly Ser Asn Lys Lys
 20 25 30

Val Gln Trp Gln Cys Pro Lys His Ser Asn His Ile Trp Thr Ala Ser
 35 40 45

Val Asn Asn Arg Thr Asn Ala Lys Asn Pro Arg Cys Pro Tyr Cys Ala
 50 55 60

Gly Thr Arg Val Leu Ala Gly Phe Asn Asp Leu Ala Thr Thr His Pro
 65 70 75 80

His Leu Ala Val Gln Leu Val Asp Gln Asp Ile Ala Val Thr Ile Ser
 85 90 95

Ala Gly Ser Gly Lys Arg Gln Leu Trp Gln Cys Val Val Asn Pro Lys
 100 105 110

His Gln Trp Leu Ala Thr Pro Asn Asn Arg Thr Ser Thr Lys Ser Ala
 115 120 125

Ser Ser Gly Cys Pro Tyr Cys Ala Asn Arg Ala Val Leu Val Gly Asp
 130 135 140
 Asn Asp Phe Ala Thr Thr Tyr Pro Glu Leu Ala Ala Gln Leu Val Asp
 145 150 155 160
 Gln Ser Ala Ala Thr Thr Phe Thr Ala Gly His Asn Lys Pro Val Glu
 165 170 175
 Trp Ile Cys Cys Lys His Glu Pro Pro Phe Ile Trp Lys Thr Ser Pro
 180 185 190
 Ile Leu Arg Val Arg Gln Asn Thr Gln Cys Pro Val Cys Ser Glu Arg
 195 200 205
 Thr Val Ala Pro Ala Leu Asn Asp Leu Ala Thr Thr His Pro Lys Leu
 210 215 220
 Ala Glu Gln Ile Ala Asp Pro Gln Pro Ser Gly Val Ser Ala Ala Ala
 225 230 235 240
 Ile Ile Pro Thr Ile Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln
 245 250 255
 Cys Ser Lys Asn His Asp His Gln Trp Val Ala Thr Val Lys Asp Arg
 260 265 270
 Val Arg Gly Thr Asp Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg
 275 280 285
 Lys Glu Ala Glu Leu Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr
 290 295 300
 Asp Val Gln Gln Gly Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly
 305 310 315 320
 Ala Ser Pro Ser Thr Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile
 325 330 335
 Glu Phe Asn Gly Leu Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys
 340 345 350
 His Tyr His Ala Asn Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln
 355 360 365
 Leu Ile His Val Trp Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val
 370 375 380
 Ile Arg Met Ile Ala His Lys Leu His Ala Thr His Asn Leu Ser Ala
 385 390 395 400
 Val Leu Pro Thr Glu Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe
 405 410 415
 Ala Val His Ser His Cys Arg Trp Ser Leu Val His Ala Leu Leu His
 420 425 430
 Ser

aag ctt cat gca acc cat aac ctc agt gct gtt ttg cct acc gaa act 691
Lys Leu His Ala Thr His Asn Leu Ser Ala Val Leu Pro Thr Glu Thr
185 190 195

act gac tca cgt gtg gca acc acc gct ttc gcc gta cac tca cac tgt 739
Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala Val His Ser His Cys
200 205 210

cgg tgg tct ctg gtt cac gcg ctg ctg cat tct tgaacagcaa ccatattcag 792
Arg Trp Ser Leu Val His Ala Leu Leu His Ser
215 220

ggt 795

<210> 1296
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 1296
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20 25 30
Ile Pro Thr Ile Ser Arg Gly Ser His Thr Gln Leu Thr Trp Gln Cys
35 40 45
Ser Lys Asn His Asp His Gln Trp Val Ala Thr Val Lys Asp Arg Val
50 55 60
Arg Gly Thr Asp Cys Pro Thr Cys Ala Asn Thr Gly Thr Ser Arg Lys
65 70 75 80
Glu Ala Glu Leu Ile Glu Val Ile Arg Ala Leu Phe Pro Asn Thr Asp
85 90 95
Val Gln Gln Gly Ala Leu Ile Asn Gly Arg Thr Gly Asn Gln Gly Ala
100 105 110
Ser Pro Ser Thr Asp Val Leu Ile Pro Ser Lys Asn Leu Ala Ile Glu
115 120 125
Phe Asn Gly Leu Tyr Trp His Ser Glu Leu Phe Ile Lys Asp Lys His
130 135 140
Tyr His Ala Asn Lys Ser Ala Leu Ala Glu Gln Ala Gly Val Gln Leu
145 150 155 160
Ile His Val Trp Glu Asp Asp Trp Asn Leu Arg Arg Asp Ile Val Ile
165 170 175
Arg Met Ile Ala His Lys Leu His Ala Thr His Asn Leu Ser Ala Val
180 185 190
Leu Pro Thr Glu Thr Thr Asp Ser Arg Val Ala Thr Thr Ala Phe Ala
195 200 205
Val His Ser His Cys Arg Trp Ser Leu Val His Ala Leu Leu His Ser

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<400> 1298
Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser Glu Asp Gln
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Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp Thr Gly Asn
             20             25             30

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tca agc gaa tcc gcg gca gaa act act gag gcg caa cca agc gag acc 432
 Ser Ser Glu Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr
 130 135 140

ccg gtc gag ccc gcc gct gct tcc cca tcc gat acc atc atc aac ctg 480
 Pro Val Glu Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu
 145 150 155 160

gat acc tca tcc aac atg gat cga gtt gtt gac ggc agc cag gaa acc 528
 Asp Thr Ser Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr
 165 170 175

tac cac acg gtt act tcc cgg act ctg gcc aac ctc gcc 567
 Tyr His Thr Val Thr Ser Arg Thr Leu Ala Asn Leu Ala
 180 185

<210> 1300

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 1300

Ala Ser Gly Thr Asp Ala Ser Thr Ile Thr Leu Asp Gln Val Ala Leu
 1 5 10 15

Pro Val Ala Thr Asn Ser Gly Ala Ser Ala Ala Val Ala Leu Ala Leu
 20 25 30

Ala Glu Thr Pro Glu Ala Ala Ala Ala Leu Asn Arg Asp Ala Asp
 35 40 45

Val Thr Ala Thr Gly Ala Ala Asp Ser Pro Ala Phe Ala Thr Val Glu
 50 55 60

Gly Ala Glu Leu Pro Glu Gly Tyr Thr Phe Glu Ala Val Asp Ser Ala
 65 70 75 80

Glu Val Pro Val Trp Ala Val Ala Ile Asn Ala Gly Asn Gly Ile Ser
 85 90 95

Glu Asp Gln Ala Arg Ala Ala Ser Asp Phe Ser Ser Phe Ser Phe Asp
 100 105 110

Thr Gly Asn Ala Asp Asn Ser Ala Leu Glu Ser Val Leu Thr Gln Ala
 115 120 125

Ser Ser Glu Ser Ala Ala Glu Thr Thr Glu Ala Gln Pro Ser Glu Thr
 130 135 140

Pro Val Glu Pro Ala Ala Ala Ser Pro Ser Asp Thr Ile Ile Asn Leu
 145 150 155 160

Asp Thr Ser Ser Asn Met Asp Arg Val Val Asp Gly Ser Gln Glu Thr
 165 170 175

Tyr His Thr Val Thr Ser Arg Thr Leu Ala Asn Leu Ala
 180 185

Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg
 35 40 45
 Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
 50 55 60
 Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
 65 70 75 80
 Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
 85 90 95
 Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
 100 105 110
 Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
 115 120 125
 Gln Phe Gly Val Gly
 130

<210> 1303

<211> 499.

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(499)

<223> FRXA02817

<400> 1303

aaaattccca cccccaaaac tccccactt cgggtaagga atcaggattc tcacaaagtt 60
 caggcagggt cccgctactt ttcagcgcta atcttggtc atg att tta ggc gta 115
 Met Ile Leu Gly Val
 1 5
 ccc att caa tat ttg ctc tat tca ttg tgg aat tgg att gtc gat acc 163
 Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn Trp Ile Val Asp Thr
 10 15 20
 ggt ttt gat gta gca att atc ctg gtc ttg gcg ttt ttg att cca cgt 211
 Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala Phe Leu Ile Pro Arg
 25 30 35
 atc ggc cga ctg gcc atg cgt att atc aag cgc cga gtg gag tct gca 259
 Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg Arg Val Glu Ser Ala
 40 45 50
 gcc gat gcg gac acc act aag aac cag ctc gcg ttc gcc ggc gtt ggc 307
 Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala Phe Ala Gly Val Gly
 55 60 65
 gtt tat atc gcg caa att gtg gcg ttt ttc atg ctt gcc gtc tcc gcg 355
 Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met Leu Ala Val Ser Ala
 70 75 80 85
 atg cag gct ttt ggt ttc tct ctc gcg ggc gct gcg att ccg gca acc 403

Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala Ala Ile Pro Ala Thr
 90 95 100

att gcg tca gct gcc att ggc ctt ggt gcg cag tcg att gtt gcg gac 451
 Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln Ser Ile Val Ala Asp
 105 110 115

ttc ttg gcc gga ttt ttc atc ctg acg gaa aag caa ttc ggc gtg ggt 499
 Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys Gln Phe Gly Val Gly
 120 125 130

<210> 1304

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 1304

Met Ile Leu Gly Val Pro Ile Gln Tyr Leu Leu Tyr Ser Leu Trp Asn
 1 5 10 15

Trp Ile Val Asp Thr Gly Phe Asp Val Ala Ile Ile Leu Val Leu Ala
 20 25 30

Phe Leu Ile Pro Arg Ile Gly Arg Leu Ala Met Arg Ile Ile Lys Arg
 35 40 45

Arg Val Glu Ser Ala Ala Asp Ala Asp Thr Thr Lys Asn Gln Leu Ala
 50 55 60

Phe Ala Gly Val Gly Val Tyr Ile Ala Gln Ile Val Ala Phe Phe Met
 65 70 75 80

Leu Ala Val Ser Ala Met Gln Ala Phe Gly Phe Ser Leu Ala Gly Ala
 85 90 95

Ala Ile Pro Ala Thr Ile Ala Ser Ala Ala Ile Gly Leu Gly Ala Gln
 100 105 110

Ser Ile Val Ala Asp Phe Leu Ala Gly Phe Phe Ile Leu Thr Glu Lys
 115 120 125

Gln Phe Gly Val Gly
 130

<210> 1305

<211> 606

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(606)

<223> RXN02818

<400> 1305

tcc tat tcc cgg aag ttt ttg acc cag gtg tgg att cga gac aat gtc 48
 Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
 1 5 10 15

ggc gat tat aaa ggc ctt acc gat acg gcg ttc cgt aag aag ctg cag 96
 Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
 20 25 30

cgc gat ctt gcc tac ctg cgc aga gtt ggc gtt ccg att gag cag ttc 144
 Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
 35 40 45

acg gtc acc tca ggc ata gct gaa ggc cag cag gcg tac cgt ctg gcc 192
 Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
 50 55 60

cag gat tct tat aag ctc ccc gag gtc gaa ttc acc cca gat gag gcc 240
 Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65 70 75 80

gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc 288
 Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
 85 90 95

gcc ttc gcg cgt tcg ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag 336
 Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
 100 105 110

cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt 384
 Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
 115 120 125

tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg 432
 Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
 130 135 140

ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc 480
 Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
 145 150 155 160

tcg ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc 528
 Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
 165 170 175

atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc 576
 Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
 180 185 190

cgc atc acc cgc gtc cgc aac atc aaa ctc 606
 Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
 195 200

<210> 1306

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 1306

Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
 1 5 10 15

Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
 20 25 30

cag gat tct tat aag ctc ccc gag gtc gaa ttc acc cca gat gag gcc 240
 Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65 70 75 80
 gcc gtg ctg ggc atg gca ggg gag atg ggc cat aat cag gaa ctc ggc 288
 Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
 85 90 95
 gcc ttc gcg cgt tct ggg tgg acc aaa ttg gcg gcc ggc ggc gcg cag 336
 Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
 100 105 110
 cgt gat ctg tcc acg tcc aca gcc ttg acc aat gcg ggc gat tta ggt 384
 Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
 115 120 125
 tcc ttg tct gca aaa acc ctc gat gcg atc atc aaa gcc cgc caa ttg 432
 Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
 130 135 140
 ggc aag caa atc agc ttc gaa tac cgg cgc gcc ccc aaa gac gcc ccc 480
 Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
 145 150 155 160
 tct ctt cga cac atg gat cct tgg ggt ctg gtc cct gag cgc gac cgc 528
 Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
 165 170 175
 atc tac ctg gtc gga ttc gac ctc gac cgc caa gaa gca cgc acc ttc 576
 Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
 180 185 190
 cgc atc acc cgc gtc cgc aac atc aaa ctc 606
 Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
 195 200

<210> 1308

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 1308

Ser Tyr Ser Arg Lys Phe Leu Thr Gln Val Trp Ile Arg Asp Asn Val
 1 5 10 15
 Gly Asp Tyr Lys Gly Leu Thr Asp Thr Ala Phe Arg Lys Lys Leu Gln
 20 25 30
 Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe
 35 40 45
 Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala
 50 55 60
 Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala
 65 70 75 80
 Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly
 85 90 95

Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln
 100 105 110

Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly
 115 120 125

Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu
 130 135 140

Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro
 145 150 155 160

Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg
 165 170 175

Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe
 180 185 190

Arg Ile Thr Arg Val Arg Asn Ile Lys Leu
 195 200

<210> 1309

<211> 1962

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1939)

<223> RXN02825

<400> 1309

tggcctgccc ctgaaacttt tacggctttc agagcgcagg gcatcatttt cttgtgtcgc 60

caacacttga gaaaaattgc ggaaaaggac actgctgttc atg aaa ctt gca cct 115
 Met Lys Leu Ala Pro
 1 5

cgt atg cgg atg agg agc ccc aaa act ttc gcg gcc ctc gcc tca ctt 163
 Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala Ala Leu Ala Ser Leu
 10 15 20

gct tta gtc ata ggt ctc ggc cag gta ccg atc gcc caa gct caa acc 211
 Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile Ala Gln Ala Gln Thr
 25 30 35

gag tat cga acc gcc tcc gac ggt tcc ctg aac tgg gga ttt agg caa 259
 Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn Trp Gly Phe Arg Gln
 40 45 50

tcg ttc cgc aat tac atc caa acc ggc gtg gcc aaa ggt tcc atc acg 307
 Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala Lys Gly Ser Ile Thr
 55 60 65

ctt ggc gac ggc gca tcc gac aac ggt ggc aac ttc gca ttc acc cca 355
 Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn Phe Ala Phe Thr Pro
 70 75 80 85

cgc acc aac ggc acc acc gtg acc agc gat tcc caa ggc acc gtg gaa 403
 Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser Gln Gly Thr Val Glu

90	95	100	
ttc aac ggc tcc gtg cac ttc ctc gga cac cag gca gag gac aaa tgg			451
Phe Asn Gly Ser Val His Phe Leu Gly His Gln Ala Glu Asp Lys Trp			
105	110	115	
atc ctg gac acc acc atg tct gac atc aaa atg gtg ttc aac gga tcc			499
Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met Val Phe Asn Gly Ser			
120	125	130	
tcc gcg cag cta gtt gtg gat ttg gtt gcc cgc gaa ttc aag ggc acc			547
Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg Glu Phe Lys Gly Thr			
135	140	145	
acc tac gat gac atc ggc gaa tac atc atc tcc gac gac atc gtg ctt			595
Thr Tyr Asp Asp Ile Gly Glu Tyr Ile Ile Ser Asp Asp Ile Val Leu			
150	155	160	165
gcc gac gtc tcc ctc aac tcc gcc gcc gac ttc tcc caa gat tcc atc			643
Ala Asp Val Ser Leu Asn Ser Ala Ala Asp Phe Ser Gln Asp Ser Ile			
170	175	180	
gac ctg tcc ggc acc acc gac ctc acc gca gct ggc gcc caa gct ttc			691
Asp Leu Ser Gly Thr Thr Asp Leu Thr Ala Ala Gly Ala Gln Ala Phe			
185	190	195	
gga gga ttc tac gaa acc ggc gaa gcc ctc gac ccg acc ggc ggc agc			739
Gly Gly Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Gly Ser			
200	205	210	
ctg acc att tcc tcc acc acc acc gcg cca tcg acc agc acg acc tcc			787
Leu Thr Ile Ser Ser Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Ser			
215	220	225	
acc tct gcc tca act tcc ggt gga acc gcc gac tgt tcc tcc ggc gca			835
Thr Ser Ala Ser Thr Ser Gly Gly Thr Ala Asp Cys Ser Ser Gly Ala			
230	235	240	245
ttg ggt gtt gtc acc acc gga acc aac gac ggc atg ctg ggc acc atc			883
Leu Gly Val Val Thr Thr Gly Thr Asn Asp Gly Met Leu Gly Thr Ile			
250	255	260	
cag gaa gta aac aac acc ttc gcg att tgg aac aac ctc atc gtc aac			931
Gln Glu Val Asn Asn Thr Phe Ala Ile Trp Asn Asn Leu Ile Val Asn			
265	270	275	
acc gag cgc atg ttc tgc aac att gat acc ctc aag gcg cgc ttc gac			979
Thr Glu Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp			
280	285	290	
acg gat gat tcc agc gat tca gcg acc tct gcg act tct ggg act act			1027
Thr Asp Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr			
295	300	305	
gcg tcc acc ggc acc acc gct gca act acc gcg gga acc acg ggt acc			1075
Ala Ser Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr			
310	315	320	325
act gga act gcc agc acc gct tcc gga act tcc gga act tcc gga acc			1123
Thr Gly Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr			
330	335	340	

tcc ggc acc gca gca act gtc gct ggc acc acc cca act gac aat ggc	1171
Ser Gly Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly	
345 350 355	
ggt tgc acc gct tcc gga tct ttg ggc gtg acc caa gca tct gcg cag	1219
Val Cys Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln	
360 365 370	
tgg ggt gtg aag gcg tcc ttc cag aac tac att cgc gga tcg atc gcc	1267
Trp Gly Val Lys Ala Ser Phe Gln Asn Tyr Ile Arg Gly Ser Ile Ala	
375 380 385	
aac ggt agc tgg act ctc aac ggc gtt ggt ttt gat aat cag cag ttc	1315
Asn Gly Ser Trp Thr Leu Asn Gly Val Gly Phe Asp Asn Gln Gln Phe	
390 395 400 405	
caa ttc tct gga aat tcc gga gca gtc gac gcg gaa aac aag acc ggc	1363
Gln Phe Ser Gly Asn Ser Gly Ala Val Asp Ala Glu Asn Lys Thr Gly	
410 415 420	
agc atc aat ttc cct ggt tcc atc cac ttc acg ggt cac ggc gga atc	1411
Ser Ile Asn Phe Pro Gly Ser Ile His Phe Thr Gly His Gly Gly Ile	
425 430 435	
ttg gac atg cag atc gca aac att gag atc agc ttc aac ggc aac tcc	1459
Leu Asp Met Gln Ile Ala Asn Ile Glu Ile Ser Phe Asn Gly Asn Ser	
440 445 450	
ggc gag ctg att gcg gat gtc gtt tcc tct gac atg gat gga aat tcc	1507
Gly Glu Leu Ile Ala Asp Val Val Ser Ser Asp Met Asp Gly Asn Ser	
455 460 465	
acc aac tac ggt cgc act gtc gtg ggc acc ctg aac ttc tct gcg ttg	1555
Thr Asn Tyr Gly Arg Thr Val Val Gly Thr Leu Asn Phe Ser Ala Leu	
470 475 480 485	
aat gtt tct gca acg gaa gct tcc ggt tcc gct tcg gtg tcc ctg tca	1603
Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser	
490 495 500	
cag tcg ggt tcg cag gcg ttc gct gat ttc tac acc cca ggc acc cag	1651
Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln	
505 510 515	
ttg gat ccg atc agt ttc agc gca act ttg ggc ggc gac gcc agc tgc	1699
Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys	
520 525 530	
gcc acc gga tcc acc tcg acc aca ggc gct gct gcc acc gcg aac act	1747
Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr	
535 540 545	
gac aac acc gaa ggt gtt gcc ggc gag gaa tcc acc acc ccc gct aac	1795
Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn	
550 555 560 565	
caa aac agc cag ttc caa atc cgc cag gcc gct gca gat tcc acc gga	1843
Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly	
570 575 580	

ctg gat acc acc acc aca atg ttg ctc atc ctc gcg gcg ttc gtt gtc 1891
 Leu Asp Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
 585 590 595

gca ggt ggc tcc atg act cgc ttc acc gtc ggc aac ccg act gga aaa 1939
 Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
 600 605 610

taaggcttca catgaataac gct 1962

<210> 1310

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 1310

Met Lys Leu Ala Pro Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala
 1 5 10 15

Ala Leu Ala Ser Leu Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile
 20 25 30

Ala Gln Ala Gln Thr Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn
 35 40 45

Trp Gly Phe Arg Gln Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala
 50 55 60

Lys Gly Ser Ile Thr Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn
 65 70 75 80

Phe Ala Phe Thr Pro Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser
 85 90 95

Gln Gly Thr Val Glu Phe Asn Gly Ser Val His Phe Leu Gly His Gln
 100 105 110

Ala Glu Asp Lys Trp Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met
 115 120 125

Val Phe Asn Gly Ser Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg
 130 135 140

Glu Phe Lys Gly Thr Thr Tyr Asp Asp Ile Gly Glu Tyr Ile Ile Ser
 145 150 155 160

Asp Asp Ile Val Leu Ala Asp Val Ser Leu Asn Ser Ala Ala Asp Phe
 165 170 175

Ser Gln Asp Ser Ile Asp Leu Ser Gly Thr Thr Asp Leu Thr Ala Ala
 180 185 190

Gly Ala Gln Ala Phe Gly Gly Phe Tyr Glu Thr Gly Glu Ala Leu Asp
 195 200 205

Pro Thr Gly Gly Ser Leu Thr Ile Ser Ser Thr Thr Thr Ala Pro Ser
 210 215 220

Thr Ser Thr Thr Ser Thr Ser Ala Ser Thr Ser Gly Gly Thr Ala Asp
 225 230 235 240

Cys Ser Ser Gly Ala Leu Gly Val Val Thr Thr Gly Thr Asn Asp Gly
 245 250 255
 Met Leu Gly Thr Ile Gln Glu Val Asn Asn Thr Phe Ala Ile Trp Asn
 260 265 270
 Asn Leu Ile Val Asn Thr Glu Arg Met Phe Cys Asn Ile Asp Thr Leu
 275 280 285
 Lys Ala Arg Phe Asp Thr Asp Asp Ser Ser Asp Ser Ala Thr Ser Ala
 290 295 300
 Thr Ser Gly Thr Thr Ala Ser Thr Gly Thr Thr Ala Ala Thr Thr Ala
 305 310 315 320
 Gly Thr Thr Gly Thr Thr Gly Thr Ala Ser Thr Ala Ser Gly Thr Ser
 325 330 335
 Gly Thr Ser Gly Thr Ser Gly Thr Ala Ala Thr Val Ala Gly Thr Thr
 340 345 350
 Pro Thr Asp Asn Gly Val Cys Thr Ala Ser Gly Ser Leu Gly Val Thr
 355 360 365
 Gln Ala Ser Ala Gln Trp Gly Val Lys Ala Ser Phe Gln Asn Tyr Ile
 370 375 380
 Arg Gly Ser Ile Ala Asn Gly Ser Trp Thr Leu Asn Gly Val Gly Phe
 385 390 395 400
 Asp Asn Gln Gln Phe Gln Phe Ser Gly Asn Ser Gly Ala Val Asp Ala
 405 410 415
 Glu Asn Lys Thr Gly Ser Ile Asn Phe Pro Gly Ser Ile His Phe Thr
 420 425 430
 Gly His Gly Gly Ile Leu Asp Met Gln Ile Ala Asn Ile Glu Ile Ser
 435 440 445
 Phe Asn Gly Asn Ser Gly Glu Leu Ile Ala Asp Val Val Ser Ser Asp
 450 455 460
 Met Asp Gly Asn Ser Thr Asn Tyr Gly Arg Thr Val Val Gly Thr Leu
 465 470 475 480
 Asn Phe Ser Ala Leu Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala
 485 490 495
 Ser Val Ser Leu Ser Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr
 500 505 510
 Thr Pro Gly Thr Gln Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly
 515 520 525
 Gly Asp Ala Ser Cys Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala
 530 535 540
 Ala Thr Ala Asn Thr Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser
 545 550 555 560

Thr Thr Pro Ala Asn Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala
 565 570 575

Ala Asp Ser Thr Gly Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu
 580 585 590

Ala Ala Phe Val Val Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly
 595 600 605

Asn Pro Thr Gly Lys
 610

<210> 1311

<211> 538

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA01322

<400> 1311

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caacacttga gaaaaattgc ggaaaaggac actgctgttc atg aaa ctt gca cct 115
 Met Lys Leu Ala Pro
 1 5

cgt atg cgg atg agg agc ccc aaa act ttc gcg gcc ctg gcc tca ctt 163
 Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala Ala Leu Ala Ser Leu
 10 15 20

gct tta gtc ata ggt ctg ggc cag gta ccg atc gcc caa gct caa acc 211
 Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile Ala Gln Ala Gln Thr
 25 30 35

gag tat cga acc gcc tcc gac ggt tcc ctg aac tgg gga ttt agg caa 259
 Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn Trp Gly Phe Arg Gln
 40 45 50

tcg ttc cgc aat tac atc caa acc ggc gtg gcc aaa ggt tcc atc acg 307
 Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala Lys Gly Ser Ile Thr
 55 60 65

ctt ggc gac ggc gca tcc gac aac ggt ggc aac ttc gca ttc acc cca 355
 Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn Phe Ala Phe Thr Pro
 70 75 80 85

cgc acc aac ggc acc acc gtg acc agc gat tcc caa ggc acc gtg gaa 403
 Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser Gln Gly Thr Val Glu
 90 95 100

ttc aac ggc tcc gtg cac ttc ctg gga cac cag gca gag gac aaa tgg 451
 Phe Asn Gly Ser Val His Phe Leu Gly His Gln Ala Glu Asp Lys Trp
 105 110 115

atc ctg gac acc acc atg tct gac atc aaa atg gtg ttc aac gga tcc 499
 Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met Val Phe Asn Gly Ser
 120 125 130

tcc gcg cag cta gtt gtg gat ttg gtt gcc cgc gaa ttc
 Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg Glu Phe
 135 140 145

538

<210> 1312
 <211> 146
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1312
 Met Lys Leu Ala Pro Arg Met Arg Met Arg Ser Pro Lys Thr Phe Ala
 1 5 10 15
 Ala Leu Ala Ser Leu Ala Leu Val Ile Gly Leu Gly Gln Val Pro Ile
 20 25 30
 Ala Gln Ala Gln Thr Glu Tyr Arg Thr Ala Ser Asp Gly Ser Leu Asn
 35 40 45
 Trp Gly Phe Arg Gln Ser Phe Arg Asn Tyr Ile Gln Thr Gly Val Ala
 50 55 60
 Lys Gly Ser Ile Thr Leu Gly Asp Gly Ala Ser Asp Asn Gly Gly Asn
 65 70 75 80
 Phe Ala Phe Thr Pro Arg Thr Asn Gly Thr Thr Val Thr Ser Asp Ser
 85 90 95
 Gln Gly Thr Val Glu Phe Asn Gly Ser Val His Phe Leu Gly His Gln
 100 105 110
 Ala Glu Asp Lys Trp Ile Leu Asp Thr Thr Met Ser Asp Ile Lys Met
 115 120 125
 Val Phe Asn Gly Ser Ser Ala Gln Leu Val Val Asp Leu Val Ala Arg
 130 135 140
 Glu Phe
 145

<210> 1313
 <211> 528
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(528)
 <223> FRXA02824

<400> 1313
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 Phe Tyr Glu Thr Gly Glu Ala Leu Asp Pro Thr Gly Asp Ser Leu Thr
 1 5 10 15
 att tcc tcc acc acc acc gcg cca tcg acc agc acg acc tcc acc tct 96
 Ile Ser Ser Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Ser Thr Ser
 20 25 30

Arg Met Phe Cys Asn Ile Asp Thr Leu Lys Ala Arg Phe Asp Thr Asp
85 90 95

Asp Ser Ser Asp Ser Ala Thr Ser Ala Thr Ser Gly Thr Thr Ala Ser
 100 105 110
 Thr Gly Thr Thr Ala Ala Thr Thr Ala Gly Thr Thr Gly Thr Thr Gly
 115 120 125
 Thr Ala Ser Thr Ala Ser Gly Thr Ser Gly Thr Ser Gly Thr Ser Gly
 130 135 140
 Thr Ala Ala Thr Val Ala Gly Thr Thr Pro Thr Asp Asn Gly Val Cys
 145 150 155 160
 Thr Ala Ser Gly Ser Leu Gly Val Thr Gln Ala Ser Ala Gln Trp Gly
 165 170 175

<210> 1315

<211> 407

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(384)

<223> FRXA02825

<400> 1315

aat gtt tct gca acg gaa gct tcc ggt tcc gct tcg gtg tcc ctg tca	48
Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser	
1 5 10 15	
cag tcg ggt tcg cag gcg ttc gct gat ttc tac acc cca ggc acc cag	96
Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln	
20 25 30	
ttg gat ccg atc agt ttc agc gca act ttg ggc ggc gac gcc agc tgc	144
Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys	
35 40 45	
gcc acc gga tcc acc tcg acc aca ggc gct gct gcc acc gcg aac act	192
Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr	
50 55 60	
gac aac acc gaa ggt gtt gcc ggc gag gaa tcc acc acc ccc gct aac	240
Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn	
65 70 75 80	
caa aac agc cag ttc caa atc cgc cag gcc gct gca gat tcc acc gga	288
Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly	
85 90 95	
ctg gat acc acc acc aca atg ttg ctc atc ctc gcg gcg ttc gtt gtc	336
Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val	
100 105 110	
gca ggt ggc tcc atg act cgc ttc acc gtc ggc aac ccg act gga aaa	384
Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys	
115 120 125	
taaggcttca catgaataac gct	407

<210> 1316

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 1316

Asn Val Ser Ala Thr Glu Ala Ser Gly Ser Ala Ser Val Ser Leu Ser
 1 5 10 15

Gln Ser Gly Ser Gln Ala Phe Ala Asp Phe Tyr Thr Pro Gly Thr Gln
 20 25 30

Leu Asp Pro Ile Ser Phe Ser Ala Thr Leu Gly Gly Asp Ala Ser Cys
 35 40 45

Ala Thr Gly Ser Thr Ser Thr Thr Gly Ala Ala Ala Thr Ala Asn Thr
 50 55 60

Asp Asn Thr Glu Gly Val Ala Gly Glu Glu Ser Thr Thr Pro Ala Asn
 65 70 75 80

Gln Asn Ser Gln Phe Gln Ile Arg Gln Ala Ala Ala Asp Ser Thr Gly
 85 90 95

Leu Asp Thr Thr Thr Thr Met Leu Leu Ile Leu Ala Ala Phe Val Val
 100 105 110

Ala Gly Gly Ser Met Thr Arg Phe Thr Val Gly Asn Pro Thr Gly Lys
 115 120 125

<210> 1317

<211> 528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(528)

<223> RXN02838

<400> 1317

aac acg ggc aag ggc ggg ggg ctg acg gtg ccg ctg ggc gac ggg cag 48
 Asn Thr Gly Lys Gly Gly Gly Leu Thr Val Pro Leu Gly Asp Gly Gln
 1 5 10 15

ggg cgg tat atc gcg aag ttc ccc tcg acc gcg ttt gtg ggg gtg tcg 96
 Gly Arg Tyr Ile Ala Lys Phe Pro Ser Thr Ala Phe Val Gly Val Ser
 20 25 30

gag aac gaa ttt gcc aat ctg gct ttg gcc gag gcg atc ggg atg gag 144
 Glu Asn Glu Phe Ala Asn Leu Ala Leu Ala Glu Ala Ile Gly Met Glu
 35 40 45

gtg ccc gcg cgc gag ttg gtg ggg cgt gcg cag ttt gaa ggc gtg ccc 192
 Val Pro Ala Arg Glu Leu Val Gly Arg Ala Gln Phe Glu Gly Val Pro
 50 55 60

ccc gag ttt gag gcc atg acc gac ggg ttg gtt ttg ctg gtg cgg cgg 240

Pro Glu Phe Glu Ala Met Thr Asp Gly Leu Val Leu Leu Val Arg Arg
65 70 75 80

ttt gat cgc gcg ggc gat ggc gtg cgc gtg cat atg gag gat ttc gca 288
Phe Asp Arg Ala Gly Asp Gly Val Arg Val His Met Glu Asp Phe Ala
85 90 95

cag gtg ttc ggc cta tac ccc gcg cgc aag tat gat ggg gcg gcc agt 336
Gln Val Phe Gly Leu Tyr Pro Ala Arg Lys Tyr Asp Gly Ala Ala Ser
100 105 110

cac gat att gcg gcg gtg ctg ggc agt gcg gtg tcg atc gcg gcg ggg 384
His Asp Ile Ala Ala Val Leu Gly Ser Ala Val Ser Ile Ala Ala Gly
115 120 125

ttg gag ttc gtg cgg cgg ctg gcg ctc tcg gtt gtg atg ggc aac ggc 432
Leu Glu Phe Val Arg Arg Leu Ala Leu Ser Val Val Met Gly Asn Gly
130 135 140

gat atg cat ttg aag aac tgg tcg ctg atc tat cgc ggg cgg ggc gat 480
Asp Met His Leu Lys Asn Trp Ser Leu Ile Tyr Arg Gly Arg Gly Asp
145 150 155 160

gtg ccg gcg ttg gcg cct gtg tat tat atg atg tcg acc gtg acc tat 528
Val Pro Ala Leu Ala Pro Val Tyr Tyr Met Met Ser Thr Val Thr Tyr
165 170 175

<210> 1318

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1318

Asn Thr Gly Lys Gly Gly Gly Leu Thr Val Pro Leu Gly Asp Gly Gln
1 5 10 15

Gly Arg Tyr Ile Ala Lys Phe Pro Ser Thr Ala Phe Val Gly Val Ser
20 25 30

Glu Asn Glu Phe Ala Asn Leu Ala Leu Ala Glu Ala Ile Gly Met Glu
35 40 45

Val Pro Ala Arg Glu Leu Val Gly Arg Ala Gln Phe Glu Gly Val Pro
50 55 60

Pro Glu Phe Glu Ala Met Thr Asp Gly Leu Val Leu Leu Val Arg Arg
65 70 75 80

Phe Asp Arg Ala Gly Asp Gly Val Arg Val His Met Glu Asp Phe Ala
85 90 95

Gln Val Phe Gly Leu Tyr Pro Ala Arg Lys Tyr Asp Gly Ala Ala Ser
100 105 110

His Asp Ile Ala Ala Val Leu Gly Ser Ala Val Ser Ile Ala Ala Gly
115 120 125

Leu Glu Phe Val Arg Arg Leu Ala Leu Ser Val Val Met Gly Asn Gly
130 135 140

Asp Met His Leu Lys Asn Trp Ser Leu Ile Tyr Arg Gly Arg Gly Asp
 145 150 155 160

Val Pro Ala Leu Ala Pro Val Tyr Tyr Met Met Ser Thr Val Thr Tyr
 165 170 175

<210> 1319

<211> 462

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(462)

<223> FRXA02838

<400> 1319

acc gtg ccg ctg ggc gac ggg cag ggg cgg tat atc gcg aag atc ccc 48
 Thr Val Pro Leu Gly Asp Gly Gln Gly Arg Tyr Ile Ala Lys Ile Pro
 1 5 10 15

tcg acc gcg ttt gtg ggg gtg tcg gag aac aaa ttt gcc aat ctg gct 96
 Ser Thr Ala Phe Val Gly Val Ser Glu Asn Lys Phe Ala Asn Leu Ala
 20 25 30

ttg gcc gag gcg atc ggg atg gag gtg ccc gcg cgc gag ttg gtg ggg 144
 Leu Ala Glu Ala Ile Gly Met Glu Val Pro Ala Arg Glu Leu Val Gly
 35 40 45

cgt gcg cag ttt gaa ggc gtg ccc ccc gag ttt gag gcc atg acc gac 192
 Arg Ala Gln Phe Glu Gly Val Pro Pro Glu Phe Glu Ala Met Thr Asp
 50 55 60

ggg ttg gtt ttg ctg gtg cgg cgg ttt gat cgc gcg ggc gat ggc gtg 240
 Gly Leu Val Leu Leu Val Arg Arg Phe Asp Arg Ala Gly Asp Gly Val
 65 70 75 80

cgc gtg cat atg gag gat ttc gca cag gtg ttc ggc cta tac ccc gcg 288
 Arg Val His Met Glu Asp Phe Ala Gln Val Phe Gly Leu Tyr Pro Ala
 85 90 95

cgc aag tat gat ggg gcg gcc agt cac gat att gcg gcg gtg ctg ggc 336
 Arg Lys Tyr Asp Gly Ala Ala Ser His Asp Ile Ala Ala Val Leu Gly
 100 105 110

agt gcg gtg tcg atc gcg gcg ggg ttg gag ttc gtg cgg cgg ctg gcg 384
 Ser Ala Val Ser Ile Ala Ala Gly Leu Glu Phe Val Arg Arg Leu Ala
 115 120 125

ctc tct gtt gtg atg ggc aac ggc gat atg cat ttg aag aac tgg tcg 432
 Leu Ser Val Val Met Gly Asn Gly Asp Met His Leu Lys Asn Trp Ser
 130 135 140

ctg atc tat cac ggg cgg ggc gat gtg ccg 462
 Leu Ile Tyr His Gly Arg Gly Asp Val Pro
 145 150

<210> 1320

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 1320

Thr Val Pro Leu Gly Asp Gly Gln Gly Arg Tyr Ile Ala Lys Ile Pro
 1 5 10 15

Ser Thr Ala Phe Val Gly Val Ser Glu Asn Lys Phe Ala Asn Leu Ala
 20 25 30

Leu Ala Glu Ala Ile Gly Met Glu Val Pro Ala Arg Glu Leu Val Gly
 35 40 45

Arg Ala Gln Phe Glu Gly Val Pro Pro Glu Phe Glu Ala Met Thr Asp
 50 55 60

Gly Leu Val Leu Leu Val Arg Arg Phe Asp Arg Ala Gly Asp Gly Val
 65 70 75 80

Arg Val His Met Glu Asp Phe Ala Gln Val Phe Gly Leu Tyr Pro Ala
 85 90 95

Arg Lys Tyr Asp Gly Ala Ala Ser His Asp Ile Ala Ala Val Leu Gly
 100 105 110

Ser Ala Val Ser Ile Ala Ala Gly Leu Glu Phe Val Arg Arg Leu Ala
 115 120 125

Leu Ser Val Val Met Gly Asn Gly Asp Met His Leu Lys Asn Trp Ser
 130 135 140

Leu Ile Tyr His Gly Arg Gly Asp Val Pro
 145 150

<210> 1321

<211> 273

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(250)

<223> RXN02840

<400> 1321

aagtgaatc aatcggcttt tccagcagca gcaactggctcg cgccagcgtg ggtggttatgg 60

tgaaggcgaa tacaccttca gcaccgctga gccggaagag atg acg gta atc agt 115
 Met Thr Val Ile Ser
 1 5

ggc gcg ctg aat gtg tta ctg cct gac gcg acc gac tgg cag gtg tat 163
 Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr Asp Trp Gln Val Tyr
 10 15 20

gaa gcc ggt tcg gtg ttt aat gtt ccc ggt cac agt gag ttt cat ctg 211
 Glu Ala Gly Ser Val Phe Asn Val Pro Gly His Ser Glu Phe His Leu
 25 30 35

caa gtt gcc gaa ccc acc tct tat ctg tgc cgc tat ctg taattcctcg 260

Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg Tyr Leu
 40 45 50

ccttccccctt gaa

273

<210> 1322
 <211> 50
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1322
 Met Thr Val Ile Ser Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr
 1 5 10 15
 Asp Trp Gln Val Tyr Glu Ala Gly Ser Val Phe Asn Val Pro Gly His
 20 25 30
 Ser Glu Phe His Leu Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg
 35 40 45
 Tyr Leu
 50

<210> 1323
 <211> 273
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(250)
 <223> FRXA02840

<400> 1323
 aagtgaaatc aatcggccttt tccagcagca gcactggtcg cgccagcgtg ggtgttatgg 60
 tgaaggcgaa tacaccttca gcaccgctga gccggaagag atg acg gta atc agt 115
 Met Thr Val Ile Ser
 1 5
 ggc gcg ctg aat gtg tta ctg cct gac gcg acc gac tgg cag gtg tat 163
 Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr Asp Trp Gln Val Tyr
 10 15 20
 gaa gcc ggt tcg gtg ttt aat gtt ccc ggt cac agt gag ttt cat ctg 211
 Glu Ala Gly Ser Val Phe Asn Val Pro Gly His Ser Glu Phe His Leu
 25 30 35
 caa gtt gcc gaa ccc acc tct tat ctg tgc cgc tat ctg taattcctcg 260
 Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg Tyr Leu
 40 45 50
 ccttccccctt gaa

273

<210> 1324
 <211> 50
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1324

Met Thr Val Ile Ser Gly Ala Leu Asn Val Leu Leu Pro Asp Ala Thr
 1 5 10 15
 Asp Trp Gln Val Tyr Glu Ala Gly Ser Val Phe Asn Val Pro Gly His
 20 25 30
 Ser Glu Phe His Leu Gln Val Ala Glu Pro Thr Ser Tyr Leu Cys Arg
 35 40 45
 Tyr Leu
 50

<210> 1325

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXN02841

<400> 1325

ctcacataac tttagccac cccataccct ttaaccctg cactgctcat ccacaagcac 60
 tgtgcagggg ttgtgttttc taacaagaaa agagaccacc atg ttc aca gct ttt 115
 Met Phe Thr Ala Phe
 1 5
 aaa agc aat cct acg acc att aaa aag ctg gtt tct gag ctc att aat 163
 Lys Ser Asn Pro Thr Thr Ile Lys Lys Leu Val Ser Glu Leu Ile Asn
 10 15 20
 ggc gac gat gca gcg ctc aac gaa cta gag cga cac gtc act aat gaa 211
 Gly Asp Asp Ala Ala Leu Asn Glu Leu Glu Arg His Val Thr Asn Glu
 25 30 35
 tca gtc cgt gct cgc gaa ctc cct aat gtc cag tac aaa gcc act gcg 259
 Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln Tyr Lys Ala Thr Ala
 40 45 50
 ggg cgc aac ttc gcc ata tcc aag ctg gtc caa aat ttg cgt cgc atc 307
 Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln Asn Leu Arg Arg Ile
 55 60 65
 aac aag gca caa aac aat cca cgt ggt gtg ccc act cat gcc acc gtg 355
 Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro Thr His Ala Thr Val
 70 75 80 85
 att ctg ctt aag gaa gac ggc agc tac gac ggt gaa gaa cag tgg cgc 403
 Ile Leu Leu Lys Glu Asp Gly Ser Tyr Asp Gly Glu Glu Gln Trp Arg
 90 95 100
 att cca gaa aag gcg atc act ccg ttc gac atg cta cgt tgc cct gac 451
 Ile Pro Glu Lys Ala Ile Thr Pro Phe Asp Met Leu Arg Ser Pro Asp
 105 110 115
 ttc aac cac aac agg ctg aag aac cgg ccg ctc atg gtc gag tcc caa 499

Phe Asn His Asn Arg Leu Lys Asn Arg Pro Leu Met Val Glu Ser Gln
 120 125 130

tac ccc tgg ggc gtc ccc gga ctc att aaa atg aac tgatcaatcc 545
 Tyr Pro Trp Gly Val Pro Gly Leu Ile Lys Met Asn
 135 140 145

ctgacacagc cat 558

<210> 1326

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 1326

Met Phe Thr Ala Phe Lys Ser Asn Pro Thr Thr Ile Lys Lys Leu Val
 1 5 10 15

Ser Glu Leu Ile Asn Gly Asp Asp Ala Ala Leu Asn Glu Leu Glu Arg
 20 25 30

His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln
 35 40 45

Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln
 50 55 60

Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro
 65 70 75 80

Thr His Ala Thr Val Ile Leu Leu Lys Glu Asp Gly Ser Tyr Asp Gly
 85 90 95

Glu Glu Gln Trp Arg Ile Pro Glu Lys Ala Ile Thr Pro Phe Asp Met
 100 105 110

Leu Arg Ser Pro Asp Phe Asn His Asn Arg Leu Lys Asn Arg Pro Leu
 115 120 125

Met Val Glu Ser Gln Tyr Pro Trp Gly Val Pro Gly Leu Ile Lys Met
 130 135 140

Asn
 145

<210> 1327

<211> 285

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (7)..(285)

<223> FRXA02841

<400> 1327

accacc atg ttc gca gct ttt aaa agc aat ctt ccg acc att aaa aag ctg 51
 Met Phe Ala Ala Phe Lys Ser Asn Leu Pro Thr Ile Lys Lys Leu
 1 5 10 15

gtt tat gag gtc att aat ggc gtc gat gca gcg ctc aac gaa cta gag 99
 Val Tyr Glu Val Ile Asn Gly Val Asp Ala Ala Leu Asn Glu Leu Glu
 20 25 30

cga cac gtc act aat gaa tca gtc cgt gct cgc gaa ctc cct aat gtc 147
 Arg His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val
 35 40 45

cag tac aaa gcc act gcg ggg cgc aac ttc gcc ata tcc aag ctg gtc 195
 Gln Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val
 50 55 60

caa aat ttg cgt cgc atc aac aag gca caa aac aat cca cgt ggt gtg 243
 Gln Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val
 65 70 75

ccc act cat gcc acc gtg att ctg ctt aag gga gac ggc agc 285
 Pro Thr His Ala Thr Val Ile Leu Leu Lys Gly Asp Gly Ser
 80 85 90

<210> 1328

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 1328

Met Phe Ala Ala Phe Lys Ser Asn Leu Pro Thr Ile Lys Lys Leu Val
 1 5 10 15

Tyr Glu Val Ile Asn Gly Val Asp Ala Ala Leu Asn Glu Leu Glu Arg
 20 25 30

His Val Thr Asn Glu Ser Val Arg Ala Arg Glu Leu Pro Asn Val Gln
 35 40 45

Tyr Lys Ala Thr Ala Gly Arg Asn Phe Ala Ile Ser Lys Leu Val Gln
 50 55 60

Asn Leu Arg Arg Ile Asn Lys Ala Gln Asn Asn Pro Arg Gly Val Pro
 65 70 75 80

Thr His Ala Thr Val Ile Leu Leu Lys Gly Asp Gly Ser
 85 90

<210> 1329

<211> 873

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(850)

<223> RXN02846

<400> 1329

tacaagcgct gaacgttgag tttgagtttg gtccattgag gggtaaaggc ttacctctcg 60

actaggtggg gtgggcgtag agcgcctatt ctgattgac gtg tta acc atc gct 115

											Val	Leu	Thr	Ile	Ala	
											1				5	
att	gta	ctt	ctc	gcg	tca	gtc	ctc	atc	ggc	gct	ctt	ctc	caa	cgc	atg	163
Ile	Val	Leu	Leu	Ala	Ser	Val	Leu	Ile	Gly	Ala	Leu	Leu	Gln	Arg	Met	
				10					15					20		
aca	gga	ttg	ggc	gtc	ggc	cta	gtt	acc	ggc	cca	gtc	ctg	act	tct	ttg	211
Thr	Gly	Leu	Gly	Val	Gly	Leu	Val	Thr	Gly	Pro	Val	Leu	Thr	Ser	Leu	
			25					30					35			
tta	ggg	ccg	cta	gca	ggc	gtg	acc	atg	gtg	aat	ggc	ctg	tcc	atc	atc	259
Leu	Gly	Pro	Leu	Ala	Gly	Val	Thr	Met	Val	Asn	Gly	Leu	Ser	Ile	Ile	
		40					45					50				
aac	gcg	gtg	aat	aat	gcg	tgg	tcg	gtg	cgc	aaa	cgc	act	gac	tgg	gcc	307
Asn	Ala	Val	Asn	Asn	Ala	Trp	Ser	Val	Arg	Lys	Arg	Thr	Asp	Trp	Ala	
	55					60					65					
aaa	ttc	cga	att	ctt	gcc	ggc	gct	ttg	gtg	ctt	ggc	tct	ggt	cct	gct	355
Lys	Phe	Arg	Ile	Leu	Ala	Gly	Ala	Leu	Val	Leu	Gly	Ser	Val	Pro	Ala	
	70				75					80					85	
gtt	gca	gtg	gtg	tat	ttc	ctt	aac	gga	cca	tgg	ctg	ttg	att	ttc	gtt	403
Val	Ala	Val	Val	Tyr	Phe	Leu	Asn	Gly	Pro	Trp	Leu	Leu	Ile	Phe	Val	
				90					95					100		
ggc	gcg	atg	gtg	ctg	ctc	gcg	ttg	ggc	gtt	tcc	ctg	ttc	cca	aca	gag	451
Gly	Ala	Met	Val	Leu	Leu	Ala	Leu	Gly	Val	Ser	Leu	Phe	Pro	Thr	Glu	
			105					110					115			
aaa	ttc	gca	ctc	aag	caa	gaa	gct	aaa	ctg	cct	atg	gtc	atc	ttc	ggc	499
Lys	Phe	Ala	Leu	Lys	Gln	Glu	Ala	Lys	Leu	Pro	Met	Val	Ile	Phe	Gly	
		120					125					130				
atg	att	ggc	gga	ttc	atg	tcc	act	gtt	gca	ggc	atc	gca	ggg	cca	tcc	547
Met	Ile	Gly	Gly	Phe	Met	Ser	Thr	Val	Ala	Gly	Ile	Ala	Gly	Pro	Ser	
						140					145					
ctg	act	gtt	tat	gcg	cgc	ctg	agc	cgc	tgg	gat	tac	cgc	gac	ttt	gtg	595
Leu	Thr	Val	Tyr	Ala	Arg	Leu	Ser	Arg	Trp	Asp	Tyr	Arg	Asp	Phe	Val	
					155					160					165	
gcc	acc	ttg	cac	cca	gtt	cta	ctc	gtg	gcc	aac	acc	gta	tcg	ttc	ctg	643
Ala	Thr	Leu	His	Pro	Val	Leu	Leu	Val	Ala	Asn	Thr	Val	Ser	Phe	Leu	
				170					175					180		
ctc	aag	gtt	atc	ttg	atc	ggc	gga	ctc	gat	ttc	ggc	ggc	gca	ccc	gca	691
Leu	Lys	Val	Ile	Leu	Ile	Gly	Gly	Leu	Asp	Phe	Gly	Gly	Ala	Pro	Ala	
				185				190					195			
tgg	ctc	tgg	atc	ggc	gcc	gta										

230

235

240

245

atc atg gaa ttg gtt tagcgggtcctt aattgggtggg aag
 Ile Met Glu Leu Val
 250

873

<210> 1330

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 1330

Val Leu Thr Ile Ala Ile Val Leu Leu Ala Ser Val Leu Ile Gly Ala
 1 5 10 15

Leu Leu Gln Arg Met Thr Gly Leu Gly Val Gly Leu Val Thr Gly Pro
 20 25 30

Val Leu Thr Ser Leu Leu Gly Pro Leu Ala Gly Val Thr Met Val Asn
 35 40 45

Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val Arg Lys
 50 55 60

Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu Val Leu
 65 70 75 80

Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly Pro Trp
 85 90 95

Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly Val Ser
 100 105 110

Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys Leu Pro
 115 120 125

Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val Ala Gly
 130 135 140

Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg Trp Asp
 145 150 155 160

Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val Ala Asn
 165 170 175

Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu Asp Phe
 180 185 190

Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met Ile Phe
 195 200 205

Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser Thr Pro
 210 215 220

Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly Ala Ala Val
 225 230 235 240

Val Leu Phe Arg Gly Ile Met Glu Leu Val
 245 250

<210> 1331
 <211> 573
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(573)
 <223> FRXA02846

<400> 1331
 gtg aat ggt ctg tcc atc atc aac gcg gtg aat aat gcg tgg tcg gtg 48
 Val Asn Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val
 1 5 10 15
 cgc aaa cgc act gac tgg gcc aaa ttc cga att ctt gcc ggc gct ttg 96
 Arg Lys Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu
 20 25 30
 gtg ctt ggt tct gtt cct gct gtt gca gtg gtg tat ttc ctt aac gga 144
 Val Leu Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly
 35 40 45
 cca tgg ctg ttg att ttc gtt ggt gcg atg gtg ctg ctc gcg ttg ggt 192
 Pro Trp Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly
 50 55 60
 gtt tcc ctg ttc cca aca gag aaa ttc gca ctc aag caa gaa gct aaa 240
 Val Ser Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys
 65 70 75 80
 ctg cct atg gtc atc ttc ggc atg att ggt gga ttc atg tcc act gtt 288
 Leu Pro Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val
 85 90 95
 gca ggc atc gca ggg cca tcc ctg act gtt tat gcg cgc ctg agc cgc 336
 Ala Gly Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg
 100 105 110
 tgg gat tac cga gac ttt gtg gcc acc ttg cac cca gtt cta ctc gtg 384
 Trp Asp Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val
 115 120 125
 gcc aac acc gta tcg ttc ctg ctc aag gtt atc ttg atc ggt gga ctc 432
 Ala Asn Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu
 130 135 140
 gat ttc ggt ggc gca ccc gca tgg ctc tgg atc ggt gcc gta gcg atg 480
 Asp Phe Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met
 145 150 155 160
 atc ttt gtc ggt gct tgg ttg ggt gaa atc gtc aac gct aag gtg tcc 528
 Ile Phe Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser
 165 170 175
 acc cca atg gcc aag cgc atc gct acg ctc ctg gca gca gct ggt 573
 Thr Pro Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly
 180 185 190

<210> 1332

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 1332

Val Asn Gly Leu Ser Ile Ile Asn Ala Val Asn Asn Ala Trp Ser Val
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Arg Lys Arg Thr Asp Trp Ala Lys Phe Arg Ile Leu Ala Gly Ala Leu
 20 25 30

Val Leu Gly Ser Val Pro Ala Val Ala Val Val Tyr Phe Leu Asn Gly
 35 40 45

Pro Trp Leu Leu Ile Phe Val Gly Ala Met Val Leu Leu Ala Leu Gly
 50 55 60

Val Ser Leu Phe Pro Thr Glu Lys Phe Ala Leu Lys Gln Glu Ala Lys
 65 70 75 80

Leu Pro Met Val Ile Phe Gly Met Ile Gly Gly Phe Met Ser Thr Val
 85 90 95

Ala Gly Ile Ala Gly Pro Ser Leu Thr Val Tyr Ala Arg Leu Ser Arg
 100 105 110

Trp Asp Tyr Arg Asp Phe Val Ala Thr Leu His Pro Val Leu Leu Val
 115 120 125

Ala Asn Thr Val Ser Phe Leu Leu Lys Val Ile Leu Ile Gly Gly Leu
 130 135 140

Asp Phe Gly Gly Ala Pro Ala Trp Leu Trp Ile Gly Ala Val Ala Met
 145 150 155 160

Ile Phe Val Gly Ala Trp Leu Gly Glu Ile Val Asn Ala Lys Val Ser
 165 170 175

Thr Pro Met Ala Lys Arg Ile Ala Thr Leu Leu Ala Ala Ala Gly
 180 185 190

<210> 1333

<211> 1135

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (47)..(1135)

<223> RXN02847

<400> 1333

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 Leu Ala Leu Thr
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gcc aga ggc ttt ctc aat tct gaa aga agc cag aca agg tgg aaa acc 106
 Ala Arg Gly Phe Leu Asn Ser Glu Arg Ser Gln Thr Arg Trp Lys Thr
 5 10 15 20

cac ttc acc acc cag aaa gtt cca cgc tcc ggc tac aga tat gac ctc	154
His Phe Thr Thr Gln Lys Val Pro Arg Ser Gly Tyr Arg Tyr Asp Leu	
25 30 35	
gat ggg ctc cgc ggc atc gcg atc gcc ttc gta gtt ttg ttc cat gtt	202
Asp Gly Leu Arg Gly Ile Ala Ile Ala Phe Val Val Leu Phe His Val	
40 45 50	
ttc gtc gga aaa gtc tcc ggc ggt gtg gat gtc ttc ctg ctg ctg tct	250
Phe Val Gly Lys Val Ser Gly Gly Val Asp Val Phe Leu Leu Leu Ser	
55 60 65	
ggc tat ttc ttc tta ggg tgc caa ttg cgt tat gca gat cgt cca gat	298
Gly Tyr Phe Phe Leu Gly Ser Gln Leu Arg Tyr Ala Asp Arg Pro Asp	
70 75 80	
tct tcc atc aac ccc tgg tgg ccg att tgg cgc acg cta cgc aga tta	346
Ser Ser Ile Asn Pro Trp Trp Pro Ile Trp Arg Thr Leu Arg Arg Leu	
85 90 95 100	
ctt cct gcg tta gtg ctg gtg ttg ggc gtt tcc atg gtc ctc atc ttg	394
Leu Pro Ala Leu Val Leu Val Leu Gly Val Ser Met Val Leu Ile Leu	
105 110 115	
gcg tgg gtg ccc aga ctg caa cca ata gaa ata gcc aac caa gca gta	442
Ala Trp Val Pro Arg Leu Gln Pro Ile Glu Ile Ala Asn Gln Ala Val	
120 125 130	
gcc agc ctc ttc tat gtc caa aac tgg gag ctc gca tcc caa ggt gct	490
Ala Ser Leu Phe Tyr Val Gln Asn Trp Glu Leu Ala Ser Gln Gly Ala	
135 140 145	
gcc tac gga gca gcc tct gca gaa gtc agt cct ttc cag cac ttg tgg	538
Ala Tyr Gly Ala Ala Ser Ala Glu Val Ser Pro Phe Gln His Leu Trp	
150 155 160	
tcc atg gct gtg caa ggg cag ttc tac ctc ttt gcc atc ttg ttg agc	586
Ser Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser	
165 170 175 180	
atg gcg atc atc ctg att cgt cga tac cgc ccc gaa tac tcc gca gtg	634
Met Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val	
185 190 195	
cga cta gcg act cct gtg ctg gca gtg ctc aca tcc gta tca ttt ttc	682
Arg Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser Val Ser Phe Phe	
200 205 210	
agt gca atc ctg tgg cat ttc att gat caa tca gtc aac tac tat tcc	730
Ser Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser	
215 220 225	
acc ttc acc agg ttc tgg gag ctc ggc ctt ggt gca cta ttg gtg ctg	778
Thr Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala Leu Leu Val Leu	
230 235 240	
cat gcg cct cga att ttg att tct gcg aag act aaa tca ata ctc gca	826
His Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala	
245 250 255 260	

gcc gtc ggt ttg ttt atg gtg cta tcc act gga ttc ttc atg gat ggc 874
 Ala Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe Phe Met Asp Gly
 265 270 275
 gca gag act ttc cct gga ttc ccc gcg ctg tat ccc atc ttg ggt gct 922
 Ala Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala
 280 285 290
 tgc tta gtc atc ctt ggc gac ggt aaa atc tcg gtc ttt ctc tcc cga 970
 Cys Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val Phe Leu Ser Arg
 295 300 305
 aaa tgg atg ctt tgg ctc ggc gat atc gcc tac ccg ctc tac ttg tgg 1018
 Lys Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp
 310 315 320
 cac tgg cct ctg ctg atc att ttc acc gct ttg ttc aac caa gaa gag 1066
 His Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu
 325 330 335 340
 cca tcc atc tgg ctg ggt atc gcc gtg att atg ctg tcc ctt ggc ttg 1114
 Pro Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu Ser Leu Gly Leu
 345 350 355
 gcg cag ctg act aac aaa tac 1135
 Ala Gln Leu Thr Asn Lys Tyr
 360

<210> 1334

<211> 363

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1334

Leu Ala Leu Thr Ala Arg Gly Phe Leu Asn Ser Glu Arg Ser Gln Thr
 1 5 10 15
 Arg Trp Lys Thr His Phe Thr Thr Gln Lys Val Pro Arg Ser Gly Tyr
 20 25 30
 Arg Tyr Asp Leu Asp Gly Leu Arg Gly Ile Ala Ile Ala Phe Val Val
 35 40 45
 Leu Phe His Val Phe Val Gly Lys Val Ser Gly Gly Val Asp Val Phe
 50 55 60
 Leu Leu Leu Ser Gly Tyr Phe Phe Leu Gly Ser Gln Leu Arg Tyr Ala
 65 70 75 80
 Asp Arg Pro Asp Ser Ser Ile Asn Pro Trp Trp Pro Ile Trp Arg Thr
 85 90 95
 Leu Arg Arg Leu Leu Pro Ala Leu Val Leu Val Leu Gly Val Ser Met
 100 105 110
 Val Leu Ile Leu Ala Trp Val Pro Arg Leu Gln Pro Ile Glu Ile Ala
 115 120 125
 Asn Gln Ala Val Ala Ser Leu Phe Tyr Val Gln Asn Trp Glu Leu Ala
 130 135 140

Ser Gln Gly Ala Ala Tyr Gly Ala Ala Ser Ala Glu Val Ser Pro Phe
 145 150 155 160
 Gln His Leu Trp Ser Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala
 165 170 175
 Ile Leu Leu Ser Met Ala Ile Ile Leu Ile Arg Arg Tyr Arg Pro Glu
 180 185 190
 Tyr Ser Ala Val Arg Leu Ala Thr Pro Val Leu Ala Val Leu Thr Ser
 195 200 205
 Val Ser Phe Phe Ser Ala Ile Leu Trp His Phe Ile Asp Gln Ser Val
 210 215 220
 Asn Tyr Tyr Ser Thr Phe Thr Arg Phe Trp Glu Leu Gly Leu Gly Ala
 225 230 235 240
 Leu Leu Val Leu His Ala Pro Arg Ile Leu Ile Ser Ala Lys Thr Lys
 245 250 255
 Ser Ile Leu Ala Ala Val Gly Leu Phe Met Val Leu Ser Thr Gly Phe
 260 265 270
 Phe Met Asp Gly Ala Glu Thr Phe Pro Gly Phe Pro Ala Leu Tyr Pro
 275 280 285
 Ile Leu Gly Ala Cys Leu Val Ile Leu Gly Asp Gly Lys Ile Ser Val
 290 295 300
 Phe Leu Ser Arg Lys Trp Met Leu Trp Leu Gly Asp Ile Ala Tyr Pro
 305 310 315 320
 Leu Tyr Leu Trp His Trp Pro Leu Leu Ile Ile Phe Thr Ala Leu Phe
 325 330 335
 Asn Gln Glu Glu Pro Ser Ile Trp Leu Gly Ile Ala Val Ile Met Leu
 340 345 350
 Ser Leu Gly Leu Ala Gln Leu Thr Asn Lys Tyr
 355 360

<210> 1335

<211> 694

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(694)

<223> FRXA02847

<400> 1335

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agcctctgca gaagtcagtc ctttccagca cttgtggtcc atg gct gtg caa ggg 115
 Met Ala Val Gln Gly
 1 5

cag ttc tac ctc ttt gcc atc ttg ttg agc atg gcg atc atc ctg att 163
 Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser Met Ala Ile Ile Leu Ile
 10 15 20

cgt cga tac cgc ccc gaa tac tcc gca gtg cga cta gcg act cct gtg 211
 Arg Arg Tyr Arg Pro Glu Tyr Ser Ala Val Arg Leu Ala Thr Pro Val
 25 30 35

ctg gca gtg ctc aca tcc gta tca ttt ttc agt gca atc ctg tgg cat 259
 Leu Ala Val Leu Thr Ser Val Ser Phe Phe Ser Ala Ile Leu Trp His
 40 45 50

ttc att gat caa tca gtc aac tac tat tcc acc ttc acc agg ttc tgg 307
 Phe Ile Asp Gln Ser Val Asn Tyr Tyr Ser Thr Phe Thr Arg Phe Trp
 55 60 65

gag ctc ggc ctt ggt gca cta ttg gtg ctg cat gcg cct cga att ttg 355
 Glu Leu Gly Leu Gly Ala Leu Leu Val Leu His Ala Pro Arg Ile Leu
 70 75 80 85

att tct gcg aag act aaa tca ata ctc gca gcc gtc ggt ttg ttt atg 403
 Ile Ser Ala Lys Thr Lys Ser Ile Leu Ala Ala Val Gly Leu Phe Met
 90 95 100

gtg cta tcc act gga ttc ttc atg gat ggc gca gag act ttc cct gga 451
 Val Leu Ser Thr Gly Phe Phe Met Asp Gly Ala Glu Thr Phe Pro Gly
 105 110 115

ttc ccc gcg ctg tat ccc atc ttg ggt gct tgc tta gtc atc ctt ggc 499
 Phe Pro Ala Leu Tyr Pro Ile Leu Gly Ala Cys Leu Val Ile Leu Gly
 120 125 130

gac ggt aaa atc tcg gtc ttt ctc tcc cga aaa tgg atg ctt tgg ctc 547
 Asp Gly Lys Ile Ser Val Phe Leu Ser Arg Lys Trp Met Leu Trp Leu
 135 140 145

ggc gat atc gcc tac ccg ctc tac ttg tgg cac tgg cct ctg ctg atc 595
 Gly Asp Ile Ala Tyr Pro Leu Tyr Leu Trp His Trp Pro Leu Leu Ile
 150 155 160 165

att ttc acc gct ttg ttc aac caa gaa gag cca tcc atc tgg ctg ggt 643
 Ile Phe Thr Ala Leu Phe Asn Gln Glu Glu Pro Ser Ile Trp Leu Gly
 170 175 180

atc gcc gtg att atg ctg tcc ctt ggc ttg gcg cag ctg act aac aaa 691
 Ile Ala Val Ile Met Leu Ser Leu Gly Leu Ala Gln Leu Thr Asn Lys
 185 190 195

tac 694
 Tyr

<210> 1336

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 1336

Met Ala Val Gln Gly Gln Phe Tyr Leu Phe Ala Ile Leu Leu Ser Met
 1 5 10 15

tca gat tgt gtg cca tca acc ggt gca cca gga ttt acc acc tca gac 192
 Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
 50 55 60

acc cga atc atc agc gat ctt tct ggc aac gaa atc acc aga gaa acc 240
 Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Thr
 65 70 75 80

gtc acc acg gtt tac gat cct tca cca aac gtg gtc tgc tcc 282
 Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
 85 90

taaaacaaaa tgccccacca gat 305

<210> 1338

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 1338

Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
 1 5 10 15

Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
 20 25 30

Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly
 35 40 45

Ser Asp Cys Val Pro Ser Thr Gly Ala Pro Gly Phe Thr Thr Ser Asp
 50 55 60

Thr Arg Ile Ile Ser Asp Leu Ser Gly Asn Glu Ile Thr Arg Glu Thr
 65 70 75 80

Val Thr Thr Val Tyr Asp Pro Ser Pro Asn Val Val Cys Ser
 85 90

<210> 1339

<211> 305

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(282)

<223> FRXA02849

<400> 1339

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 Ser Pro Tyr Pro Val Met Ile Ser Thr Ser Ala Asp Ala Ser Asn Val
 1 5 10 15

acc gtg cgc atc atg ggt gtg gac acc acc tcc gtg gaa tcc atc aac 96
 Thr Val Arg Ile Met Gly Val Asp Thr Thr Ser Val Glu Ser Ile Asn
 20 25 30

aac gga cgt tgg tcc acc acc cag ccc aac aca gtt cga gta tcg ggt 144
 Asn Gly Arg Trp Ser Thr Thr Gln Pro Asn Thr Val Arg Val Ser Gly

10	15	20	
ctc gag acg ctg agt tac gat tcg ctc gcc gag gcg acc ggt ctg tcc			211
Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu Ala Thr Gly Leu Ser			
25	30	35	
aag tcg ggc ttg att tat cat ttc ccc agc cgc cat gcg ctg ctt tta			259
Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg His Ala Leu Leu Leu			
40	45	50	
ggc atg cac gag ttg ctt gcc gac gac tgg gac aag gaa ttg cgc gac			307
Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp Lys Glu Leu Arg Asp			
55	60	65	
ata acc cgc gac cca gag gat cca ctt gag cga ttg cgc gcc gtc gtg			355
Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg Leu Arg Ala Val Val			
70	75	80	85
gtt acg ctt gct gaa aac gtt tcg cgc ccc gag ctg gtt ttg ctt atg			403
Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu Leu Val Leu Leu Met			
90	95	100	
gac gcc ccc tcc cac ccg gga ttt ctt aac gcc tgg cgc act gta aat			451
Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala Trp Arg Thr Val Asn			
105	110	115	
cat caa tgg atc ccc gac acc gat gat ctg gaa aac gat gcc cac aaa			499
His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu Asn Asp Ala His Lys			
120	125	130	
cgc gcc gtc tac tct ggt gca gct cgc agc cga tgg cct ctt cgt gca			547
Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg Trp Pro Leu Arg Ala			
135	140	145	
cga tta cat tca tgatgatgtc ctcagcaagt cca			582
Arg Leu His Ser			
150			

<210> 1342

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 1342

Met Arg Thr Ser Lys Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr			
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Ile Gly Glu Tyr Ser Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu			
20	25	30	
Ala Thr Gly Leu Ser Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg			
35	40	45	
His Ala Leu Leu Leu Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp			
50	55	60	
Lys Glu Leu Arg Asp Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg			
65	70	75	80
Leu Arg Ala Val Val Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu			

	85		90		95
Leu Val Leu Leu Met Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala					
	100		105		110
Trp Arg Thr Val Asn His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu					
	115		120		125
Asn Asp Ala His Lys Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg					
	130		135		140
Trp Pro Leu Arg Ala Arg Leu His Ser					
	145		150		

<210> 1343

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(643)

<223> RXN02914

<400> 1343

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caaaaaccgc cgtgatggcg tactgactgc cgtaggcatc	atg gtg gga aac tcc	115
	Met Val Gly Asn Ser	
	1 5	

atc tgg atc ata gcc agc ctc ctt ggg ctc tcg gca ctg atc tcc acg	163
Ile Trp Ile Ile Ala Ser Leu Leu Gly Leu Ser Ala Leu Ile Ser Thr	
	10 15 20

tat cca gca att ttg aac ctg ttg cag ctc gtc ggt ggc ggt tat ttg	211
Tyr Pro Ala Ile Leu Asn Leu Leu Gln Leu Val Gly Gly Gly Tyr Leu	
	25 30 35

acc tgg atg ggc atc ggg gcg gtg agg tca tgg tgg acg aaa cgc tcc	259
Thr Trp Met Gly Ile Gly Ala Val Arg Ser Trp Trp Thr Lys Arg Ser	
	40 45 50

aca cag caa gct gca gcg gat tct caa gct gta gag aat acg ttg gtg	307
Thr Gln Gln Ala Ala Ala Asp Ser Gln Ala Val Glu Asn Thr Leu Val	
	55 60 65

aca gcc acg gct gca tct gtc gga gtg tgg cca gct att cga tct ggc	355
Thr Ala Thr Ala Ala Ser Val Gly Val Trp Pro Ala Ile Arg Ser Gly	
	70 75 80 85

att gct acc aac ttg tcc aac ccc aaa gct gtg ctg ttt ttt ggt tcc	403
Ile Ala Thr Asn Leu Ser Asn Pro Lys Ala Val Leu Phe Phe Gly Ser	
	90 95 100

gtt ttc gcc caa ttt gtt aga cct gac atg gga atc ggg tgg agt att	451
Val Phe Ala Gln Phe Val Arg Pro Asp Met Gly Ile Gly Trp Ser Ile	
	105 110 115

ttc att gga gtc ttc ctc acc ctc act ggc ctg ctg tgg ttt gtg ggg	499
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Phe Ile Gly Val Phe Leu Thr Leu Thr Gly Leu Leu Trp Phe Val Gly
 120 125 130

ttc gcc gtc ttg gtc cgc aaa cta gcc gct ggc ctc acc cga aat gga 547
 Phe Ala Val Leu Val Arg Lys Leu Ala Ala Gly Leu Thr Arg Asn Gly
 135 140 145

gcc atc atc gac ctg cta acg ggg gtg att ttc atc ggg ctg gga atg 595
 Ala Ile Ile Asp Leu Leu Thr Gly Val Ile Phe Ile Gly Leu Gly Met
 150 155 160 165

ttc atg atc ttc gag ggg gtt gta gga atc ggt ggc agg gta gtg ggt 643
 Phe Met Ile Phe Glu Gly Val Val Gly Ile Gly Gly Arg Val Val Gly
 170 175 180

tagccccgcc cccaggacgt cac 666

<210> 1344
 <211> 181
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1344
 Met Val Gly Asn Ser Ile Trp Ile Ile Ala Ser Leu Leu Gly Leu Ser
 1 5 10 15

Ala Leu Ile Ser Thr Tyr Pro Ala Ile Leu Asn Leu Leu Gln Leu Val
 20 25 30

Gly Gly Gly Tyr Leu Thr Trp Met Gly Ile Gly Ala Val Arg Ser Trp
 35 40 45

Trp Thr Lys Arg Ser Thr Gln Gln Ala Ala Ala Asp Ser Gln Ala Val
 50 55 60

Glu Asn Thr Leu Val Thr Ala Thr Ala Ala Ser Val Gly Val Trp Pro
 65 70 75 80

Ala Ile Arg Ser Gly Ile Ala Thr Asn Leu Ser Asn Pro Lys Ala Val
 85 90 95

Leu Phe Phe Gly Ser Val Phe Ala Gln Phe Val Arg Pro Asp Met Gly
 100 105 110

Ile Gly Trp Ser Ile Phe Ile Gly Val Phe Leu Thr Leu Thr Gly Leu
 115 120 125

Leu Trp Phe Val Gly Phe Ala Val Leu Val Arg Lys Leu Ala Ala Gly
 130 135 140

Leu Thr Arg Asn Gly Ala Ile Ile Asp Leu Leu Thr Gly Val Ile Phe
 145 150 155 160

Ile Gly Leu Gly Met Phe Met Ile Phe Glu Gly Val Val Gly Ile Gly
 165 170 175

Gly Arg Val Val Gly
 180

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<210> 1346
<211> 157
<212> PRT
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<213> Corynebacterium glutamicum

<400> 1346

Val Ser Ala Leu Glu Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys
 1 5 10 15

Ala Ala Asp Glu Lys Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser
 20 25 30

Asp Met Ile Ala Ile Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn
 35 40 45

Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr
 50 55 60

Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
 65 70 75 80

Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
 85 90 95

Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
 100 105 110

Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp
 115 120 125

Ser Asp Glu Ala Asp Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro
 130 135 140

Pro Leu Pro Ala Glu Tyr Glu Pro Gly Tyr Glu Asp Asp
 145 150 155

<210> 1347

<211> 672

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(649)

<223> RXN02924

<400> 1347

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cggattgttg atcacgaaaa agcatgtcac agacaccttt gtg cct tct gta gca 115
 Val Pro Ser Val Ala
 1 5

tcc atc tca gag cgc gcc acg ttt att ctc acc gcc gat cac ttt ttg 163
 Ser Ile Ser Glu Arg Ala Thr Phe Ile Leu Thr Ala Asp His Phe Leu
 10 15 20

cgc agc tgc tgc aaa gta att tat gtc cgg ggc gaa aat ttc acc gcc 211
 Arg Ser Cys Ser Lys Val Ile Tyr Val Arg Gly Glu Asn Phe Thr Ala
 25 30 35

aca gca acc acc agc ctg tct gta ttt ggc aca gat ctg ggt ttg atc 259
 Thr Ala Thr Thr Ser Leu Ser Val Phe Gly Thr Asp Leu Gly Leu Ile

40	45	50	
aaa tta gac ggc aaa gcc ccc acc atg cca ctt cca ctt ttc gca gat			307
Lys Leu Asp Gly Lys Ala Pro Thr Met Pro Leu Pro Leu Phe Ala Asp			
55	60	65	
aag cca ctt cgc gtg ggc atg aaa acc acc acg ttc gga ttc ggc ggt			355
Lys Pro Leu Arg Val Gly Met Lys Thr Thr Thr Phe Gly Phe Gly Gly			
70	75	80	85
ctg cca tca gcc acc gtt gct aaa gaa atc cac ggg cgc gtt atc tct			403
Leu Pro Ser Ala Thr Val Ala Lys Glu Ile His Gly Arg Val Ile Ser			
90	95	100	
gcc atc ccc cat ggc gta tca aga aac cgc atc acc cga gtc cat cac			451
Ala Ile Pro His Gly Val Ser Arg Asn Arg Ile Thr Arg Val His His			
105	110	115	
ggt gcc ttg atc ttt aac tcc cca gaa aag gca gta aag gga gac tcc			499
Gly Ala Leu Ile Phe Asn Ser Pro Glu Lys Ala Val Lys Gly Asp Ser			
120	125	130	
ggc gga cct gtg ctg gtt aat gga cga gta gcc gga atc caa tca atg			547
Gly Gly Pro Val Leu Val Asn Gly Arg Val Ala Gly Ile Gln Ser Met			
135	140	145	
atc tct gac ccc ggt gga ttt aac acc ggg gtc gcc act gcc gca tcc			595
Ile Ser Asp Pro Gly Gly Phe Asn Thr Gly Val Ala Thr Ala Ala Ser			
150	155	160	165
ctt atc cag cac atg cct gcc cta gct caa gcg ctt gaa ctg ctc gaa			643
Leu Ile Gln His Met Pro Ala Leu Ala Gln Ala Leu Glu Leu Leu Glu			
170	175	180	
cat agc tagctcgcta ggaaccgatac gcc			672
His Ser			

<210> 1348

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 1348

Val	Pro	Ser	Val	Ala	Ser	Ile	Ser	Glu	Arg	Ala	Thr	Phe	Ile	Leu	Thr
1				5					10					15	

Ala	Asp	His	Phe	Leu	Arg	Ser	Cys	Ser	Lys	Val	Ile	Tyr	Val	Arg	Gly
		20						25					30		

Glu	Asn	Phe	Thr	Ala	Thr	Ala	Thr	Thr	Ser	Leu	Ser	Val	Phe	Gly	Thr
	35					40						45			

Asp	Leu	Gly	Leu	Ile	Lys	Leu	Asp	Gly	Lys	Ala	Pro	Thr	Met	Pro	Leu
	50					55					60				

Pro	Leu	Phe	Ala	Asp	Lys	Pro	Leu	Arg	Val	Gly	Met	Lys	Thr	Thr	Thr
	65				70					75				80	

Phe	Gly	Phe	Gly	Gly	Leu	Pro	Ser	Ala	Thr	Val	Ala	Lys	Glu	Ile	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

<400> 1349																
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ttgtctgcag tgggacagat tcgaagaaca gtggttctgc																
										gtg	gca	gac	gaa	ggt		115
										Val	Ala	Asp	Glu	Gly		
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 Val Leu Gly Gln Gly Gly His Val Val His Val Ala Val Ala Thr Gly
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 Cys Gln Asp Asn Gly Met Ala Gly Val Cys Gly Glu Leu Ala Gly Asp
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Gly Leu Ala Phe Ala Ala Pro Asp Ala Asp Glu Arg Glu Glu Arg Glu
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 Gln Leu Val Gly Leu Val Ser Val Gln Leu Arg Ser Ser Phe Ser Glu
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 Pro Ala Thr Glu Glu Ala Glu Asp Thr Glu Ala Glu Ser Pro Thr Thr
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 Pro Thr Gly Leu Pro Ala Ala Ala Ser Ile Ala Thr Leu Asp Asn
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 His Val
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Met Asn Leu His Ser
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tta gag att cgc caa att tca tcc ggc aca att tca gaa cga aaa act 163
Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile Ser Glu Arg Lys Thr
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Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn Gln Asn Leu Val His
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Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly Val Ile Leu Ala Met
40 45 50

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Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser Val Glu Tyr Pro Thr
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Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala Ile Ser Trp Pro Leu
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Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu Pro His Ser Ile Ser
90 95 100

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Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg Tyr Arg Ile Gly Asp
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390					395					400					405					
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Asn	Ala	Gly	Arg	Val	Glu	Asp	Leu	Tyr	Phe	Val	Gln	Phe	Trp	Gly	Met					
410					415					420										
acc	gtc	ttt	ttg	aat	tcc	aac	ttt	caa	gtg	caa	agt	gcc	gaa	gaa	cat	1411				
Thr	Val	Phe	Leu	Asn	Ser	Asn	Phe	Gln	Val	Gln	Ser	Ala	Glu	Glu	His					
425					430					435										

cag ctt ggt gcg aaa cgt gaa cgc tgg att aca caa gaa ggc gta gct 1459
 Gln Leu Gly Ala Lys Arg Glu Arg Trp Ile Thr Gln Glu Gly Val Ala
 440 445 450

gcc aag ttc acc gaa gaa gat gaa atc gta ttc ctc gat cag ata tct 1507
 Ala Lys Phe Thr Glu Glu Asp Glu Ile Val Phe Leu Asp Gln Ile Ser
 455 460 465

gaa agc gaa ata acc agg tgg aaa aca cca gaa gga tac ttc act gag 1555
 Glu Ser Glu Ile Thr Arg Trp Lys Thr Pro Glu Gly Tyr Phe Thr Glu
 470 475 480 485

gtc aga att ctg tca cca aac cac ttc aac ata ctg gtt act ccg cct 1603
 Val Arg Ile Leu Ser Pro Asn His Phe Asn Ile Leu Val Thr Pro Pro
 490 495 500

act ggt tct gac tat ctc aaa cca gta cct tcc tct gtc tca gtg ttt 1651
 Thr Gly Ser Asp Tyr Leu Lys Pro Val Pro Ser Ser Val Ser Val Phe
 505 510 515

aga gac ggt caa tgg agc aac att aaa ttc gag gac gtc tct gta gaa 1699
 Arg Asp Gly Gln Trp Ser Asn Ile Lys Phe Glu Asp Val Ser Val Glu
 520 525 530

atc tagggctttc gacgcttgag ccc 1725
 Ile

<210> 1362

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 1362

Met Asn Leu His Ser Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile
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 20 25 30

Gln Asn Leu Val His Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly
 35 40 45

Val Ile Leu Ala Met Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser
 50 55 60

Val Glu Tyr Pro Thr Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala
 65 70 75 80

Ile Ser Trp Pro Leu Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu
 85 90 95

Pro His Ser Ile Ser Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His
 100 105 110

Leu Arg Val Ser Ile Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg
 115 120 125

Tyr Arg Ile Gly Asp Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp

130	135	140
Thr Pro Phe Met Ser Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu 145 150 155 160		
Ala Ala Thr Glu Met Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr 165 170 175		
Gly Asp Gly Trp Thr Ala Leu Ser His Ser Asp Lys Pro Ile Arg His 180 185 190		
Glu Ala Glu Leu Lys Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu 195 200 205		
Met Pro Leu Thr Asp Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly 210 215 220		
Thr Phe Asp Ser Gly Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp 225 230 235 240		
Asp Ala Tyr Thr Glu Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp 245 250 255		
Ala Thr Leu Asp Gly Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe 260 265 270		
Glu Ala Ser Ile Thr His Ile Val Asp Glu Gln Leu Trp Val Leu Gly 275 280 285		
Gln Met Leu Pro Val Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr 290 295 300		
Leu Gly Gln Thr Tyr Val Pro Ile Ser Val Ser His Ser Ser Arg Leu 305 310 315 320		
Gln Phe Ser Glu Gly Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu 325 330 335		
Asn Pro Gly Val Arg Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro 340 345 350		
Val Ile Glu Leu Asp Val Pro Ala Pro Trp Glu Leu Gln Glu Ser Phe 355 360 365		
Pro Asp Gly Leu Tyr Ser Leu Thr Asp Gly Glu Gln Thr Ala Leu Gly 370 375 380		
Arg Ser Thr Pro Ala Gly Gln Leu Glu Ile Cys Val Ile Ser Asn Asp 385 390 395 400		
Gly Ser Arg Ile Leu Asn Ala Gly Arg Val Glu Asp Leu Tyr Phe Val 405 410 415		
Gln Phe Trp Gly Met Thr Val Phe Leu Asn Ser Asn Phe Gln Val Gln 420 425 430		
Ser Ala Glu Glu His Gln Leu Gly Ala Lys Arg Glu Arg Trp Ile Thr 435 440 445		
Gln Glu Gly Val Ala Ala Lys Phe Thr Glu Glu Asp Glu Ile Val Phe 450 455 460		

Leu Asp Gln Ile Ser Glu Ser Glu Ile Thr Arg Trp Lys Thr Pro Glu
 465 470 475 480

Gly Tyr Phe Thr Glu Val Arg Ile Leu Ser Pro Asn His Phe Asn Ile
 485 490 495

Leu Val Thr Pro Pro Thr Gly Ser Asp Tyr Leu Lys Pro Val Pro Ser
 500 505 510

Ser Val Ser Val Phe Arg Asp Gly Gln Trp Ser Asn Ile Lys Phe Glu
 515 520 525

Asp Val Ser Val Glu Ile
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<210> 1363

<211> 1243

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1243)

<223> FRXA01383

<400> 1363

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cttagacaac ttcataaatc cccttgagat gattgagata atg aat ctc cac tcc 115
 Met Asn Leu His Ser
 1 5

tta gag att cgc caa att tca tcc ggc aca att tca gaa cga aaa act 163
 Leu Glu Ile Arg Gln Ile Ser Ser Gly Thr Ile Ser Glu Arg Lys Thr
 10 15 20

tgg atc ttt ccc act gct gct cgc tca ttc aat caa aat cta gta cac 211
 Trp Ile Phe Pro Thr Ala Ala Arg Ser Phe Asn Gln Asn Leu Val His
 25 30 35

ccg caa agc att gaa atc gat gca caa acc ggc gtt att ttg gct atg 259
 Pro Gln Ser Ile Glu Ile Asp Ala Gln Thr Gly Val Ile Leu Ala Met
 40 45 50

gaa aac cga cta caa cgt acc gaa gtt gaa tca gta gag tac cca acg 307
 Glu Asn Arg Leu Gln Arg Thr Glu Val Glu Ser Val Glu Tyr Pro Thr
 55 60 65

gat ctt cct aat cct gca tgg aca ggt cca gcc att tct tgg cca cta 355
 Asp Leu Pro Asn Pro Ala Trp Thr Gly Pro Ala Ile Ser Trp Pro Leu
 70 75 80 85

aaa gac cca tca atc gat ttc cct gac ccg ctc ccc cac agc att tcc 403
 Lys Asp Pro Ser Ile Asp Phe Pro Asp Pro Leu Pro His Ser Ile Ser
 90 95 100

gaa tta cca cct caa tcc gat aat cct cgg cat ttg cga gta tcc atc 451
 Glu Leu Pro Pro Gln Ser Asp Asn Pro Arg His Leu Arg Val Ser Ile
 105 110 115

agc tta gat gca gtg gaa ggt gct ttt ccg cgc tac cgg atc gga gat	499
Ser Leu Asp Ala Val Glu Gly Ala Phe Pro Arg Tyr Arg Ile Gly Asp	
120 125 130	
tca ata cgt att ccg ctt gtc ttt gcc cgg gac acg ccc ttc atg tcc	547
Ser Ile Arg Ile Pro Leu Val Phe Ala Arg Asp Thr Pro Phe Met Ser	
135 140 145	
ggc tta gaa aca aca cgt cgc gcc tgg att gag gcg gcc acg gaa atg	595
Gly Leu Glu Thr Thr Arg Arg Ala Trp Ile Glu Ala Ala Thr Glu Met	
150 155 160 165	
gac atc cat aac aca tgg ccc ata atc ctc acc ggt gac ggc tgg act	643
Asp Ile His Asn Thr Trp Pro Ile Ile Leu Thr Gly Asp Gly Trp Thr	
170 175 180	
gca ctc tct cat tca gac aaa cca ata cgc cac gaa gcc gag tta aag	691
Ala Leu Ser His Ser Asp Lys Pro Ile Arg His Glu Ala Glu Leu Lys	
185 190 195	
gga tgg ttt ttc cac agt ttg ttc ggc agt gaa atg ccc ttg act gat	739
Gly Trp Phe Phe His Ser Leu Phe Gly Ser Glu Met Pro Leu Thr Asp	
200 205 210	
ctg aag att gaa cga atc tac gga ggc ctg ggt act ttc gac agc gga	787
Leu Lys Ile Glu Arg Ile Tyr Gly Gly Leu Gly Thr Phe Asp Ser Gly	
215 220 225	
gcc acc cgg tgg caa gaa ctc aca gac aca gat gat gcc tac aca gaa	835
Ala Thr Arg Trp Gln Glu Leu Thr Asp Thr Asp Asp Ala Tyr Thr Glu	
230 235 240 245	
aat ggc agc tgg ctg ttg gaa gtt atc gtc gat gcc acc ctt gac ggt	883
Asn Gly Ser Trp Leu Leu Glu Val Ile Val Asp Ala Thr Leu Asp Gly	
250 255 260	
gca att cca cca cca ctt cag cca caa cag ttt gaa gca tcc atc act	931
Ala Ile Pro Pro Pro Leu Gln Pro Gln Gln Phe Glu Ala Ser Ile Thr	
265 270 275	
cac atc gtc gat gag caa cta tgg gtc ctt ggg cag atg ctt cca gtt	979
His Ile Val Asp Glu Gln Leu Trp Val Leu Gly Gln Met Leu Pro Val	
280 285 290	
cta cga tgc tgg gat ctt gaa acc gga aaa tac ctg ggg caa acc tat	1027
Leu Arg Cys Trp Asp Leu Glu Thr Gly Lys Tyr Leu Gly Gln Thr Tyr	
295 300 305	
gta cct att tcg gtt tct cat agt tct cgg ctt cag ttt tcg gaa ggg	1075
Val Pro Ile Ser Val Ser His Ser Ser Arg Leu Gln Phe Ser Glu Gly	
310 315 320 325	
ttg att cac gat tat gaa aat gcc tgg tcg ctg aat cct ggg gtg cgc	1123
Leu Ile His Asp Tyr Glu Asn Ala Trp Ser Leu Asn Pro Gly Val Arg	
330 335 340	
atg ctt gcg gag cca cag ccg tgg ata gag cct gtc att gaa ctc gac	1171
Met Leu Ala Glu Pro Gln Pro Trp Ile Glu Pro Val Ile Glu Leu Asp	
345 350 355	

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ttc cta act gat ggc aag caa aca
Phe Leu Thr Asp Gly Lys Gln Thr
      375                380

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			20					25					30		
Gln	Asn	Leu	Val	His	Pro	Gln	Ser	Ile	Glu	Ile	Asp	Ala	Gln	Thr	Gly
		35					40					45			
Val	Ile	Leu	Ala	Met	Glu	Asn	Arg	Leu	Gln	Arg	Thr	Glu	Val	Glu	Ser
	50					55					60				
Val	Glu	Tyr	Pro	Thr	Asp	Leu	Pro	Asn	Pro	Ala	Trp	Thr	Gly	Pro	Ala
65					70					75					80
Ile	Ser	Trp	Pro	Leu	Lys	Asp	Pro	Ser	Ile	Asp	Phe	Pro	Asp	Pro	Leu
				85					90					95	
Pro	His	Ser	Ile	Ser	Glu	Leu	Pro	Pro	Gln	Ser	Asp	Asn	Pro	Arg	His
			100					105					110		
Leu	Arg	Val	Ser	Ile	Ser	Leu	Asp	Ala	Val	Glu	Gly	Ala	Phe	Pro	Arg
		115					120					125			
Tyr	Arg	Ile	Gly	Asp	Ser	Ile	Arg	Ile	Pro	Leu	Val	Phe	Ala	Arg	Asp
	130					135					140				
Thr	Pro	Phe	Met	Ser	Gly	Leu	Glu	Thr	Thr	Arg	Arg	Ala	Trp	Ile	Glu
145					150					155					160
Ala	Ala	Thr	Glu	Met	Asp	Ile	His	Asn	Thr	Trp	Pro	Ile	Ile	Leu	Thr
				165					170					175	
Gly	Asp	Gly	Trp	Thr	Ala	Leu	Ser	His	Ser	Asp	Lys	Pro	Ile	Arg	His
			180					185					190		
Glu	Ala	Glu	Leu	Lys	Gly	Trp	Phe	Phe	His	Ser	Leu	Phe	Gly	Ser	Glu
		195					200					205			
Met	Pro	Leu	Thr	Asp	Leu	Lys	Ile	Glu	Arg	Ile	Tyr	Gly	Gly	Leu	Gly
	210					215					220				
Thr	Phe	Asp	Ser	Gly	Ala	Thr	Arg	Trp	Gln	Glu	Leu	Thr	Asp	Thr	Asp
225					230					235					240
Asp	Ala	Tyr	Thr	Glu	Asn	Gly	Ser	Trp	Leu	Leu	Glu	Val	Ile	Val	Asp

245	250	255
Ala Thr Leu Asp Gly Ala Ile Pro	Pro Pro Leu Gln Pro	Gln Gln Phe
260	265	270
Glu Ala Ser Ile Thr His Ile Val	Asp Glu Gln Leu Trp	Val Leu Gly
275	280	285
Gln Met Leu Pro Val Leu Arg Cys	Trp Asp Leu Glu Thr	Gly Lys Tyr
290	295	300
Leu Gly Gln Thr Tyr Val Pro Ile	Ser Val Ser His Ser	Ser Arg Leu
305	310	315
Gln Phe Ser Glu Gly Leu Ile His	Asp Tyr Glu Asn Ala	Trp Ser Leu
325	330	335
Asn Pro Gly Val Arg Met Leu Ala	Glu Pro Gln Pro Trp	Ile Glu Pro
340	345	350
Val Ile Glu Leu Asp Val Pro Ala	Pro Trp Glu Leu Gln	Glu Ser Phe
355	360	365
Pro Asp Gly Leu Tyr Phe Leu Thr	Asp Gly Lys Gln Thr	
370	375	380

<210> 1365

<211> 447

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> RXN02950

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acctatcttt agtgagccgt actagcgaga aagctgcccc	atg act gtt ttc aat	115
	Met Thr Val Phe Asn	
	1 5	

gtt ctc cat gac gca ccc gca cca cag ccg gat aaa aac cgc ccc ggt	163
Val Leu His Asp Ala Pro Ala Pro Gln Pro Asp Lys Asn Arg Pro Gly	
10 15 20	

gtc aaa cgt ctc ctc caa ggt gat ggc gca aac ctc atc gcc ttc act	211
Val Lys Arg Leu Leu Gln Gly Asp Gly Ala Asn Leu Ile Ala Phe Thr	
25 30 35	

ttc agc cct gga cag tca ctt ccc gac cac cgc gcc gca cat ccc atc	259
Phe Ser Pro Gly Gln Ser Leu Pro Asp His Arg Ala Ala His Pro Ile	
40 45 50	

acc gtg acc gca ttt tct ggc cag ctc acc ttc agc tat ggc gag gaa	307
Thr Val Thr Ala Phe Ser Gly Gln Leu Thr Phe Ser Tyr Gly Glu Glu	
55 60 65	

acc ttt gag ctc tcc ccc ggt gtg aca gtg cac ttg gaa gca gga gtt	355
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Thr Phe Glu Leu Ser Pro Gly Val Thr Val His Leu Glu Ala Gly Val
 70 75 80 85

acc cac cgc gtg gac tgc ccg cca gaa gca cca ggc gat gca agt aat 403
 Thr His Arg Val Asp Cys Pro Pro Glu Ala Pro Gly Asp Ala Ser Asn
 90 95 100

gct gtt aac tat gct cac tgg tgaaaaaacac tcagtcaacc agg 447
 Ala Val Asn Tyr Ala His Trp
 105

<210> 1366

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1366

Met Thr Val Phe Asn Val Leu His Asp Ala Pro Ala Pro Gln Pro Asp
 1 5 10 15

Lys Asn Arg Pro Gly Val Lys Arg Leu Leu Gln Gly Asp Gly Ala Asn
 20 25 30

Leu Ile Ala Phe Thr Phe Ser Pro Gly Gln Ser Leu Pro Asp His Arg
 35 40 45

Ala Ala His Pro Ile Thr Val Thr Ala Phe Ser Gly Gln Leu Thr Phe
 50 55 60

Ser Tyr Gly Glu Glu Thr Phe Glu Leu Ser Pro Gly Val Thr Val His
 65 70 75 80

Leu Glu Ala Gly Val Thr His Arg Val Asp Cys Pro Pro Glu Ala Pro
 85 90 95

Gly Asp Ala Ser Asn Ala Val Asn Tyr Ala His Trp
 100 105

<210> 1367

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(709)

<223> RXN02951

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tcagaaatta atccatagcc gatatttaag gtgagaacac atg agc tcc acg ctc 115
 Met Ser Ser Thr Leu
 1 5

gca cga aaa gct tca ggc gac ggt tcc gaa aag aag aag cct ggc ttg 163
 Ala Arg Lys Ala Ser Gly Asp Gly Ser Glu Lys Lys Lys Pro Gly Leu
 10 15 20

ttt aga cgt gcg ctt cgt ttc ctc acc cac cca cct cac aaa cag gta 211
 Phe Arg Arg Ala Leu Arg Phe Leu Thr His Pro Pro His Lys Gln Val
 25 30 35

gac aac agc ctt gcg gat atc cgt gaa gga tta ggc ctc ggg gtg gac 259
 Asp Asn Ser Leu Ala Asp Ile Arg Glu Gly Leu Gly Leu Gly Val Asp
 40 45 50

gat tcc cac gaa gga tcc aaa ccc agc aac gat cat tct ttg ctg cat 307
 Asp Ser His Glu Gly Ser Lys Pro Ser Asn Asp His Ser Leu Leu His
 55 60 65

gaa aag cct gaa att tcc gtc atg ccg acc gaa tca atg gca cgg ctg 355
 Glu Lys Pro Glu Ile Ser Val Met Pro Thr Glu Ser Met Ala Arg Leu
 70 75 80 85

atc ttt tat gcg cct gat atg gat ggg caa aca gac ccc ggt gaa gta 403
 Ile Phe Tyr Ala Pro Asp Met Asp Gly Gln Thr Asp Pro Gly Glu Val
 90 95 100

gtg tgg att tgg gca cca gcc gat ggc ccc cag caa cca ccc cgt aaa 451
 Val Trp Ile Trp Ala Pro Ala Asp Gly Pro Gln Gln Pro Pro Arg Lys
 105 110 115

cgt gcc atc gtt gtt gtt gga aga aac cga aac gcc att tta ggt ctg 499
 Arg Ala Ile Val Val Val Gly Arg Asn Arg Asn Ala Ile Leu Gly Leu
 120 125 130

ctc att tcc tgc aac ccc gag cac cgc act gat gaa gac tgg atc gac 547
 Leu Ile Ser Cys Asn Pro Glu His Arg Thr Asp Glu Asp Trp Ile Asp
 135 140 145

att gga tct ggc agc tgg gac cct cga ggt cgc caa agt tgg gta cga 595
 Ile Gly Ser Gly Ser Trp Asp Pro Arg Gly Arg Gln Ser Trp Val Arg
 150 155 160 165

ctc gac cgc gtt ctg gag gta ccc gaa ttg ggt atc cgg cgc caa gga 643
 Leu Asp Arg Val Leu Glu Val Pro Glu Leu Gly Ile Arg Arg Gln Gly
 170 175 180

aca gtc gtc ccc ccg ggg cgc ttt gag cgt atc gcc aac cgc ctc cgc 691
 Thr Val Val Pro Pro Gly Arg Phe Glu Arg Ile Ala Asn Arg Leu Arg
 185 190 195

aac gat ttc aac tgg gtc taacatttat ttggtattg ggc 732
 Asn Asp Phe Asn Trp Val
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<210> 1368

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 1368

Met Ser Ser Thr Leu Ala Arg Lys Ala Ser Gly Asp Gly Ser Glu Lys
 1 5 10 15

Lys Lys Pro Gly Leu Phe Arg Arg Ala Leu Arg Phe Leu Thr His Pro
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<210> 1369
<211> 414
<212> DNA
<213> Corynebacterium glutamicum
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						Met	Gln	Thr	Ala	Gln							
						1				5							
gga gga agg gtc tac acc tca ctg atg gac gag aag tcc ctt tcc ccg																163	
Gly	Gly	Arg	Val	Tyr	Thr	Ser	Leu	Met	Asp	Glu	Lys	Ser	Leu	Ser	Pro		
				10					15					20			
ttg atc ggt ctg ccg ggt cgg gag aac atc ggc ctg ggc cga cac tgg																211	
Leu	Ile	Gly	Leu	Pro	Gly	Arg	Glu	Asn	Ile	Gly	Leu	Gly	Arg	His	Trp		
			25					30					35				
cac ggt ctg tcg acg atg ttg cgg gtg ctc aac ggc atc gtc tac gtc																259	
His	Gly	Leu	Ser	Thr	Met	Leu	Arg	Val	Leu	Asn	Gly	Ile	Val	Tyr	Val		

40	45	50	
gtt ctg ctg ttc gcc acc ggg ctg tgg caa ggc att atc ccc acc tcc			307
Val Leu Leu Phe Ala Thr Gly Leu Trp Gln Gly Ile Ile Pro Thr Ser			
55	60	65	
tgg gac gtc ttc ccc gag gcg tgg gag aca ttg aag gtt tac ctg ggc			355
Trp Asp Val Phe Pro Glu Ala Trp Glu Thr Leu Lys Val Tyr Leu Gly			
70	75	80	85
ttt cgt gcc cca ggc atc gag cac ttc acc ccc cta tgacgccttg			401
Phe Arg Ala Pro Gly Ile Glu His Phe Thr Pro Leu			
90	95		
caaatgctgg gct			414

<210> 1370

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 1370

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Lys	Ser	Leu	Ser	Pro	Leu	Ile	Gly	Leu	Pro	Gly	Arg	Glu	Asn	Ile	Gly
			20					25					30		

Leu	Gly	Arg	His	Trp	His	Gly	Leu	Ser	Thr	Met	Leu	Arg	Val	Leu	Asn
		35					40					45			

Gly	Ile	Val	Tyr	Val	Val	Leu	Leu	Phe	Ala	Thr	Gly	Leu	Trp	Gln	Gly
50						55					60				

Ile	Ile	Pro	Thr	Ser	Trp	Asp	Val	Phe	Pro	Glu	Ala	Trp	Glu	Thr	Leu
65					70					75					80

Lys	Val	Tyr	Leu	Gly	Phe	Arg	Ala	Pro	Gly	Ile	Glu	His	Phe	Thr	Pro
				85					90					95	

Leu

<210> 1371

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXN02967

<400> 1371

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				Met	Asp	Leu	Leu	Val		
				1				5		

gtt gcc gtg cat gag ggt gga cag cca cgt cag tcc gat tgc aat gcc 163
 Val Ala Val His Glu Gly Gly Gln Pro Arg Gln Ser Asp Cys Asn Ala
 10 15 20

ccc ggc tgc gcc cat acc tgg ctt tgt gcc atc aac ttc cag ttg ggc 211
 Pro Gly Cys Ala His Thr Trp Leu Cys Ala Ile Asn Phe Gln Leu Gly
 25 30 35

gca ggc gtg gtg gag ggc ggc gtc gag aag cga aat gtc ttt ttc ggt 259
 Ala Gly Val Val Glu Gly Gly Val Glu Lys Arg Asn Val Phe Phe Gly
 40 45 50

ggc acc ttt ttg ggg ccc gaa tac ggt ggc cgc gcc ctg cgg gcc ggt 307
 Gly Thr Phe Leu Gly Pro Glu Tyr Gly Gly Arg Ala Leu Arg Ala Gly
 55 60 65

ggc ggg ggc gtc gac atc ggt gag cag gat cca ttc gac ggc ggc tgc 355
 Gly Gly Gly Val Asp Ile Gly Glu Gln Asp Pro Phe Asp Gly Gly Cys
 70 75 80 85

ggg gat gtt gag ttc ggc ggt atc gat gta atc gag gtt gat gag gtc 403
 Gly Asp Val Glu Phe Gly Gly Ile Asp Val Ile Glu Val Asp Glu Val
 90 95 100

ggc gcc acc ggt tcg tagtgcgtag ccctctttgt tgc 441
 Gly Ala Thr Gly Ser
 105

<210> 1372

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1372

Met Asp Leu Leu Val Val Ala Val His Glu Gly Gly Gln Pro Arg Gln
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Ser Asp Cys Asn Ala Pro Gly Cys Ala His Thr Trp Leu Cys Ala Ile
 20 25 30

Asn Phe Gln Leu Gly Ala Gly Val Val Glu Gly Gly Val Glu Lys Arg
 35 40 45

Asn Val Phe Phe Gly Gly Thr Phe Leu Gly Pro Glu Tyr Gly Gly Arg
 50 55 60

Ala Leu Arg Ala Gly Gly Gly Gly Val Asp Ile Gly Glu Gln Asp Pro
 65 70 75 80

Phe Asp Gly Gly Cys Gly Asp Val Glu Phe Gly Gly Ile Asp Val Ile
 85 90 95

Glu Val Asp Glu Val Gly Ala Thr Gly Ser
 100 105

<210> 1373

<211> 435

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(412)

<223> RXN02971

<400> 1373

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gaattcaaac	ttaaggttat	ctaaatcgct	aaccattg	cg	ttg	att	gcc	atc	gtc	115
					Leu	Ile	Ala	Ile	Val	
					1				5	

gct	ctc	atc	gtg	gca	ctt	gtg	gtg	tgg	ctt	ttt	aac	cgt	tca	gat	gat	163
Ala	Leu	Ile	Val	Ala	Leu	Val	Val	Trp	Leu	Phe	Asn	Arg	Ser	Asp	Asp	
			10					15						20		

tct	ggc	tcc	acc	acg	acc	acc	tca	caa	gag	tgc	atc	tcc	gga	aac	ttg	211
Ser	Gly	Ser	Thr	Thr	Thr	Thr	Ser	Gln	Glu	Cys	Ile	Ser	Gly	Asn	Leu	
			25					30					35			

agt	ctg	ccc	gtt	ggg	ggc	gat	tcc	acc	gca	gcc	gaa	gaa	tta	gtg	aac	259
Ser	Leu	Pro	Val	Gly	Gly	Asp	Ser	Thr	Ala	Ala	Glu	Glu	Leu	Val	Asn	
		40					45					50				

aaa	ttt	aat	gac	tca	tca	cct	gtc	agc	cgt	gat	ttc	tgt	gtt	gag	gcg	307
Lys	Phe	Asn	Asp	Ser	Ser	Pro	Val	Ser	Arg	Asp	Phe	Cys	Val	Glu	Ala	
	55					60					65					

gaa	gct	gtg	gac	ggg	aac	gtc	ccc	gct	gcc	acg	tac	ctg	ttc	gct	ggg	355
Glu	Ala	Val	Asp	Gly	Asn	Val	Pro	Ala	Ala	Thr	Tyr	Leu	Phe	Ala	Gly	
	70				75				80						85	

tct	cgt	tct	gat	gct	gcc	acc	gca	ctt	gct	gaa	acc	ggg	gcc	gta	gca	403
Ser	Arg	Ser	Asp	Ala	Ala	Thr	Ala	Leu	Ala	Glu	Thr	Gly	Ala	Val	Ala	
			90					95						100		

agc	agc	tct	taaagctctt	ggccctaggt	tgg	435
Ser	Ser	Ser				

<210> 1374

<211> 104

<212> PRT

<213> Corynebacterium glutamicum

<400> 1374

Leu	Ile	Ala	Ile	Val	Ala	Leu	Ile	Val	Ala	Leu	Val	Val	Trp	Leu	Phe
1				5					10					15	

Asn	Arg	Ser	Asp	Asp	Ser	Gly	Ser	Thr	Thr	Thr	Thr	Ser	Gln	Glu	Cys
			20					25					30		

Ile	Ser	Gly	Asn	Leu	Ser	Leu	Pro	Val	Gly	Gly	Asp	Ser	Thr	Ala	Ala
		35					40					45			

Glu	Glu	Leu	Val	Asn	Lys	Phe	Asn	Asp	Ser	Ser	Pro	Val	Ser	Arg	Asp
		50				55					60				

Phe Cys Val Glu Ala Glu Ala Val Asp Gly Asn Val Pro Ala Ala Thr
 65 70 75 80

Tyr Leu Phe Ala Gly Ser Arg Ser Asp Ala Ala Thr Ala Leu Ala Glu
 85 90 95

Thr Gly Ala Val Ala Ser Ser Ser
 100

<210> 1375

<211> 1632

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1609)

<223> RXN02978

<400> 1375

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gaacgctcga tagggctgtg tacctcaacg gaggtaaaac gtg att gat cga cct 115
 Val Ile Asp Arg Pro
 1 5

gta tgg ttg ttt gaa ctt tat aac acc gcg aaa gaa gta gta tat tcg 163
 Val Trp Leu Phe Glu Leu Tyr Asn Thr Ala Lys Glu Val Val Tyr Ser
 10 15 20

cta ctc att gat caa gta act ggg gaa aat aca ata ctc aag aag gat 211
 Leu Leu Ile Asp Gln Val Thr Gly Glu Asn Thr Ile Leu Lys Lys Asp
 25 30 35

gat ggt tgg cga gat caa ttc atg att gag tct ttc ttt gct tat gat 259
 Asp Gly Trp Arg Asp Gln Phe Met Ile Glu Ser Phe Phe Ala Tyr Asp
 40 45 50

tca gaa gct gac gcg acc tcg tgg agc ggt aag aac atg aat agc tac 307
 Ser Glu Ala Asp Ala Thr Ser Trp Ser Gly Lys Asn Met Asn Ser Tyr
 55 60 65

tgg ttc gtt agc gat cta atc agc aat ata tcc ttc gct gag cga tcc 355
 Trp Phe Val Ser Asp Leu Ile Ser Asn Ile Ser Phe Ala Glu Arg Ser
 70 75 80 85

ttg gaa agc ttt tct tgg gct ctt cga gat ctt gag gat ctt tct tct 403
 Leu Glu Ser Phe Ser Trp Ala Leu Arg Asp Leu Glu Asp Leu Ser Ser
 90 95 100

agt gaa act gaa ttt gaa ggg ctt gaa gag ctg aat cta aag ttt agt 451
 Ser Glu Thr Glu Phe Glu Gly Leu Glu Glu Leu Asn Leu Lys Phe Ser
 105 110 115

gag ctc caa gaa tgg tat acg aac ctg gaa ctt cct ttt cag ccg tcg 499
 Glu Leu Gln Glu Trp Tyr Thr Asn Leu Glu Leu Pro Phe Gln Pro Ser
 120 125 130

gct gct gat gtt gat gag gtg gag cag tat ctg caa gct gaa gtg aca 547
 Ala Ala Asp Val Asp Glu Val Glu Gln Tyr Leu Gln Ala Glu Val Thr

135	140	145	
agg caa cgg ggt gac tat caa tgg tct cct gag ttt tgg ata cca aag			595
Arg Gln Arg Gly Asp Tyr Gln Trp Ser Pro Glu Phe Trp Ile Pro Lys			
150	155	160	165
ccg gat tca tac tat atc gac cat gca cta gcg gtt gtc aca gat gtt			643
Pro Asp Ser Tyr Tyr Ile Asp His Ala Leu Ala Val Val Thr Asp Val			
	170	175	180
ttg gga gct att gaa caa ggg gag ctg cgt gaa gaa gta gag gtg cag			691
Leu Gly Ala Ile Glu Gln Gly Glu Leu Arg Glu Glu Val Glu Val Gln			
	185	190	195
cag gct tta gac gag gta tct gaa aat tgg aat cct ttg gaa gat tct			739
Gln Ala Leu Asp Glu Val Ser Glu Asn Trp Asn Pro Leu Glu Asp Ser			
	200	205	210
gat tac tac tta cag gat cac cgt ggg cgc cct gta caa gat ctt tcc			787
Asp Tyr Tyr Leu Gln Asp His Arg Gly Arg Pro Val Gln Asp Leu Ser			
	215	220	225
cgg gaa atg gag gag ttg gtc aga tgt cta atg ctt gac caa gag tgg			835
Arg Glu Met Glu Glu Leu Val Arg Cys Leu Met Leu Asp Gln Glu Trp			
	230	235	240
ttg ggt gca gag gca agg att aga aag ctt gtt gaa tca gtt gag tgg			883
Trp Gly Ala Glu Ala Arg Ile Arg Lys Leu Val Glu Ser Val Glu Trp			
	250	255	260
gag gat act cag gcg atc agc tct tta att gaa cac gag caa tat tgg			931
Glu Asp Thr Gln Ala Ile Ser Ser Leu Ile Glu His Glu Gln Tyr Trp			
	265	270	275
gag gat ggt cgt ttt cgc cca cct cta cat aag ttt tgc gaa gga cta			979
Glu Asp Gly Arg Phe Arg Pro Pro Leu His Lys Phe Ser Glu Gly Leu			
	280	285	290
gac gag cca gag ccc ttg ccg atg acg aga aaa atg ata ctt gcg acg			1027
Asp Glu Pro Glu Pro Leu Pro Met Thr Arg Lys Met Ile Leu Ala Thr			
	295	300	305
aat cac cct gat gtt tta cgc gta aac att gct gat tat tat cag cag			1075
Asn His Pro Asp Val Leu Arg Val Asn Ile Ala Asp Tyr Tyr Gln Gln			
	310	315	320
cat agg cgc att gct act cag aag gtg gaa tgt tat aag gaa gtt ttg			1123
His Arg Arg Ile Ala Thr Gln Lys Val Glu Cys Tyr Lys Glu Val Leu			
	330	335	340
gca ttg tat cca gag att ctt aag aaa ttt gat gat tca tct ttc gtc			1171
Ala Leu Tyr Pro Glu Ile Leu Lys Lys Phe Asp Asp Ser Ser Phe Val			
	345	350	355
aat cga cat tgg atc tat agg gcg ttt gat cgc gaa ggt cag ctt ttg			1219
Asn Arg His Trp Ile Tyr Arg Ala Phe Asp Arg Glu Gly Gln Leu Leu			
	360	365	370
tat atc ggg gag aca ata aac cct ctt gta cgg ttg agg gag cat gcc			1267
Tyr Ile Gly Glu Thr Ile Asn Pro Leu Val Arg Leu Arg Glu His Ala			
	375	380	385

ggc tta ggg tct att aac cac gca cat cat agg cta gta tcg ccg tgg 1315
 Gly Leu Gly Ser Ile Asn His Ala His His Arg Leu Val Ser Pro Trp
 390 395 400 405
 ttt tct acg atg gct aca ttt cat ctt gaa tct tgc ttt acc cag gct 1363
 Phe Ser Thr Met Ala Thr Phe His Leu Glu Ser Cys Phe Thr Gln Ala
 410 415 420
 gag gca aaa gag aag gag gct tta tat att aag ctg gaa cag cca aga 1411
 Glu Ala Lys Glu Lys Glu Ala Leu Tyr Ile Lys Leu Glu Gln Pro Arg
 425 430 435
 tat aat aag acg cat aat tct gct aga ttg gcg gtt tct gaa gaa ggg 1459
 Tyr Asn Lys Thr His Asn Ser Ala Arg Leu Ala Val Ser Glu Glu Gly
 440 445 450
 gtg ccg gtg aac gag gtg ccg tca aga aat gat ccg agg aat gtc ggt 1507
 Val Pro Val Asn Glu Val Pro Ser Arg Asn Asp Pro Arg Asn Val Gly
 455 460 465
 tgg aag ggt cat agg cac gtg cca cca atg ttg ccg att gtt gca cgt 1555
 Trp Lys Gly His Arg His Val Pro Pro Met Leu Pro Ile Val Ala Arg
 470 475 480 485
 gtt gtc gat gaa tcg aca aca cgt gag gga tat gcg ttt tac gag gac 1603
 Val Val Asp Glu Ser Thr Thr Arg Glu Gly Tyr Ala Phe Tyr Glu Asp
 490 495 500
 aac cgg tagcgttgcg atctctcgtg gaa 1632
 Asn Arg

<210> 1376

<211> 503

<212> PRT

<213> Corynebacterium glutamicum

<400> 1376

Val Ile Asp Arg Pro Val Trp Leu Phe Glu Leu Tyr Asn Thr Ala Lys
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Glu Val Val Tyr Ser Leu Leu Ile Asp Gln Val Thr Gly Glu Asn Thr
 20 25 30

Ile Leu Lys Lys Asp Asp Gly Trp Arg Asp Gln Phe Met Ile Glu Ser
 35 40 45

Phe Phe Ala Tyr Asp Ser Glu Ala Asp Ala Thr Ser Trp Ser Gly Lys
 50 55 60

Asn Met Asn Ser Tyr Trp Phe Val Ser Asp Leu Ile Ser Asn Ile Ser
 65 70 75 80

Phe Ala Glu Arg Ser Leu Glu Ser Phe Ser Trp Ala Leu Arg Asp Leu
 85 90 95

Glu Asp Leu Ser Ser Glu Thr Glu Phe Glu Gly Leu Glu Glu Leu
 100 105 110

Asn Leu Lys Phe Ser Glu Leu Gln Glu Trp Tyr Thr Asn Leu Glu Leu
 115 120 125
 Pro Phe Gln Pro Ser Ala Ala Asp Val Asp Glu Val Glu Gln Tyr Leu
 130 135 140
 Gln Ala Glu Val Thr Arg Gln Arg Gly Asp Tyr Gln Trp Ser Pro Glu
 145 150 155 160
 Phe Trp Ile Pro Lys Pro Asp Ser Tyr Tyr Ile Asp His Ala Leu Ala
 165 170 175
 Val Val Thr Asp Val Leu Gly Ala Ile Glu Gln Gly Glu Leu Arg Glu
 180 185 190
 Glu Val Glu Val Gln Gln Ala Leu Asp Glu Val Ser Glu Asn Trp Asn
 195 200 205
 Pro Leu Glu Asp Ser Asp Tyr Tyr Leu Gln Asp His Arg Gly Arg Pro
 210 215 220
 Val Gln Asp Leu Ser Arg Glu Met Glu Glu Leu Val Arg Cys Leu Met
 225 230 235 240
 Leu Asp Gln Glu Trp Trp Gly Ala Glu Ala Arg Ile Arg Lys Leu Val
 245 250 255
 Glu Ser Val Glu Trp Glu Asp Thr Gln Ala Ile Ser Ser Leu Ile Glu
 260 265 270
 His Glu Gln Tyr Trp Glu Asp Gly Arg Phe Arg Pro Pro Leu His Lys
 275 280 285
 Phe Ser Glu Gly Leu Asp Glu Pro Glu Pro Leu Pro Met Thr Arg Lys
 290 295 300
 Met Ile Leu Ala Thr Asn His Pro Asp Val Leu Arg Val Asn Ile Ala
 305 310 315 320
 Asp Tyr Tyr Gln Gln His Arg Arg Ile Ala Thr Gln Lys Val Glu Cys
 325 330 335
 Tyr Lys Glu Val Leu Ala Leu Tyr Pro Glu Ile Leu Lys Lys Phe Asp
 340 345 350
 Asp Ser Ser Phe Val Asn Arg His Trp Ile Tyr Arg Ala Phe Asp Arg
 355 360 365
 Glu Gly Gln Leu Leu Tyr Ile Gly Glu Thr Ile Asn Pro Leu Val Arg
 370 375 380
 Leu Arg Glu His Ala Gly Leu Gly Ser Ile Asn His Ala His His Arg
 385 390 395 400
 Leu Val Ser Pro Trp Phe Ser Thr Met Ala Thr Phe His Leu Glu Ser
 405 410 415
 Cys Phe Thr Gln Ala Glu Ala Lys Glu Lys Glu Ala Leu Tyr Ile Lys
 420 425 430
 Leu Glu Gln Pro Arg Tyr Asn Lys Thr His Asn Ser Ala Arg Leu Ala

435	440	445
Val Ser Glu Glu Gly Val	Pro Val Asn Glu Val	Pro Ser Arg Asn Asp
450	455	460
Pro Arg Asn Val Gly Trp Lys Gly His Arg His	Val Pro Pro Met Leu	
465	470	475 480
Pro Ile Val Ala Arg Val Val Asp Glu Ser Thr Thr Arg Glu Gly Tyr		
	485 490	495
Ala Phe Tyr Glu Asp Asn Arg		
500		

<210> 1377
 <211> 1689
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1666)
 <223> RXN02995

<400> 1377
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 tcgcgcaaca gggatacaat gagcaaccgt gacgcagcaa ttg aac cac gca aag 115
 Leu Asn His Ala Lys
 1 5
 gta aat caa cat ccc ggt caa gcc acc ctc cca gaa acc gca gag ggg 163
 Val Asn Gln His Pro Gly Gln Ala Thr Leu Pro Glu Thr Ala Glu Gly
 10 15 20
 cag gtt cgc acc tac gag gta aaa acc tac ggc tgt cag atg aat gtg 211
 Gln Val Arg Thr Tyr Glu Val Lys Thr Tyr Gly Cys Gln Met Asn Val
 25 30 35
 cac gat tct gag cgc ctt tcg ggc ctg ctc gag gag gct gga tac gtt 259
 His Asp Ser Glu Arg Leu Ser Gly Leu Leu Glu Glu Ala Gly Tyr Val
 40 45 50
 gct gct ccg gag gac acc act ccg gat ctt gtc gta ttt aat acg tgc 307
 Ala Ala Pro Glu Asp Thr Thr Pro Asp Leu Val Val Phe Asn Thr Cys
 55 60 65
 gcc gtg cgt gaa aac gcc gat atg cgc ctc tat ggc act ttg ggc aac 355
 Ala Val Arg Glu Asn Ala Asp Met Arg Leu Tyr Gly Thr Leu Gly Asn
 70 75 80 85
 ctg cgc agc gtg aaa gaa aag aac cca ggc atg caa atc gct gtc ggt 403
 Leu Arg Ser Val Lys Glu Lys Asn Pro Gly Met Gln Ile Ala Val Gly
 90 95 100
 ggt tgt ttg gct caa aaa gac aaa gat acc gtg gtg aaa aaa gca ccg 451
 Gly Cys Leu Ala Gln Lys Asp Lys Asp Thr Val Val Lys Lys Ala Pro
 105 110 115
 tgg gtg gac gtg gtg ttt ggt acc cac aac att ggt tcc ttg cca acc 499

Trp	Val	Asp	Val	Val	Phe	Gly	Thr	His	Asn	Ile	Gly	Ser	Leu	Pro	Thr		
	120						125					130					
ttg	ctt	cag	cgc	gcg	gag	cac	aat	gcc	caa	gcg	gaa	gtc	gaa	att	gtc	547	
Leu	Leu	Gln	Arg	Ala	Glu	His	Asn	Ala	Gln	Ala	Glu	Val	Glu	Ile	Val		
	135					140					145						
gat	tcc	ctc	gag	cag	ttc	ccg	tca	gta	ctt	cct	gca	aag	cgc	gag	tct	595	
Asp	Ser	Leu	Glu	Gln	Phe	Pro	Ser	Val	Leu	Pro	Ala	Lys	Arg	Glu	Ser		
150					155					160					165		
gct	tac	gct	ggg	tgg	gtg	tcc	gta	tca	gtc	gga	tgt	aac	aac	acc	tgt	643	
Ala	Tyr	Ala	Gly	Trp	Val	Ser	Val	Ser	Val	Gly	Cys	Asn	Asn	Thr	Cys		
				170					175					180			
act	ttc	tgc	atc	gtt	ccg	tcg	ctg	cgc	ggg	aaa	gag	cag	gac	cgt	cga	691	
Thr	Phe	Cys	Ile	Val	Pro	Ser	Leu	Arg	Gly	Lys	Glu	Gln	Asp	Arg	Arg		
			185					190					195				
cca	gga	gac	atc	ctc	gca	gag	gta	caa	gca	ctg	gtg	gat	cag	gga	gtt	739	
Pro	Gly	Asp	Ile	Leu	Ala	Glu	Val	Gln	Ala	Leu	Val	Asp	Gln	Gly	Val		
		200					205					210					
acc	gag	gta	act	cta	ctt	ggc	caa	aac	gta	aat	gct	tac	ggc	gtg	aac	787	
Thr	Glu	Val	Thr	Leu	Leu	Gly	Gln	Asn	Val	Asn	Ala	Tyr	Gly	Val	Asn		
	215					220				225							
ttt	gtt	gat	cct	gag	cta	gag	cgc	gat	cgc	agt	gca	ttt	tcc	aag	ctg	835	
Phe	Val	Asp	Pro	Glu	Leu	Glu	Arg	Asp	Arg	Ser	Ala	Phe	Ser	Lys	Leu		
230					235					240					245		
ctt	cgt	gcc	tgt	ggg	gag	atc	gaa	ggc	ctc	gag	cgg	gtt	cgc	ttc	acc	883	
Leu	Arg	Ala	Cys	Gly	Glu	Ile	Glu	Gly	Leu	Glu	Arg	Val	Arg	Phe	Thr		
				250					255					260			
agc	cct	cac	cct	gca	gaa	ttc	acc	tct	gat	gtc	att	gac	gcc	atg	gca	931	
Ser	Pro	His	Pro	Ala	Glu	Phe	Thr	Ser	Asp	Val	Ile	Asp	Ala	Met	Ala		
			265					270					275				
gag	acc	cca	aac	atc	tgc	ccg	cag	ctg	cac	atg	cca	ctg	cag	tcc	gga	979	
Glu	Thr	Pro	Asn	Ile	Cys	Pro	Gln	Leu	His	Met	Pro	Leu	Gln	Ser	Gly		
		280					285					290					
tct	gac	aag	gtg	ctc	aaa	gag	atg	cgc	cgt	tcc	tac	cga	tcc	aag	aag	1027	
Ser	Asp	Lys	Val	Leu	Lys	Glu	Met	Arg	Arg	Ser	Tyr	Arg	Ser	Lys	Lys		
	295					300					305						
ttc	ctc	tcc	atc	ttg	gat	gag	gtc	cgt	gcg	aag	atc	cct	cac	gcc	tct	1075	
Phe	Leu	Ser	Ile	Leu	Asp	Glu	Val	Arg	Ala	Lys	Ile	Pro	His	Ala	Ser		
310					315					320					325		
atc	acc	acc	gat	att	att	gtc	gga	ttc	cct	ggc	gaa	aca	gag	gag	gat	1123	
Ile	Thr	Thr	Asp	Ile	Ile	Val	Gly	Phe	Pro	Gly	Glu	Thr	Glu	Glu	Asp		
				330					335					340			
ttc	caa	gca	acc	ctc	gac	gtt	gtc	aag	aag	gca	cgc	ttt	act	tct	gct	1171	
Phe	Gln	Ala	Thr	Leu	Asp	Val	Val	Lys	Lys	Ala	Arg	Phe	Thr	Ser	Ala		
			345					350					355				
tac	acc	ttc	caa	tac	agc	cca	cgc	cct	ggc	acc	cct	gca	gcg	gaa	tat	1219	
Tyr	Thr	Phe	Gln	Tyr	Ser	Pro	Arg	Pro	Gly	Thr	Pro	Ala	Ala	Glu	Tyr		

360	365	370	
gaa aac cag ctt cca aaa gaa gtt gtg cag gaa cgc tac gag cgc ctc			1267
Glu Asn Gln Leu Pro Lys Glu Val Val Gln Glu Arg Tyr Glu Arg Leu			
375	380	385	
atg gtc gtt cag gaa caa gtc tgc gaa gaa gaa aac caa aag ctc atc			1315
Met Val Val Gln Glu Gln Val Cys Glu Glu Glu Asn Gln Lys Leu Ile			
390	395	400	405
ggc acc acc gtc gaa ttg ctg gtc cag gct ggc gga ggc cgc aag aac			1363
Gly Thr Thr Val Glu Leu Leu Val Gln Ala Gly Gly Gly Arg Lys Asn			
410	415	420	
gat gcc acc aag cgc atg agt ggt cgc gca cgc gat gga cgc ctc gtg			1411
Asp Ala Thr Lys Arg Met Ser Gly Arg Ala Arg Asp Gly Arg Leu Val			
425	430	435	
cac ttt gcg cca gag ggc gac att gat ggt gag atc cgc ccc ggc gat			1459
His Phe Ala Pro Glu Gly Asp Ile Asp Gly Glu Ile Arg Pro Gly Asp			
440	445	450	
ttt gtc act gtc acg gtg act gag gcc aag cct ttc ttc ctc atc gca			1507
Phe Val Thr Val Thr Val Thr Glu Ala Lys Pro Phe Phe Leu Ile Ala			
455	460	465	
gac tcc ggt gtg cag acc cac cgc cgc acc aaa gct ggt gac aac tct			1555
Asp Ser Gly Val Gln Thr His Arg Arg Thr Lys Ala Gly Asp Asn Ser			
470	475	480	485
gca gtt ggt caa gtt cca acc aca gca ccg atc ggt gtg ggc ttg gga			1603
Ala Val Gly Gln Val Pro Thr Thr Ala Pro Ile Gly Val Gly Leu Gly			
490	495	500	
ctg cca caa atc ggc gca cca aag gtg gct cct gcc aca gaa tct gcc			1651
Leu Pro Gln Ile Gly Ala Pro Lys Val Ala Pro Ala Thr Glu Ser Ala			
505	510	515	
tgc tgc tcc att aac taaaaattgc aggctagaat aga			1689
Cys Cys Ser Ile Asn			
520			

<210> 1378

<211> 522

<212> PRT

<213> Corynebacterium glutamicum

<400> 1378

Leu	Asn	His	Ala	Lys	Val	Asn	Gln	His	Pro	Gly	Gln	Ala	Thr	Leu	Pro
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Glu	Thr	Ala	Glu	Gly	Gln	Val	Arg	Thr	Tyr	Glu	Val	Lys	Thr	Tyr	Gly
		20					25						30		

Cys	Gln	Met	Asn	Val	His	Asp	Ser	Glu	Arg	Leu	Ser	Gly	Leu	Leu	Glu
		35					40					45			

Glu	Ala	Gly	Tyr	Val	Ala	Ala	Pro	Glu	Asp	Thr	Thr	Pro	Asp	Leu	Val
	50					55					60				

Val Phe Asn Thr Cys Ala Val Arg Glu Asn Ala Asp Met Arg Leu Tyr
65 70 75 80

Gly Thr Leu Gly Asn Leu Arg Ser Val Lys Glu Lys Asn Pro Gly Met
85 90 95

Gln Ile Ala Val Gly Gly Cys Leu Ala Gln Lys Asp Lys Asp Thr Val
100 105 110

Val Lys Lys Ala Pro Trp Val Asp Val Val Phe Gly Thr His Asn Ile
115 120 125

Gly Ser Leu Pro Thr Leu Leu Gln Arg Ala Glu His Asn Ala Gln Ala
130 135 140

Glu Val Glu Ile Val Asp Ser Leu Glu Gln Phe Pro Ser Val Leu Pro
145 150 155 160

Ala Lys Arg Glu Ser Ala Tyr Ala Gly Trp Val Ser Val Ser Val Gly
165 170 175

Cys Asn Asn Thr Cys Thr Phe Cys Ile Val Pro Ser Leu Arg Gly Lys
180 185 190

Glu Gln Asp Arg Arg Pro Gly Asp Ile Leu Ala Glu Val Gln Ala Leu
195 200 205

Val Asp Gln Gly Val Thr Glu Val Thr Leu Leu Gly Gln Asn Val Asn
210 215 220

Ala Tyr Gly Val Asn Phe Val Asp Pro Glu Leu Glu Arg Asp Arg Ser
225 230 235 240

Ala Phe Ser Lys Leu Leu Arg Ala Cys Gly Glu Ile Glu Gly Leu Glu
245 250 255

Arg Val Arg Phe Thr Ser Pro His Pro Ala Glu Phe Thr Ser Asp Val
260 265 270

Ile Asp Ala Met Ala Glu Thr Pro Asn Ile Cys Pro Gln Leu His Met
275 280 285

Pro Leu Gln Ser Gly Ser Asp Lys Val Leu Lys Glu Met Arg Arg Ser
290 295 300

Tyr Arg Ser Lys Lys Phe Leu Ser Ile Leu Asp Glu Val Arg Ala Lys
305 310 315 320

Ile Pro His Ala Ser Ile Thr Thr Asp Ile Ile Val Gly Phe Pro Gly
325 330 335

Glu Thr Glu Glu Asp Phe Gln Ala Thr Leu Asp Val Val Lys Lys Ala
340 345 350

Arg Phe Thr Ser Ala Tyr Thr Phe Gln Tyr Ser Pro Arg Pro Gly Thr
355 360 365

Pro Ala Ala Glu Tyr Glu Asn Gln Leu Pro Lys Glu Val Val Gln Glu
370 375 380

Arg Tyr Glu Arg Leu Met Val Val Gln Glu Gln Val Cys Glu Glu Glu

385 390 395 400
 Asn Gln Lys Leu Ile Gly Thr Thr Val Glu Leu Leu Val Gln Ala Gly
 405 410 415
 Gly Gly Arg Lys Asn Asp Ala Thr Lys Arg Met Ser Gly Arg Ala Arg
 420 425 430
 Asp Gly Arg Leu Val His Phe Ala Pro Glu Gly Asp Ile Asp Gly Glu
 435 440 445
 Ile Arg Pro Gly Asp Phe Val Thr Val Thr Val Thr Glu Ala Lys Pro
 450 455 460
 Phe Phe Leu Ile Ala Asp Ser Gly Val Gln Thr His Arg Arg Thr Lys
 465 470 475 480
 Ala Gly Asp Asn Ser Ala Val Gly Gln Val Pro Thr Thr Ala Pro Ile
 485 490 495
 Gly Val Gly Leu Gly Leu Pro Gln Ile Gly Ala Pro Lys Val Ala Pro
 500 505 510
 Ala Thr Glu Ser Ala Cys Cys Ser Ile Asn
 515 520

<210> 1379

<211> 752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(729)

<223> RXN02997

<400> 1379

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 Pro Leu Pro Gly Gln Pro Phe Glu Gly Glu Ala Leu Thr Leu Ile Asn
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 gcc ctc ctc cac cac gcc gaa aac gtc gca gcc tcc aac ccc tgg aag 96
 Ala Leu Leu His His Ala Glu Asn Val Ala Ala Ser Asn Pro Trp Lys
 20 25 30

 cgc acc acc ttc cac acc gct cac atg cac cct cca ggg agt aat gcg 144
 Arg Thr Thr Phe His Thr Ala His Met His Pro Pro Gly Ser Asn Ala
 35 40 45

 gat tgt gac tac tgc ctg gtg ctg caa cgc cgc gga tac gtt aaa gcc 192
 Asp Cys Asp Tyr Cys Leu Val Leu Gln Arg Arg Gly Tyr Val Lys Ala
 50 55 60

 cac gaa gaa atc caa caa acc atc ccg ctt cct tca ggt gac tgg tcc 240
 His Glu Glu Ile Gln Gln Thr Ile Pro Leu Pro Ser Gly Asp Trp Ser
 65 70 75 80

 gct gga gaa ttc acc gtg gtg gac gtt gaa ggc acc gcc ttc cca agc 288
 Ala Gly Glu Phe Thr Val Val Asp Val Glu Gly Thr Ala Phe Pro Ser
 85 90 95

gcg ctg atc ccc agc atc gtg gaa ctc caa cac cgc gca gcc ctc gat 336
 Ala Leu Ile Pro Ser Ile Val Glu Leu Gln His Arg Ala Ala Leu Asp
 100 105 110

gtg ccc cac gga aac tta agt gtt gcg cct gca cag tgg gat gaa cac 384
 Val Pro His Gly Asn Leu Ser Val Ala Pro Ala Gln Trp Asp Glu His
 115 120 125

cgc ttg gcg cag caa tct gaa aga atc ctt aaa aca gga acg aaa ctg 432
 Arg Leu Ala Gln Gln Ser Glu Arg Ile Leu Lys Thr Gly Thr Lys Leu
 130 135 140

ttc acc gta ctg ttt gcc gaa gga tcc aca gtc gct gcc atg tcc tcc 480
 Phe Thr Val Leu Phe Ala Glu Gly Ser Thr Val Ala Ala Met Ser Ser
 145 150 155 160

atc gcg att ccc cca ggc tcc aac cct gac atc gcc gaa cag gga ctg 528
 Ile Ala Ile Pro Pro Gly Ser Asn Pro Asp Ile Ala Glu Gln Gly Leu
 165 170 175

acc atc gtg cac cca gat ttc aga ggc cgt ggt ctt gga acc gct gtg 576
 Thr Ile Val His Pro Asp Phe Arg Gly Arg Gly Leu Gly Thr Ala Val
 180 185 190

aaa tta gcg gga ctg tca cta ctt tcg agg tgc cac cca gaa att caa 624
 Lys Leu Ala Gly Leu Ser Leu Ser Arg Cys His Pro Glu Ile Gln
 195 200 205

cgc gta gcc acc tca aat gca gta gac aac cat gcg atg ctg gcg att 672
 Arg Val Ala Thr Ser Asn Ala Val Asp Asn His Ala Met Leu Ala Ile
 210 215 220

aac cgc tcc ata ggg gca aca gag atc gcc cga acc acc ctg tgg gag 720
 Asn Arg Ser Ile Gly Ala Thr Glu Ile Ala Arg Thr Thr Leu Trp Glu
 225 230 235 240

aag aaa ctc taggtgatgg aattcgagac caa 752
 Lys Lys Leu

<210> 1380

<211> 243

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1380

Pro Leu Pro Gly Gln Pro Phe Glu Gly Glu Ala Leu Thr Leu Ile Asn
 1 5 10 15

Ala Leu Leu His His Ala Glu Asn Val Ala Ala Ser Asn Pro Trp Lys
 20 25 30

Arg Thr Thr Phe His Thr Ala His Met His Pro Pro Gly Ser Asn Ala
 35 40 45

Asp Cys Asp Tyr Cys Leu Val Leu Gln Arg Arg Gly Tyr Val Lys Ala
 50 55 60

His Glu Glu Ile Gln Gln Thr Ile Pro Leu Pro Ser Gly Asp Trp Ser

65	70	75	80
Ala Gly Glu Phe Thr Val Val Asp Val Glu Gly Thr Ala Phe Pro Ser	85	90	95
Ala Leu Ile Pro Ser Ile Val Glu Leu Gln His Arg Ala Ala Leu Asp	100	105	110
Val Pro His Gly Asn Leu Ser Val Ala Pro Ala Gln Trp Asp Glu His	115	120	125
Arg Leu Ala Gln Gln Ser Glu Arg Ile Leu Lys Thr Gly Thr Lys Leu	130	135	140
Phe Thr Val Leu Phe Ala Glu Gly Ser Thr Val Ala Ala Met Ser Ser	145	150	155
Ile Ala Ile Pro Pro Gly Ser Asn Pro Asp Ile Ala Glu Gln Gly Leu	165	170	175
Thr Ile Val His Pro Asp Phe Arg Gly Arg Gly Leu Gly Thr Ala Val	180	185	190
Lys Leu Ala Gly Leu Ser Leu Leu Ser Arg Cys His Pro Glu Ile Gln	195	200	205
Arg Val Ala Thr Ser Asn Ala Val Asp Asn His Ala Met Leu Ala Ile	210	215	220
Asn Arg Ser Ile Gly Ala Thr Glu Ile Ala Arg Thr Thr Leu Trp Glu	225	230	235
Lys Lys Leu			

<210> 1381
 <211> 553
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(553)
 <223> RXN03001

<400> 1381
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 acgctacgac atctaactac tttaaaagga cgaaaatatt atg gac tgg tta acc 115
 Met Asp Trp Leu Thr
 1 5
 att cct ctt ttc ctc gtt aat gaa atc ctt gcg gtt ccg gct ttc ctc 163
 Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala Val Pro Ala Phe Leu
 10 15 20
 atc ggt atc atc acc gcc gtg gga ttg ggt gcc atg ggg cgt tcc gtc 211
 Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala Met Gly Arg Ser Val
 25 30 35

ggt cag gtt atc ggt gga gca atc aaa gca acg ttg ggc ttt ttg ctc 259
 Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr Leu Gly Phe Leu Leu
 40 45 50

 att ggt gcg ggt gcc acg ttg gtc act gcc tcc ctg gag cca ctg ggt 307
 Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser Leu Glu Pro Leu Gly
 55 60 65

 gcg atg atc atg ggt gcc aca ggc atg cgt ggt gtt gtc cca acg aat 355
 Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly Val Val Pro Thr Asn
 70 75 80 85

 gaa gcc atc gcc gga atc gca cag gct gaa tac ggc gcg cag gtg gcg 403
 Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr Gly Ala Gln Val Ala
 90 95 100

 tgg ctg atg att ctg ggc ttc gcc atc tct ttg gtg ttg gct cgt ttc 451
 Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu Val Leu Ala Arg Phe
 105 110 115

 acc aac ctg cgt tat gtc ttg ctc aac gga cac cac gtg ctg ttg atg 499
 Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His His Val Leu Leu Met
 120 125 130

 tgc acc atg ctc acc atg gtc ttg gcc acc gga aga gtt gat gcg tgg 547
 Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly Arg Val Asp Ala Trp
 135 140 145

 atc ttc 553
 Ile Phe
 150

<210> 1382

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 1382

Met Asp Trp Leu Thr Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala
 1 5 10 15

Val Pro Ala Phe Leu Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala
 20 25 30

Met Gly Arg Ser Val Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr
 35 40 45

Leu Gly Phe Leu Leu Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser
 50 55 60

Leu Glu Pro Leu Gly Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly
 65 70 75 80

Val Val Pro Thr Asn Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr
 85 90 95

Gly Ala Gln Val Ala Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu
 100 105 110

Val Leu Ala Arg Phe Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His

115	120	125	
His Val Leu Leu Met Cys Thr	Met Leu Thr Met	Val Leu Ala Thr Gly	
130	135	140	
Arg Val Asp Ala Trp Ile Phe			
145	150		
 <210> 1383			
<211> 891			
<212> DNA			
<213> Corynebacterium glutamicum			
 <220>			
<221> CDS			
<222> (101)..(868)			
<223> RXN03005			
 <400> 1383			
taggtaaacc ttaaacagtc gccattgaag aatttttaaaa acaaacaacc ttcaacgcgc			60
taacaagcat cttcccactc tcgttacgg agtttctcac			
		atg tct cac aag ttt	115
		Met Ser His Lys Phe	
		1 5	
tcc cgc cgt gct ttc gca gta ctg acc gct gcc gca att tcc act tcc			163
Ser Arg Arg Ala Phe Ala Val Leu Thr Ala Ala Ala Ile Ser Thr Ser			
	10	15	20
gct ttc gca acc act gct ccg tct gcg att gca gag cca gtt cta atg			211
Ala Phe Ala Thr Thr Ala Pro Ser Ala Ile Ala Glu Pro Val Leu Met			
	25	30	35
tcg cac tgc aga cga ttc cag cgt cgc aac ttc aga aaa ctc cct cga			259
Ser His Cys Arg Arg Phe Gln Arg Arg Asn Phe Arg Lys Leu Pro Arg			
	40	45	50
ctg ggg ctt caa ggc ttc ctg gcg cac cta tgt cac cgg acc ttg gac			307
Leu Gly Leu Gln Gly Phe Leu Ala His Leu Cys His Arg Thr Leu Asp			
	55	60	65
tgg tgg aac cgt gac gca act ggc ggt gca act gtc aac gaa gat gga			355
Trp Trp Asn Arg Asp Ala Thr Gly Gly Ala Thr Val Asn Glu Asp Gly			
	70	75	80
acc tac aac ttc acc ctc gga act ggc tcc aat tac gac gtc gac acc			403
Thr Tyr Asn Phe Thr Leu Gly Thr Gly Ser Asn Tyr Asp Val Asp Thr			
	90	95	100
gag aag ggc cag ctg aac tac gaa gga act gtt gcc ttc gcc agt gac			451
Glu Lys Gly Gln Leu Asn Tyr Glu Gly Thr Val Ala Phe Ala Ser Asp			
	105	110	115
gct cac ggc ttc aac atc acc ttg tcc aac ccg cag atc acc gtc gag			499
Ala His Gly Phe Asn Ile Thr Leu Ser Asn Pro Gln Ile Thr Val Glu			
	120	125	130
ggc gac act gca act ttg agc gcc gag ctg tct gac aat gcc gct ccc			547
Gly Asp Thr Ala Thr Leu Ser Ala Glu Leu Ser Asp Asn Ala Ala Pro			
	135	140	145

gaa gag acc tcc act act cgc gtt gat gtt gct gag ttc gaa ctg acc 595
 Glu Glu Thr Ser Thr Thr Arg Val Asp Val Ala Glu Phe Glu Leu Thr
 150 155 160 165

gct cct gag gtt tca gaa acc gat gcg gac att acc tac acc tgg acc 643
 Ala Pro Glu Val Ser Glu Thr Asp Ala Asp Ile Thr Tyr Thr Trp Thr
 170 175 180

gat gct tcc ggc act ttc ttg gag acc ctg cag cct gaa gaa ttg agc 691
 Asp Ala Ser Gly Thr Phe Leu Glu Thr Leu Gln Pro Glu Glu Leu Ser
 185 190 195

cgt tac gca ggc cag gaa gcg gat gcg ctg agc ttc tcc atc acc gtg 739
 Arg Tyr Ala Gly Gln Glu Ala Asp Ala Leu Ser Phe Ser Ile Thr Val
 200 205 210

gac aag gct tca gag aac cct tcc gat gat gtt gct acc gga tct tcc 787
 Asp Lys Ala Ser Glu Asn Pro Ser Asp Asp Val Ala Thr Gly Ser Ser
 215 220 225

tcc agc ttc ctc tcc acc atc ttg aac ttc ctt cag cag ctg gcg agc 835
 Ser Ser Phe Leu Ser Thr Ile Leu Asn Phe Leu Gln Gln Leu Ala Ser
 230 235 240 245

cca ctg ctc aag ctc ttc ggt tcg ctt tct tcc taaataatca gtaatgcccc 888
 Pro Leu Leu Lys Leu Phe Gly Ser Leu Ser
 250 255

acc 891

<210> 1384

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 1384

Met Ser His Lys Phe Ser Arg Arg Ala Phe Ala Val Leu Thr Ala Ala
 1 5 10 15

Ala Ile Ser Thr Ser Ala Phe Ala Thr Thr Ala Pro Ser Ala Ile Ala
 20 25 30

Glu Pro Val Leu Met Ser His Cys Arg Arg Phe Gln Arg Arg Asn Phe
 35 40 45

Arg Lys Leu Pro Arg Leu Gly Leu Gln Gly Phe Leu Ala His Leu Cys
 50 55 60

His Arg Thr Leu Asp Trp Trp Asn Arg Asp Ala Thr Gly Gly Ala Thr
 65 70 75 80

Val Asn Glu Asp Gly Thr Tyr Asn Phe Thr Leu Gly Thr Gly Ser Asn
 85 90 95

Tyr Asp Val Asp Thr Glu Lys Gly Gln Leu Asn Tyr Glu Gly Thr Val
 100 105 110

Ala Phe Ala Ser Asp Ala His Gly Phe Asn Ile Thr Leu Ser Asn Pro
 115 120 125

Gln Ile Thr Val Glu Gly Asp Thr Ala Thr Leu Ser Ala Glu Leu Ser
 130 135 140

Asp Asn Ala Ala Pro Glu Glu Thr Ser Thr Thr Arg Val Asp Val Ala
 145 150 155 160

Glu Phe Glu Leu Thr Ala Pro Glu Val Ser Glu Thr Asp Ala Asp Ile
 165 170 175

Thr Tyr Thr Trp Thr Asp Ala Ser Gly Thr Phe Leu Glu Thr Leu Gln
 180 185 190

Pro Glu Glu Leu Ser Arg Tyr Ala Gly Gln Glu Ala Asp Ala Leu Ser
 195 200 205

Phe Ser Ile Thr Val Asp Lys Ala Ser Glu Asn Pro Ser Asp Asp Val
 210 215 220

Ala Thr Gly Ser Ser Ser Ser Phe Leu Ser Thr Ile Leu Asn Phe Leu
 225 230 235 240

Gln Gln Leu Ala Ser Pro Leu Leu Lys Leu Phe Gly Ser Leu Ser Ser
 245 250 255

<210> 1385

<211> 448

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(448)

<223> RXN03009

<400> 1385

atgtgaacct gatgctggca cctgaagata gccacagccc aggcaccgca acagtgaacct 60

accgtcatgg tttcagcgat caccgtttac cctgcactgc gtg gct aat atc gcc 115
 Val Ala Asn Ile Ala
 1 5

agc ttg tac gga ctg tgg gaa ggc agc aca tcc aca cca atc gaa cag 163
 Ser Leu Tyr Gly Leu Trp Glu Gly Ser Thr Ser Thr Pro Ile Glu Gln
 10 15 20

ctc gta cct gcg aaa ggt tcc agc ttt cgt ttg gtg agg tct ttt tac 211
 Leu Val Pro Ala Lys Gly Ser Ser Phe Arg Leu Val Arg Ser Phe Tyr
 25 30 35

agg cga att gac ggc caa gca gtt cag gct cgt ctc aag gag aag att 259
 Arg Arg Ile Asp Gly Gln Ala Val Gln Ala Arg Leu Lys Glu Lys Ile
 40 45 50

ctc aac acc gcg gaa aac ccg ctt cct cgc ttg gac att cca ggt aag 307
 Leu Asn Thr Ala Glu Asn Pro Leu Pro Arg Leu Asp Ile Pro Gly Lys
 55 60 65

gag cgc act gcg cag tac cca gaa aat ccg gat acc ttc gcc caa aaa 355
 Glu Arg Thr Ala Gln Tyr Pro Glu Asn Pro Asp Thr Phe Ala Gln Lys

70	75	80	85	
gca gct caa gaa att ctt gat gag ttc aga act cca ctg atc ggt gaa				403
Ala Ala Gln Glu Ile Leu Asp Glu Phe Arg Thr Pro Leu Ile Gly Glu				
	90	95	100	
gaa gct gca gct cat gtt gag aaa acg aag acg att ttc tgg aag				448
Glu Ala Ala Ala His Val Glu Lys Thr Lys Thr Ile Phe Trp Lys				
	105	110	115	

<210> 1386

<211> 116

<212> PRT

<213> Corynebacterium glutamicum

<400> 1386

Val Ala Asn Ile Ala Ser Leu Tyr Gly Leu Trp Glu Gly Ser Thr Ser				
1	5	10	15	
Thr Pro Ile Glu Gln Leu Val Pro Ala Lys Gly Ser Ser Phe Arg Leu				
	20	25	30	
Val Arg Ser Phe Tyr Arg Arg Ile Asp Gly Gln Ala Val Gln Ala Arg				
	35	40	45	
Leu Lys Glu Lys Ile Leu Asn Thr Ala Glu Asn Pro Leu Pro Arg Leu				
	50	55	60	
Asp Ile Pro Gly Lys Glu Arg Thr Ala Gln Tyr Pro Glu Asn Pro Asp				
	65	70	75	80
Thr Phe Ala Gln Lys Ala Ala Gln Glu Ile Leu Asp Glu Phe Arg Thr				
	85	90	95	
Pro Leu Ile Gly Glu Glu Ala Ala Ala His Val Glu Lys Thr Lys Thr				
	100	105	110	
Ile Phe Trp Lys				
	115			

<210> 1387

<211> 360

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(337)

<223> RXN03010

<400> 1387

tgggcgccctt caatcggcac ccaactgaatg gattcttccg ggcctagttt tagggctgat	60
cagcctggga ctcaatgcgt ggattacctt cgggtgcgcca gtg ccc acc gat aat	115
	Val Pro Thr Asp Asn
	1 5
ctt ttt ctc atc gtt gct gga att gcg tgg gtg ttg gca gga att ttg	163
Leu Phe Leu Ile Val Ala Gly Ile Ala Trp Val Leu Ala Gly Ile Leu	

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<210> 1388
<211> 79
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1388
Val Pro Thr Asp Asn Leu Phe Leu Ile Val Ala Gly Ile Ala Trp Val
  1                    5                10              15

Leu Ala Gly Ile Leu Ser Val Leu Ser Ile Gly Lys Tyr Met Ser Ala
      20                25              30

Val Asn Glu Arg Lys Ser Thr Gly Phe Tyr Thr Glu Val Pro Trp Lys
      35                40              45

Lys Ala Leu Phe Thr Ala Thr Ala Val Leu Leu Val Phe Ala Val Val
  50                    55                60

Trp Ser Ala Leu Asp Ile Ala Leu Trp Val Gly Lys Gln Ser Trp
  65                70                75

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<210> 1389
<211> 324
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(301)  
<223> RXN03011
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<400> 1389
ccgacgtacc agtttttgtc gttccacccc tggactaaaa ccgagacgag aaccaagaag 60

atgaaaccaa ggggtaaaaa ctggtagtct cttccacgtc atg gca tac gaa act 115
                                         Met Ala Tyr Glu Thr
                                         1                               5

gat tcc ctc aac cga cgc acc ctc ggg ccc gcg att gca agc gca gtc 163

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Asp Ser Leu Asn Arg Arg Thr Leu Gly Pro Ala Ile Ala Ser Ala Val
 10 15 20
 gtg gga atc gcc gtc ggc gca gtc gca gta gtt ggg gtt tca atg atc 211
 Val Gly Ile Ala Val Gly Ala Val Ala Val Val Gly Val Ser Met Ile
 25 30 35
 tca ggg cag gac act gtt ccc act ggt aac gcc gta act gca gac gat 259
 Ser Gly Gln Asp Thr Val Pro Thr Gly Asn Ala Val Thr Ala Asp Asp
 40 45 50
 gcc ctg ctc ggt ggc cct gag tat ggt tca cgc gaa gca gac 301
 Ala Leu Leu Gly Gly Pro Glu Tyr Gly Ser Arg Glu Ala Asp
 55 60 65
 taagaagcca cttccccggtt ttc 324

<210> 1390

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 1390

Met Ala Tyr Glu Thr Asp Ser Leu Asn Arg Arg Thr Leu Gly Pro Ala
 1 5 10 15

Ile Ala Ser Ala Val Val Gly Ile Ala Val Gly Ala Val Ala Val Val
 20 25 30

Gly Val Ser Met Ile Ser Gly Gln Asp Thr Val Pro Thr Gly Asn Ala
 35 40 45

Val Thr Ala Asp Asp Ala Leu Leu Gly Gly Pro Glu Tyr Gly Ser Arg
 50 55 60

Glu Ala Asp
 65

<210> 1391

<211> 593

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(570)

<223> RXN03012

<400> 1391

acc act atc aac atc atc atc acc aat ggc gct gca cca cac cca act 48
 Thr Thr Ile Asn Ile Ile Ile Thr Asn Gly Ala Ala Pro His Pro Thr
 1 5 10 15

aat ctc aat cgc gca gaa att cat gat cac cta ccc ctc act gcc tct 96
 Asn Leu Asn Arg Ala Glu Ile His Asp His Leu Pro Leu Thr Ala Ser
 20 25 30

gat tcg gag cta acc cgc ccc tcc cag gaa tca gtt ctc tat gac cat 144
 Asp Ser Glu Leu Thr Arg Pro Ser Gln Glu Ser Val Leu Tyr Asp His

35	40	45	
gaa tcc gaa act gtc ttg cgc acc atg gtc atc cct gca gac ctg cac			192
Glu Ser Glu Thr Val Leu Arg Thr Met Val Ile Pro Ala Asp Leu His			
50	55	60	
gtc gct atg aag cat cta gct aaa aaa cac aac ctc acg gtc aca gag			240
Val Ala Met Lys His Leu Ala Lys Lys His Asn Leu Thr Val Thr Glu			
65	70	75	80
atc tcg cgc atc ctt ctg cag cgc tac atc gac cgc aat att aac cat			288
Ile Ser Arg Ile Leu Leu Gln Arg Tyr Ile Asp Arg Asn Ile Asn His			
85	90	95	
gta gag caa aac cag gct gaa tcc gac atg gtg gaa gtc ttt gcc agc			336
Val Glu Gln Asn Gln Ala Glu Ser Asp Met Val Glu Val Phe Ala Ser			
100	105	110	
caa cca acc aat gca acc gca atg atc cct gta cct gga acc agc ttc			384
Gln Pro Thr Asn Ala Thr Ala Met Ile Pro Val Pro Gly Thr Ser Phe			
115	120	125	
agg caa ata ttt atc aag cac agc act ggt ttc tgg aaa aac att gat			432
Arg Gln Ile Phe Ile Lys His Ser Thr Gly Phe Trp Lys Asn Ile Asp			
130	135	140	
cat gat ctt gtc gat ctc gac gcc tct aag acc ccg cgt gta cgc gac			480
His Asp Leu Val Asp Leu Asp Ala Ser Lys Thr Pro Arg Val Arg Asp			
145	150	155	160
cgc agt gtc tta cca caa cct caa ctc cac aga gcg ttg tta tca gat			528
Arg Ser Val Leu Pro Gln Pro Gln Leu His Arg Ala Leu Leu Ser Asp			
165	170	175	
gct gat atg gct cgc ctt gca gca caa ctg acc gac aaa cac			570
Ala Asp Met Ala Arg Leu Ala Ala Gln Leu Thr Asp Lys His			
180	185	190	
taaaacctcc acaacaagga cat			593

<210> 1392

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 1392

Thr Thr Ile Asn Ile Ile Ile Thr Asn Gly Ala Ala Pro His Pro Thr	
1 5 10 15	

Asn Leu Asn Arg Ala Glu Ile His Asp His Leu Pro Leu Thr Ala Ser	
20 25 30	

Asp Ser Glu Leu Thr Arg Pro Ser Gln Glu Ser Val Leu Tyr Asp His	
35 40 45	

Glu Ser Glu Thr Val Leu Arg Thr Met Val Ile Pro Ala Asp Leu His	
50 55 60	

Val Ala Met Lys His Leu Ala Lys Lys His Asn Leu Thr Val Thr Glu	
65 70 75 80	

Lys	Glu	Lys	Asn	Arg	Glu	Asp	Lys	Gly	Thr	Ile	Ile	Asn	Leu	Val	Val		
				90					95					100			
aac	gat	gat	att	cat	tcc	gtt	gtc	act	cca	gaa	ctt	ctt	gac	agc	gat	451	
Asn	Asp	Asp	Ile	His	Ser	Val	Val	Thr	Pro	Glu	Leu	Leu	Asp	Ser	Asp		
			105					110					115				
gtg	ctt	ggt	gtc	att	cct	gat	gca	gat	tct	ttc	gat	cgc	atg	gat	gag	499	
Val	Leu	Gly	Val	Ile	Pro	Asp	Ala	Asp	Ser	Phe	Asp	Arg	Met	Asp	Glu		
		120					125					130					
ttt	gat	tta	ctg	cgt	aac	aaa	gca	cgc	tgg	cac	tac	gga	gtg	gct	gca	547	
Phe	Asp	Leu	Leu	Arg	Asn	Lys	Ala	Arg	Trp	His	Tyr	Gly	Val	Ala	Ala		
	135					140					145						
att	gaa	cct	gac	acg	ggt	gag	ctg	gtg	gtg	ttt	aag	gtg	ccc	gcg	aaa	595	
Ile	Glu	Pro	Asp	Thr	Gly	Glu	Leu	Val	Val	Phe	Lys	Val	Pro	Ala	Lys		
150					155					160					165		
aat	agc	gct	tcg	gca	cgc	ggt	gac	att	ttt	tcc	gag	gtc	ggc	gat	gtg	643	
Asn	Ser	Ala	Ser	Ala	Arg	Gly	Asp	Ile	Phe	Ser	Glu	Val	Gly	Asp	Val		
				170					175					180			
ctt	agc	ggt	gct	gct	gac	ctc	gaa	gac	gtg	gtt	gat	ttt	gag	gtc	att	691	
Leu	Ser	Gly	Ala	Ala	Asp	Leu	Glu	Asp	Val	Val	Asp	Phe	Glu	Val	Ile		
			185					190					195				
gcc	acc	ttc	cta	gag	gtg	ctg	aat	gag	acc	tct	gag	gtg	gat	att	gat	739	
Ala	Thr	Phe	Leu	Glu	Val	Leu	Asn	Glu	Thr	Ser	Glu	Val	Asp	Ile	Asp		
		200					205					210					
gac	gaa	gat	ggc	gac	gtg	cct	tat	ggt	ctt	gag	ggt	gtc	aat	gca	gcg	787	
Asp	Glu	Asp	Gly	Asp	Val	Pro	Tyr	Gly	Leu	Glu	Gly	Val	Asn	Ala	Ala		
	215					220					225						
gga	gtt	atc	acg	gat	gac	ctc	att	cgc	gag	aag	ctt	gat	gtg	gat	tcc	835	
Gly	Val	Ile	Thr	Asp	Asp	Leu	Ile	Arg	Glu	Lys	Leu	Asp	Val	Asp	Ser		
230					235					240					245		
tat	ccg	agc	agt	gca	gag	atc	att	gac	aat	att	gtg	cat	gtg	ttc	acc	883	
Tyr	Pro	Ser	Ser	Ala	Glu	Ile	Ile	Asp	Asn	Ile	Val	His	Val	Phe	Thr		
				250					255					260			
aag	ttg	cag	ggc	aag	cat	cat	gtg	gca	cca	cag	ccg	gtg	ctt	cac	agc	931	
Lys	Leu	Gln	Gly	Lys	His	His	Val	Ala	Pro	Gln	Pro	Val	Leu	His	Ser		
			265					270					275				
gca	gac	gta	gtg	gat	gtt	gat	gca	cag	gag	tcc	cat	gac	aca	gtg	gtt	979	
Ala	Asp	Val	Val	Asp	Val	Asp	Ala	Gln	Glu	Ser	His	Asp	Thr	Val	Val		
		280					285					290					
att	gag	agc	cct	gat	gat	gtc	gca	cta	gca	gaa	cag	gtg	gat	gta	ccg	1027	
Ile	Glu	Ser	Pro	Asp	Asp	Val	Ala	Leu	Ala	Glu	Gln	Val	Asp	Val	Pro		
	295					300					305						
gat	ttc	agt	gat	gga	ttt	ggt	att	gac	gat	gcc	gag	gtt	act	gag	cca	1075	
Asp	Phe	Ser	Asp	Gly	Phe	Gly	Ile	Asp	Asp	Ala	Glu	Val	Thr	Glu	Pro		
310					315					320					325		
gag	gat	gag	gag	gtt	gtc	gaa	gca	aca	gct	gat	gca	gat	cct	ttt	ggt	1123	
Glu	Asp	Glu	Glu	Val	Val	Glu	Ala	Thr	Ala	Asp	Ala	Asp	Pro	Phe	Gly		

330	335	340	
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ggt gca tcc gat gtt gtt gct gca ccg gca cct gta gcc ggc atg tcc Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro Val Ala Gly Met Ser 360 365 370			1219
gat gag cag atc cag gcg ctg att cgt ggt gtg tct gag tcc gtg caa Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val Ser Glu Ser Val Gln 375 380 385			1267
gca aag act ggt tca gaa ctt aat gct ttg cga gaa gaa ctt gca caa Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg Glu Glu Leu Ala Gln 390 395 400 405			1315
gca ctg gct tac aat ccg gtt cag gat tca cag gca gca ttg gca cag Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln Ala Ala Leu Ala Gln 410 415 420			1363
gtg cac gca gct gat gcc cgc agc ttt gat gcc gat caa gtg ggt gat Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala Asp Gln Val Gly Asp 425 430 435			1411
gct gtc acc aaa cgt tat gtt aat gac gac ttg ggg ctg tat gtc gat Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu Gly Leu Tyr Val Asp 440 445 450			1459
gag gca aac ttc aat aat gct ttg acc agg gca ccg ttc cag gtg gcg Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala Pro Phe Gln Val Ala 455 460 465			1507
atg ccg caa ttc cag gag act aca ccg tgg tta ggt gat cag ctt cgt Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu Gly Asp Gln Leu Arg 470 475 480 485			1555
aca ttg gtg gct gtg ttt aat ggt cag ctg ctt gat cag cat cag cgt Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu Asp Gln His Gln Arg 490 495 500			1603
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<400> 1394

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		20						25					30		

Arg Lys Glu Glu Arg Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly
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 Ala Ala Val Glu Val Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly
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 Glu Thr Gly Trp Val Val Met Leu Leu Pro Thr His Asp Ser Gln Phe
 65 70 75 80
 Gly Gly Leu Asn Ala Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile
 85 90 95
 Ile Asn Leu Val Val Asn Asp Asp Ile His Ser Val Val Thr Pro Glu
 100 105 110
 Leu Leu Asp Ser Asp Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe
 115 120 125
 Asp Arg Met Asp Glu Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His
 130 135 140
 Tyr Gly Val Ala Ala Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe
 145 150 155 160
 Lys Val Pro Ala Lys Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser
 165 170 175
 Glu Val Gly Asp Val Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val
 180 185 190
 Asp Phe Glu Val Ile Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser
 195 200 205
 Glu Val Asp Ile Asp Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu
 210 215 220
 Gly Val Asn Ala Ala Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys
 225 230 235 240
 Leu Asp Val Asp Ser Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile
 245 250 255
 Val His Val Phe Thr Lys Leu Gln Gly Lys His His Val Ala Pro Gln
 260 265 270
 Pro Val Leu His Ser Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser
 275 280 285
 His Asp Thr Val Val Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu
 290 295 300
 Gln Val Asp Val Pro Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala
 305 310 315 320
 Glu Val Thr Glu Pro Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp
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 Ala Asp Pro Phe Gly Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp
 340 345 350
 Asp Glu Pro Asp Phe Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro

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Val Ala Gly Met Ser Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val 370 375 380		
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Glu Glu Leu Ala Gln Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln 405 410 415		
Ala Ala Leu Ala Gln Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala 420 425 430		
Asp Gln Val Gly Asp Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu 435 440 445		
Gly Leu Tyr Val Asp Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala 450 455 460		
Pro Phe Gln Val Ala Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu 465 470 475 480		
Gly Asp Gln Leu Arg Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu 485 490 495		
Asp Gln His Gln Arg Asp Tyr Arg Arg Ser Ala Arg Asp Val His Cys 500 505 510		

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 <212> DNA
 <213> Corynebacterium glutamicum

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 Met Leu Asp Ser Leu 5
 aaa aat cgc ttc acc aaa gcg aaa ggt tct cat gga gtg ggg gag ggg 163
 Lys Asn Arg Phe Thr Lys Ala Lys Gly Ser His Gly Val Gly Glu Gly 20
 10 15 20
 gct gtt tct ggc gat gca gca gta aag cca ctg cgc aaa gaa gaa cga 211
 Ala Val Ser Gly Asp Ala Ala Val Lys Pro Leu Arg Lys Glu Glu Arg 35
 25 30 35
 ctc gcc tca gtc att cag gaa acc gaa cca ggt gct gca gtc gag gtc 259
 Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly Ala Ala Val Glu Val 50
 40 45 50

atg cgt cgc aat gac gca ttc gct ttg cca ggt gag acc ggt tgg gta	307
Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly Glu Thr Gly Trp Val	
55 60 65	
gtc atg ctg ttg cca act cac gat tca caa ttc ggt ggg ctc aac gct	355
Val Met Leu Leu Pro Thr His Asp Ser Gln Phe Gly Gly Leu Asn Ala	
70 75 80 85	
aag gaa aag aac cgc gag gat aaa ggc acg atc atc aac ctg gtg gtc	403
Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile Ile Asn Leu Val Val	
90 95 100	
aac gat gat att cat tcc gtt gtc act cca gaa ctt ctt gac agc gat	451
Asn Asp Asp Ile His Ser Val Val Thr Pro Glu Leu Leu Asp Ser Asp	
105 110 115	
gtg ctt ggt gtc att cct gat gca gat tct ttc gat cgc atg gat gag	499
Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe Asp Arg Met Asp Glu	
120 125 130	
ttt gat tta ctg cgt aac aaa gca cgc tgg cac tac gga gtg gct gca	547
Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His Tyr Gly Val Ala Ala	
135 140 145	
att gaa cct gac acg ggt gag ctg gtg gtg ttt aag gtg ccc gcg aaa	595
Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe Lys Val Pro Ala Lys	
150 155 160 165	
aat agc gct tcg gca cgc ggt gac att ttt tcc gag gtc ggc gat gtg	643
Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser Glu Val Gly Asp Val	
170 175 180	
ctt agc ggt gct gct gac ctc gaa gac gtg gtt gat ttt gag gtc att	691
Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val Asp Phe Glu Val Ile	
185 190 195	
gcc acc ttc cta gag gtg ctg aat gag acc tct gag gtg gat att gat	739
Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser Glu Val Asp Ile Asp	
200 205 210	
gac gaa gat ggc gac gtg cct tat ggt ctt gag ggt gtc aat gca gcg	787
Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu Gly Val Asn Ala Ala	
215 220 225	
gga gtt atc acg gat gac ctc att cgc gag aag ctt gat gtg gat tcc	835
Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys Leu Asp Val Asp Ser	
230 235 240 245	
tat ccg agc agt gca gag atc att gac aat att gtg cat gtg ttc acc	883
Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile Val His Val Phe Thr	
250 255 260	
aag ttg cag ggc aag cat cat gtg gca cca cag ccg gtg ctt cac agc	931
Lys Leu Gln Gly Lys His His Val Ala Pro Gln Pro Val Leu His Ser	
265 270 275	
gca gac gta gtg gat gtt gat gca cag gag tcc cat gac aca gtg gtt	979
Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser His Asp Thr Val Val	
280 285 290	

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Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu Gln Val Asp Val Pro	
295 300 305	
gat ttc agt gat gga ttt ggt att gac gat gcc gag gtt act gag cca	1075
Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala Glu Val Thr Glu Pro	
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Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp Ala Asp Pro Phe Gly	
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Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp Asp Glu Pro Asp Phe	
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Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro Val Ala Gly Met Ser	
360 365 370	
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Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val Ser Glu Ser Val Gln	
375 380 385	
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Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg Glu Glu Leu Ala Gln	
390 395 400 405	
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Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln Ala Ala Leu Ala Gln	
410 415 420	
gtg cac gca gct gat gcc cgc agc ttt gat gcc gat caa gtg ggt gat	1411
Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala Asp Gln Val Gly Asp	
425 430 435	
gct gtc acc aaa cgt tat gtt aat gac gac ttg ggg ctg tat gtc gat	1459
Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu Gly Leu Tyr Val Asp	
440 445 450	
gag gca aac ttc aat aat gct ttg acc agg gca ccg ttc cag gtg gcg	1507
Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala Pro Phe Gln Val Ala	
455 460 465	
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Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu Gly Asp Gln Leu Arg	
470 475 480 485	
aca ttg gtg gct gtg ttt aat ggt cag ctg ctt gat cag cat cag cgt	1603
Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu Asp Gln His Gln Arg	
490 495 500	
gac tac gaa gaa gtg cgc gcg atg tac att gcg ctt aat gat cgc tct	1651
Asp Tyr Glu Glu Val Arg Ala Met Tyr Ile Ala Leu Asn Asp Arg Ser	
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aat ctt gag atc gct cgt gat ctt gga ctg gat aat aag gat tcc gaa	1699
Asn Leu Glu Ile Ala Arg Asp Leu Gly Leu Asp Asn Lys Asp Ser Glu	
520 525 530	
ttc tac gag gtt tac cgt gcc att gag cgt gac cgc gat gtt atg gct	1747

Phe	Tyr	Glu	Val	Tyr	Arg	Ala	Ile	Glu	Arg	Asp	Arg	Asp	Val	Met	Ala		
535						540					545						
ggt	gat	caa	cag	cgt	gtg	gag	tca	gag	cgt	cgt	cag	caa	ttg	cag	cag		1795
Gly	Asp	Gln	Gln	Arg	Val	Glu	Ser	Glu	Arg	Arg	Gln	Gln	Leu	Gln	Gln		
550					555					560					565		
gag	tat	gag	gcg	aac	cgt	gaa	gaa	tat	gtc	atg	gca	aag	atc	gcg	gag		1843
Glu	Tyr	Glu	Ala	Asn	Arg	Glu	Glu	Tyr	Val	Met	Ala	Lys	Ile	Ala	Glu		
				570					575					580			
cag	cgc	gtg	gag	tat	gat	cgc	cgt	cat	atg	cct	cgc	cat	acc	gca	tca		1891
Gln	Arg	Val	Glu	Tyr	Asp	Arg	Arg	His	Met	Pro	Arg	His	Thr	Ala	Ser		
			585					590					595				
cta	gaa	gcg	gta	ggt	cga	gag	ctg	acg	agc	ctg	cgg	gat	cgc	acc	att		1939
Leu	Glu	Ala	Val	Gly	Arg	Glu	Leu	Thr	Ser	Leu	Arg	Asp	Arg	Thr	Ile		
		600					605					610					
gag	gat	tac	acc	gca	cgc	atg	aac	acg	ctg	cgt	cgt	gca	cgt	gct	ggt		1987
Glu	Asp	Tyr	Thr	Ala	Arg	Met	Asn	Thr	Leu	Arg	Arg	Ala	Arg	Ala	Gly		
	615					620					625						
gaa	cgg	gct	aac	gct	gca	gaa	tct	cgc	att	att	gac	gaa	ttg	cgc	ccg		2035
Glu	Arg	Ala	Asn	Ala	Ala	Glu	Ser	Arg	Ile	Ile	Asp	Glu	Leu	Arg	Pro		
630					635					640					645		
att	gtg	gag	cgc	cag	gca	gaa	ctg	caa	cga	gca	gct	ttc	gat	ggt	ttc		2083
Ile	Val	Glu	Arg	Gln	Ala	Glu	Leu	Gln	Arg	Ala	Ala	Phe	Asp	Gly	Phe		
				650					655					660			
att	gtt	gat	ctt	gac	aag	ttt	att	gct	gat	cac	cgc	gaa	gat	gac	ctg		2131
Ile	Val	Asp	Leu	Asp	Lys	Phe	Ile	Ala	Asp	His	Arg	Glu	Asp	Asp	Leu		
			665					670					675				
cgt	ttg	gca	tcg	gtg	aat	gag	cag	aag	ctt	gct	gca	gat	aat	cgt	gtg		2179
Arg	Leu	Ala	Ser	Val	Asn	Glu	Gln	Lys	Leu	Ala	Ala	Asp	Asn	Arg	Val		
		680					685					690					
gca	cag	ttg	acc	aag	gaa	gcc	gaa	gag	cgc	atc	gag	ggt	atc	cgc	gtc		2227
Ala	Gln	Leu	Thr	Lys	Glu	Ala	Glu	Glu	Arg	Ile	Glu	Gly	Ile	Arg	Val		
		695				700					705						
gag	acc	gat	aag	atg	atc	gcc	tcc	cag	cgc	aag	gca	ctt	gag	cgt	cag		2275
Glu	Thr	Asp	Lys	Met	Ile	Ala	Ser	Gln	Arg	Lys	Ala	Leu	Glu	Arg	Gln		
710					715					720					725		
gaa	gcg	gaa	ttc	gca	gca	gag	ctt	aag	cgt	cgc	gac	act	att	gtc	gct		2323
Glu	Ala	Glu	Phe	Ala	Ala	Glu	Leu	Lys	Arg	Arg	Asp	Thr	Ile	Val	Ala		
				730					735					740			
gca	tcg	gag	gaa	cgt	gct	gag	cgg	gaa	att	acc	aca	gca	cgt	ctt	gat		2371
Ala	Ser	Glu	Glu	Arg	Ala	Glu	Arg	Glu	Ile	Thr	Thr	Ala	Arg	Leu	Asp		
			745				750						755				
gct	gag	gcg	gcg	ctc	aag	cgc	atg	gaa	gag	caa	att	cgt	gta	aat	aat		2419
Ala	Glu	Ala	Ala	Leu	Lys	Arg	Met	Glu	Glu	Gln	Ile	Arg	Val	Asn	Asn		
		760					765					770					
gag	gcg	cat	gag	gcg	gag	att	gtt	att	gag	cgc	gat	cga	gcc	acc	caa		2467
Glu	Ala	His	Glu	Ala	Glu	Ile	Val	Ile	Glu	Arg	Asp	Arg	Ala	Thr	Gln		

775	780	785	
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Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln Asp			
790	795	800	805
cgc agc aac aac atc att ttg att gcc gtc ctc att gtg ggg ctg att			2563
Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu Ile			
	810	815	820
gcc ggc atg gtc gct ggc gca gcc ttc ttc taaaagatcg ttgcgcgggc			2613
Ala Gly Met Val Ala Gly Ala Ala Phe Phe			
	825	830	
tgt			2616
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Arg Lys Glu Glu Arg Leu Ala Ser Val Ile Gln Glu Thr Glu Pro Gly			
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Ala Ala Val Glu Val Met Arg Arg Asn Asp Ala Phe Ala Leu Pro Gly			
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Glu Thr Gly Trp Val Val Met Leu Leu Pro Thr His Asp Ser Gln Phe			
	65	70	75
Gly Gly Leu Asn Ala Lys Glu Lys Asn Arg Glu Asp Lys Gly Thr Ile			
	85	90	95
Ile Asn Leu Val Val Asn Asp Asp Ile His Ser Val Val Thr Pro Glu			
	100	105	110
Leu Leu Asp Ser Asp Val Leu Gly Val Ile Pro Asp Ala Asp Ser Phe			
	115	120	125
Asp Arg Met Asp Glu Phe Asp Leu Leu Arg Asn Lys Ala Arg Trp His			
	130	135	140
Tyr Gly Val Ala Ala Ile Glu Pro Asp Thr Gly Glu Leu Val Val Phe			
	145	150	155
Lys Val Pro Ala Lys Asn Ser Ala Ser Ala Arg Gly Asp Ile Phe Ser			
	165	170	175
Glu Val Gly Asp Val Leu Ser Gly Ala Ala Asp Leu Glu Asp Val Val			
	180	185	190
Asp Phe Glu Val Ile Ala Thr Phe Leu Glu Val Leu Asn Glu Thr Ser			
	195	200	205

Glu Val Asp Ile Asp Asp Glu Asp Gly Asp Val Pro Tyr Gly Leu Glu
210 215 220

Gly Val Asn Ala Ala Gly Val Ile Thr Asp Asp Leu Ile Arg Glu Lys
225 230 235 240

Leu Asp Val Asp Ser Tyr Pro Ser Ser Ala Glu Ile Ile Asp Asn Ile
245 250 255

Val His Val Phe Thr Lys Leu Gln Gly Lys His His Val Ala Pro Gln
260 265 270

Pro Val Leu His Ser Ala Asp Val Val Asp Val Asp Ala Gln Glu Ser
275 280 285

His Asp Thr Val Val Ile Glu Ser Pro Asp Asp Val Ala Leu Ala Glu
290 295 300

Gln Val Asp Val Pro Asp Phe Ser Asp Gly Phe Gly Ile Asp Asp Ala
305 310 315 320

Glu Val Thr Glu Pro Glu Asp Glu Glu Val Val Glu Ala Thr Ala Asp
325 330 335

Ala Asp Pro Phe Gly Asp Val Ala Glu Asp Asp Pro Phe Gly Ser Asp
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Asp Glu Pro Asp Phe Gly Ala Ser Asp Val Val Ala Ala Pro Ala Pro
355 360 365

Val Ala Gly Met Ser Asp Glu Gln Ile Gln Ala Leu Ile Arg Gly Val
370 375 380

Ser Glu Ser Val Gln Ala Lys Thr Gly Ser Glu Leu Asn Ala Leu Arg
385 390 395 400

Glu Glu Leu Ala Gln Ala Leu Ala Tyr Asn Pro Val Gln Asp Ser Gln
405 410 415

Ala Ala Leu Ala Gln Val His Ala Ala Asp Ala Arg Ser Phe Asp Ala
420 425 430

Asp Gln Val Gly Asp Ala Val Thr Lys Arg Tyr Val Asn Asp Asp Leu
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Gly Leu Tyr Val Asp Glu Ala Asn Phe Asn Asn Ala Leu Thr Arg Ala
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Pro Phe Gln Val Ala Met Pro Gln Phe Gln Glu Thr Thr Pro Trp Leu
465 470 475 480

Gly Asp Gln Leu Arg Thr Leu Val Ala Val Phe Asn Gly Gln Leu Leu
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Asp Gln His Gln Arg Asp Tyr Glu Glu Val Arg Ala Met Tyr Ile Ala
500 505 510

Leu Asn Asp Arg Ser Asn Leu Glu Ile Ala Arg Asp Leu Gly Leu Asp
515 520 525

Asn Lys Asp Ser Glu Phe Tyr Glu Val Tyr Arg Ala Ile Glu Arg Asp
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 Ala Lys Ile Ala Glu Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro
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 Arg His Thr Ala Ser Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu
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 Arg Asp Arg Thr Ile Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg
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 Arg Ala Arg Ala Gly Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile
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 Asp Glu Leu Arg Pro Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala
 645 650 655
 Ala Phe Asp Gly Phe Ile Val Asp Leu Asp Lys Phe Ile Ala Asp His
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 Arg Glu Asp Asp Leu Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala
 675 680 685
 Ala Asp Asn Arg Val Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile
 690 695 700
 Glu Gly Ile Arg Val Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys
 705 710 715 720
 Ala Leu Glu Arg Gln Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg
 725 730 735
 Asp Thr Ile Val Ala Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr
 740 745 750
 Thr Ala Arg Leu Asp Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln
 755 760 765
 Ile Arg Val Asn Asn Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg
 770 775 780
 Asp Arg Ala Thr Gln Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser
 785 790 795 800
 Val Lys Gln Gln Asp Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu
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<210> 1397

<211> 1116

<212> DNA

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aag gaa gcc gaa gag cgc atc gag ggt atc cgc gtc gag acc gat aag 739
Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg Val Glu Thr Asp Lys
200 205 210

atg atc gcc tcc cag cgc aag gca ctt gag cgt cag gaa gcg gaa ttc 787
Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg Gln Glu Ala Glu Phe
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gca gca gag ctt aag cgt cgc gac act att gtc gct gca tcg gag gaa 835
Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val Ala Ala Ser Glu Glu
230 235 240 245

cgt gct gag cgg gaa att acc aca gca cgt ctt gat gct gag gcg gcg 883
Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu Asp Ala Glu Ala Ala
250 255 260

ctc aag cgc atg gaa gag caa att cgt gta aat aat gag gcg cat gag 931
Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn Asn Glu Ala His Glu
265 270 275

gcg gag att gtt att gag cgc gat cga gcc acc caa gca gag gcg aac 979
Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr Gln Ala Glu Ala Asn
280 285 290

tcc atg acg ttt gtt gag tca gtc aag cag cag gat cgc agc aac aac 1027
Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln Asp Arg Ser Asn Asn
295 300 305

atc att ttg att gcc gtc ctc att gtg ggg ctg att gcc ggc atg gtc 1075
Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu Ile Ala Gly Met Val
310 315 320 325

gct ggc gca gcc ttc ttc taaaagatcg ttgcgcgggc tgt 1116
Ala Gly Ala Ala Phe
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<210> 1398

<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 1398

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20 25 30

Glu Phe Tyr Glu Val Tyr Arg Ala Ile Glu Arg Asp Arg Asp Val Met
35 40 45

Ala Gly Asp Gln Gln Arg Val Glu Ser Glu Arg Arg Gln Gln Leu Gln
50 55 60

Gln Glu Tyr Glu Ala Asn Arg Glu Glu Tyr Val Met Ala Lys Ile Ala
65 70 75 80

Glu Gln Arg Val Glu Tyr Asp Arg Arg His Met Pro Arg His Thr Ala
85 90 95

Ser Leu Glu Ala Val Gly Arg Glu Leu Thr Ser Leu Arg Asp Arg Thr
100 105 110
Ile Glu Asp Tyr Thr Ala Arg Met Asn Thr Leu Arg Arg Ala Arg Ala
115 120 125
Gly Glu Arg Ala Asn Ala Ala Glu Ser Arg Ile Ile Asp Glu Leu Arg
130 135 140
Pro Ile Val Glu Arg Gln Ala Glu Leu Gln Arg Ala Ala Phe Asp Gly
145 150 155 160
Phe Ile Val Asp Leu Asp Lys Phe Ile Ala Asp His Arg Glu Asp Asp
165 170 175
Leu Arg Leu Ala Ser Val Asn Glu Gln Lys Leu Ala Ala Asp Asn Arg
180 185 190
Val Ala Gln Leu Thr Lys Glu Ala Glu Glu Arg Ile Glu Gly Ile Arg
195 200 205
Val Glu Thr Asp Lys Met Ile Ala Ser Gln Arg Lys Ala Leu Glu Arg
210 215 220
Gln Glu Ala Glu Phe Ala Ala Glu Leu Lys Arg Arg Asp Thr Ile Val
225 230 235 240
Ala Ala Ser Glu Glu Arg Ala Glu Arg Glu Ile Thr Thr Ala Arg Leu
245 250 255
Asp Ala Glu Ala Ala Leu Lys Arg Met Glu Glu Gln Ile Arg Val Asn
260 265 270
Asn Glu Ala His Glu Ala Glu Ile Val Ile Glu Arg Asp Arg Ala Thr
275 280 285
Gln Ala Glu Ala Asn Ser Met Thr Phe Val Glu Ser Val Lys Gln Gln
290 295 300
Asp Arg Ser Asn Asn Ile Ile Leu Ile Ala Val Leu Ile Val Gly Leu
305 310 315 320
Ile Ala Gly Met Val Ala Gly Ala Ala Phe Phe
325 330

<210> 1399

<211> 1539

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1516)

<223> RXN03024

<400> 1399

ctctacccac ttaaaatgga cgcatattcg caagataagg catgcttgga tgaatagatt 60

ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca 115

	Met	Leu	Glu	Arg	Thr	
	1				5	
cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct						163
Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser						
	10				20	
tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta						211
Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val						
	25				35	
gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta						259
Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val						
	40				50	
caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc						307
Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg						
	55				65	
tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc						355
Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly						
	70				80	85
caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc						403
Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr						
	90				95	100
cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc						451
Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser						
	105				110	115
gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa						499
Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln						
	120				125	130
gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg						547
Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp						
	135				140	145
gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att						595
Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile						
	150				155	160
ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc						643
Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu						
	170				175	180
gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca						691
Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala						
	185				190	195
gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca						739
Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser						
	200				205	210
cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca						787
Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro						
	215				220	225
agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat						835
Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr						

230	235	240	245	
gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc				883
Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr	250	255	260	
gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa				931
Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu	265	270	275	
cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa				979
Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu	280	285	290	
gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag				1027
Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys	295	300	305	
act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act				1075
Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr	310	315	320	325
cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca				1123
Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro	330	335	340	
gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca				1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser	345	350	355	
cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt				1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu	360	365	370	
cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga				1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly	375	380	385	
ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt				1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe	390	395	400	405
gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct				1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser	410	415	420	
ggg ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct				1411
Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala	425	430	435	
tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct				1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala	440	445	450	
tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag				1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln	455	460	465	
cga gat agc tagaatcaca aaaaactggg gct				1539
Arg Asp Ser				
470				

<210> 1400

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 1400

Met Leu Glu Arg Thr Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala
1 5 10 15

Ser Phe Tyr Asn Ser Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile
20 25 30

Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
35 40 45

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
50 55 60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
65 70 75 80

Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
85 90 95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
100 105 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
115 120 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
130 135 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145 150 155 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
165 170 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
180 185 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
195 200 205

Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
210 215 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225 230 235 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
245 250 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
260 265 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
275 280 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
 290 295 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
 305 310 315 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
 325 330 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
 340 345 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
 355 360 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
 370 375 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
 385 390 395 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
 405 410 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
 420 425 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
 435 440 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
 450 455 460

Val Leu Leu Asn Gln Arg Asp Ser
 465 470

<210> 1401
 <211> 996
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(973)
 <223> RXN03025

<400> 1401
 agcgaatcgg attcagtgat ttgcttgccg gcgcagaaat gatttttcaa ttagacacac 60
 ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc 115
 Met Ala Asn Pro Leu
 1 5

agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat 163
 Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
 10 15 20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc 211
 Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala

25	30	35	
cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly 40 45 50			259
cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg 55 60 65			307
gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys 70 75 80 85			355
tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr 90 95 100			403
gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu 105 110 115			451
cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala 120 125 130			499
gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser 135 140 145			547
cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu 150 155 160 165			595
agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp 170 175 180			643
tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg 185 190 195			691
tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser 200 205 210			739
gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgg gcg tca Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser 215 220 225			787
gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr 230 235 240 245			835
cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile 250 255 260			883
gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu 265 270 275			931

gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa
 Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
 280 285 290

973

taacctaacc acaaaaaact ggg

996

<210> 1402

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 1402

Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
 1 5 10 15

Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
 20 25 30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
 35 40 45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
 50 55 60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
 65 70 75 80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
 85 90 95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
 100 105 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
 115 120 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
 130 135 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
 145 150 155 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
 165 170 175

Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
 180 185 190

Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
 195 200 205

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
 210 215 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
 225 230 235 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
 245 250 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
260 265 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
275 280 285

Glu Lys Lys
290

<210> 1403

<211> 174

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (17)..(151)

<223> RXN03027

<400> 1403

aataggagaa tttaaa atg gaa aac gtt tac gag ttc ctt gga aac ctt gat 52
Met Glu Asn Val Tyr Glu Phe Leu Gly Asn Leu Asp
1 5 10

gtc ctt tcc ggc tcc ggc ctc atc ggc tac gtc ttc gac ttc ctc ggc 100
Val Leu Ser Gly Ser Gly Leu Ile Gly Tyr Val Phe Asp Phe Leu Gly
15 20 25

gct tcc agc aag tgg gct ggc gca gtt gct gac ctc atc ggt ctg ctt 148
Ala Ser Ser Lys Trp Ala Gly Ala Val Ala Asp Leu Ile Gly Leu Leu
30 35 40

ggc taattaactt cgcccacggg caa 174
Gly
45

<210> 1404

<211> 45

<212> PRT

<213> Corynebacterium glutamicum

<400> 1404

Met Glu Asn Val Tyr Glu Phe Leu Gly Asn Leu Asp Val Leu Ser Gly
1 5 10 15

Ser Gly Leu Ile Gly Tyr Val Phe Asp Phe Leu Gly Ala Ser Ser Lys
20 25 30

Trp Ala Gly Ala Val Ala Asp Leu Ile Gly Leu Leu Gly
35 40 45

<210> 1405

<211> 630

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (95)..(607)

<223> RXN03029

<400> 1405

gggtgtggctt cctattcgct gcatacctgaa tatgccatca aaatcttcac tctgaggccg 60

aaaaatccgg ttatgacatt aagtacctag gaca atg ttt gga gtg ggc tat tat 115

Met Phe Gly Val Gly Tyr Tyr
1 5aca acc gcc cac cga ttg tcc acc ctg cag cgc ccc aac ttg cgc ggc 163
Thr Thr Ala His Arg Leu Ser Thr Leu Gln Arg Pro Asn Leu Arg Gly
10 15 20atc ccc tta acc ttc gtg agc gtc gac cga gcc ggc aac atg tcc aaa 211
Ile Pro Leu Thr Phe Val Ser Val Asp Arg Ala Gly Asn Met Ser Lys
25 30 35cgc caa tcc gcc acg ggc ttc cac ttc acc cat tac ggc ggc acc tgc 259
Arg Gln Ser Ala Thr Gly Phe His Phe Thr His Tyr Gly Gly Thr Cys
40 45 50 55ccc ctg tgg aac gtg ttt gaa acc ttc acc aac ccc ggc caa gtg ctc 307
Pro Leu Trp Asn Val Phe Glu Thr Phe Thr Asn Pro Gly Gln Val Leu
60 65 70cgc caa ttc gcg caa atg ccc gac gga cgc aac tac ctg tgg atc tca 355
Arg Gln Phe Ala Gln Met Pro Asp Gly Arg Asn Tyr Leu Trp Ile Ser
75 80 85cgc acc gtg cga cac cac gaa gcc cgg ttc ggc gaa gta gac aaa atg 403
Arg Thr Val Arg His His Glu Ala Arg Phe Gly Glu Val Asp Lys Met
90 95 100ttc gcc atc ggc ttg ggc tgc gaa gcg cgc cac gcc gac cgc act gtg 451
Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg His Ala Asp Arg Thr Val
105 110 115tac tcc cgc ggt ttc aac ctc cag gac ctc tcc acc gcc acc ccc atc 499
Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu Ser Thr Ala Thr Pro Ile
120 125 130 135ggg tcc ggc tgc cga gtg tgc acc cgc gag aac tgc gcg cag cgc gca 547
Gly Ser Gly Cys Arg Val Cys Thr Arg Glu Asn Cys Ala Gln Arg Ala
140 145 150ttc cca tcc gtc cac ggc cgc atc aac atc gac gcg cac gaa tcc act 595
Phe Pro Ser Val His Gly Arg Ile Asn Ile Asp Ala His Glu Ser Thr
155 160 165atc gcg ccg tac taagaaaagg agcttgcttt acg 630
Ile Ala Pro Tyr
170

<210> 1406

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1406

Met Phe Gly Val Gly Tyr Tyr Thr Thr Ala His Arg Leu Ser Thr Leu
 1 5 10 15
 Gln Arg Pro Asn Leu Arg Gly Ile Pro Leu Thr Phe Val Ser Val Asp
 20 25 30
 Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe
 35 40 45
 Thr His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe
 50 55 60
 Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly
 65 70 75 80
 Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg
 85 90 95
 Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala
 100 105 110
 Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp
 115 120 125
 Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg
 130 135 140
 Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg Ile Asn
 145 150 155 160
 Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
 165 170

<210> 1407

<211> 789

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(789)

<223> RXN03031

<400> 1407

aac aac ggc ctt aac gcc atg gcc gcg atg acc aac ctc cca cac ctg 48
 Asn Asn Gly Leu Asn Ala Met Ala Ala Met Thr Asn Leu Pro His Leu
 1 5 10 15
 cgc gcc atc caa gaa cgc tac tac ttc ctg agc atc cgc tac ctc gcc 96
 Arg Ala Ile Gln Glu Arg Tyr Tyr Phe Leu Ser Ile Arg Tyr Leu Ala
 20 25 30
 tcc atc atg atc gcc gtg gcc aaa gca gac ccc acc ctg tgg gaa gaa 144
 Ser Ile Met Ile Ala Val Ala Lys Ala Asp Pro Thr Leu Trp Glu Glu
 35 40 45
 ctc gac ctg cgc atc acc gac gcc tta aca cca gtc acc gca ggg gaa 192
 Leu Asp Leu Arg Ile Thr Asp Ala Leu Thr Pro Val Thr Ala Gly Glu
 50 55 60

gtg atg atc caa tcc tcc acc ctg tcc aaa cgc atc gcc gcc tgg atc	240
Val Met Ile Gln Ser Ser Thr Leu Ser Lys Arg Ile Ala Ala Trp Ile	
65 70 75 80	
aaa gaa ctc gac ccc gaa ccc aca cca gag ccc ata ccg aaa gag gac	288
Lys Glu Leu Asp Pro Glu Pro Thr Pro Glu Pro Ile Pro Lys Glu Asp	
85 90 95	
tat gtt cac gtc cac acc act gat gag gcg acc tat gtc cgc atc aaa	336
Tyr Val His Val His Thr Thr Asp Glu Ala Thr Tyr Val Arg Ile Lys	
100 105 110	
atc agc ggc ccc aac cgc ctg atc ctc aat gac atc atc acc caa ctc	384
Ile Ser Gly Pro Asn Arg Leu Ile Leu Asn Asp Ile Ile Thr Gln Leu	
115 120 125	
aaa gac aca gac acc gag gac agc ctg cct gaa gcg ctc atg gcg ttc	432
Lys Asp Thr Asp Thr Glu Asp Ser Leu Pro Glu Ala Leu Met Ala Phe	
130 135 140	
ctg atg gag aaa atc cag tta aag atc acc aag tac ctt ttc acc cca	480
Leu Met Glu Lys Ile Gln Leu Lys Ile Thr Lys Tyr Leu Phe Thr Pro	
145 150 155 160	
cat aag cac cct gag cag gtg tgg tca ccg gac tac ggt gac att ggt	528
His Lys His Pro Glu Gln Val Trp Ser Pro Asp Tyr Gly Asp Ile Gly	
165 170 175	
ccc gaa gcc tat gcc aat gcc acc ctc gtg tgc gcc aag gac tta gat	576
Pro Glu Ala Tyr Ala Asn Ala Thr Leu Val Cys Ala Lys Asp Leu Asp	
180 185 190	
gag gtc gct gga gcc acg gag aag agc tac acc ccg agt gag aag atg	624
Glu Val Ala Gly Ala Thr Glu Lys Ser Tyr Thr Pro Ser Glu Lys Met	
195 200 205	
aaa gcc ctg atc aga gct cgg gat ggg cat tgc cgc ttc cca ggg tgt	672
Lys Ala Leu Ile Arg Ala Arg Asp Gly His Cys Arg Phe Pro Gly Cys	
210 215 220	
tgc gtc ccg gcg agt aaa tgc cag gtc gat cac att atc ccg tgg gcg	720
Cys Val Pro Ala Ser Lys Cys Gln Val Asp His Ile Ile Pro Trp Ala	
225 230 235 240	
gag ggc ggc ccg aca gcg gcg tgg aac ctg cag ttg ttg tgc cag cgg	768
Glu Gly Gly Pro Thr Ala Ala Trp Asn Leu Gln Leu Leu Cys Gln Arg	
245 250 255	
cat cac aat atg aaa acc gat	789
His His Asn Met Lys Thr Asp	
260	

<210> 1408

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 1408

Asn Asn Gly Leu Asn Ala Met Ala Ala Met Thr Asn Leu Pro His Leu

1 5 10 15
Arg Ala Ile Gln Glu Arg Tyr Tyr Phe Leu Ser Ile Arg Tyr Leu Ala
20 25 30
Ser Ile Met Ile Ala Val Ala Lys Ala Asp Pro Thr Leu Trp Glu Glu
35 40 45
Leu Asp Leu Arg Ile Thr Asp Ala Leu Thr Pro Val Thr Ala Gly Glu
50 55 60
Val Met Ile Gln Ser Ser Thr Leu Ser Lys Arg Ile Ala Ala Trp Ile
65 70 75 80
Lys Glu Leu Asp Pro Glu Pro Thr Pro Glu Pro Ile Pro Lys Glu Asp
85 90 95
Tyr Val His Val His Thr Thr Asp Glu Ala Thr Tyr Val Arg Ile Lys
100 105 110
Ile Ser Gly Pro Asn Arg Leu Ile Leu Asn Asp Ile Ile Thr Gln Leu
115 120 125
Lys Asp Thr Asp Thr Glu Asp Ser Leu Pro Glu Ala Leu Met Ala Phe
130 135 140
Leu Met Glu Lys Ile Gln Leu Lys Ile Thr Lys Tyr Leu Phe Thr Pro
145 150 155 160
His Lys His Pro Glu Gln Val Trp Ser Pro Asp Tyr Gly Asp Ile Gly
165 170 175
Pro Glu Ala Tyr Ala Asn Ala Thr Leu Val Cys Ala Lys Asp Leu Asp
180 185 190
Glu Val Ala Gly Ala Thr Glu Lys Ser Tyr Thr Pro Ser Glu Lys Met
195 200 205
Lys Ala Leu Ile Arg Ala Arg Asp Gly His Cys Arg Phe Pro Gly Cys
210 215 220
Cys Val Pro Ala Ser Lys Cys Gln Val Asp His Ile Ile Pro Trp Ala
225 230 235 240
Glu Gly Gly Pro Thr Ala Ala Trp Asn Leu Gln Leu Leu Cys Gln Arg
245 250 255
His His Asn Met Lys Thr Asp
260

<210> 1409

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXN03032

<400> 1409

cctgggtcata ggataacttag ctcaaccaca cggtcagggc cagcaattcc tcacgtttta 60

ccaactccgt aagcacacca tcatggcctg gtgcgccgct atg acc gac ggg gac 115
Met Thr Asp Gly Asp
1 5

tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc acc cga 163
Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr Thr Arg
10 15 20

acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa caa cta 211
Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln Gln Leu
25 30 35

gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc gca gcg 259
Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile Ala Ala
40 45 50

ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag aat caa 307
Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln Asn Gln
55 60 65

atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc aat cct 355
Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro Asn Pro
70 75 80 85

ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga tgagcaacgc 405
Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
90 95

gcc 408

<210> 1410

<211> 95

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1410

Met Thr Asp Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly
1 5 10 15

Leu Met Thr Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met
20 25 30

Ile Ala Gln Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu
35 40 45

Lys Glu Ile Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys
50 55 60

Asp His Gln Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly
65 70 75 80

Thr Arg Pro Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
85 90 95

<210> 1411

<211> 683

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(660)

<223> RXN03034

<400> 1411

ttc cca cca gat cga atc tcc gcc aac ggg cga cgc tat tac gag cca	48
Phe Pro Pro Asp Arg Ile Ser Ala Asn Gly Arg Arg Tyr Tyr Glu Pro	
1 5 10 15	
caa aca cga ctc gag ttc atg cgg atc tac acc acc ctg ccg cac ggc	96
Gln Thr Arg Leu Glu Phe Met Arg Ile Tyr Thr Thr Leu Pro His Gly	
20 25 30	
tac cgc cag ccc ttc ctt aaa gcc aac aac atc ggc cac tgc acc gtt	144
Tyr Arg Gln Pro Phe Leu Lys Ala Asn Asn Ile Gly His Cys Thr Val	
35 40 45	
cga acc tgg cta gca gca ata agc acc ttc agc cga ctt ccc cat gct	192
Arg Thr Trp Leu Ala Ala Ile Ser Thr Phe Ser Arg Leu Pro His Ala	
50 55 60	
ttt gat gat gcc cac cgc ttc ggg atc gaa cgc acc acc cca gtc gac	240
Phe Asp Asp Ala His Arg Phe Gly Ile Glu Arg Thr Thr Pro Val Asp	
65 70 75 80	
gat gtc acc aca cta acg gct gat gac aaa cgt gac ctg gtc ata gga	288
Asp Val Thr Thr Leu Thr Ala Asp Asp Lys Arg Asp Leu Val Ile Gly	
85 90 95	
tac tta gct caa cca cac ggt cag ggc cag caa ttc ctc acg ttt tac	336
Tyr Leu Ala Gln Pro His Gly Gln Gly Gln Gln Phe Leu Thr Phe Tyr	
100 105 110	
caa ctc cgt aag cac acc atc atg gcc tgg tgc gcc gct atg acc gac	384
Gln Leu Arg Lys His Thr Ile Met Ala Trp Cys Ala Ala Met Thr Asp	
115 120 125	
ggg gac tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc	432
Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr	
130 135 140	
acc cga acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa	480
Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln	
145 150 155 160	
caa cta gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc	528
Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile	
165 170 175	
gca gcg ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag	576
Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln	
180 185 190	
aat caa atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc	624
Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro	
195 200 205	

aat cct ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga 670
Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
210 215 220

tgagcaacgc gcc

683

<210> 1412
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 1412
Phe Pro Pro Asp Arg Ile Ser Ala Asn Gly Arg Arg Tyr Tyr Glu Pro
1 5 10 15
Gln Thr Arg Leu Glu Phe Met Arg Ile Tyr Thr Thr Leu Pro His Gly
20 25 30
Tyr Arg Gln Pro Phe Leu Lys Ala Asn Asn Ile Gly His Cys Thr Val
35 40 45
Arg Thr Trp Leu Ala Ala Ile Ser Thr Phe Ser Arg Leu Pro His Ala
50 55 60
Phe Asp Asp Ala His Arg Phe Gly Ile Glu Arg Thr Thr Pro Val Asp
65 70 75 80
Asp Val Thr Thr Leu Thr Ala Asp Asp Lys Arg Asp Leu Val Ile Gly
85 90 95
Tyr Leu Ala Gln Pro His Gly Gln Gly Gln Gln Phe Leu Thr Phe Tyr
100 105 110
Gln Leu Arg Lys His Thr Ile Met Ala Trp Cys Ala Ala Met Thr Asp
115 120 125
Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr
130 135 140
Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln
145 150 155 160
Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile
165 170 175
Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln
180 185 190
Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro
195 200 205
Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
210 215 220

<210> 1413
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> FRXA00063

<400> 1413

cctggtcata ggatacttag ctcaaccaca cggtcagggc cagcaattcc tcacgtttta 60
ccaactccgt aagcacacca tcatggcctg gtgcgccgct atg acc gac ggg gac 115
Met Thr Asp Gly Asp
1 5
tta gac gct gat atc tca ccc cgc cag atc ggg ttg atg acc acc cga 163
Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly Leu Met Thr Thr Arg
10 15 20
acc gtg gtc gaa atc gtt cga cta cgc cac atg att gcc caa caa cta 211
Thr Val Val Glu Ile Val Arg Leu Arg His Met Ile Ala Gln Gln Leu
25 30 35
gaa aga gcc acg atc atg gaa aac gag tac ctc aaa gaa atc gca gcg 259
Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu Lys Glu Ile Ala Ala
40 45 50
ctg aag aaa gaa ctc gcg cac tac aag caa aaa gac cat cag aat caa 307
Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys Asp His Gln Asn Gln
55 60 65
atg gtg atc gat atc ttg gga aaa gct att ggg acc agg ccc aat cct 355
Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly Thr Arg Pro Asn Pro
70 75 80 85
ggc gag ggc tta gac gag gag gac gcc acc taaacgtgga tgagcaacgc 405
Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr
90 95
gcc 408

<210> 1414

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1414

Met Thr Asp Gly Asp Leu Asp Ala Asp Ile Ser Pro Arg Gln Ile Gly
1 5 10 15
Leu Met Thr Thr Arg Thr Val Val Glu Ile Val Arg Leu Arg His Met
20 25 30
Ile Ala Gln Gln Leu Glu Arg Ala Thr Ile Met Glu Asn Glu Tyr Leu
35 40 45
Lys Glu Ile Ala Ala Leu Lys Lys Glu Leu Ala His Tyr Lys Gln Lys
50 55 60
Asp His Gln Asn Gln Met Val Ile Asp Ile Leu Gly Lys Ala Ile Gly
65 70 75 80
Thr Arg Pro Asn Pro Gly Glu Gly Leu Asp Glu Glu Asp Ala Thr

85

90

95

<210> 1415
<211> 309
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(286)
<223> RXN03037

<400> 1415
cgctaaaaga caaatgacag cgaagctgca ttcggataca cacctgaaga acactcttca 60
ccactagcat tocaccaacg cctcggaaag ggctatctcc atg tct gtt gac gat 115
Met Ser Val Asp Asp
1 5
ctt tac gct gtt gct ctc gat act cac acc ggt aag cct atc ccc tgc 163
Leu Tyr Ala Val Ala Leu Asp Thr His Thr Gly Lys Pro Ile Pro Cys
10 15 20
gta ctc tgt gaa aat gct cca cag att gtt atc tac gat ggt tgc tgc 211
Val Leu Cys Glu Asn Ala Pro Gln Ile Val Ile Tyr Asp Gly Cys Cys
25 30 35
tcg ctt gca tat acc caa gca ctt ggc gat ctc gcc gaa gcg gaa tac 259
Ser Leu Ala Tyr Thr Gln Ala Leu Gly Asp Leu Ala Glu Ala Glu Tyr
40 45 50
tac ggc gcc gat ctt gct gca gct gcc taaacaaact tcatagaacg 306
Tyr Gly Ala Asp Leu Ala Ala Ala Ala
55 60
aca 309

<210> 1416
<211> 62
<212> PRT
<213> Corynebacterium glutamicum

<400> 1416
Met Ser Val Asp Asp Leu Tyr Ala Val Ala Leu Asp Thr His Thr Gly
1 5 10 15
Lys Pro Ile Pro Cys Val Leu Cys Glu Asn Ala Pro Gln Ile Val Ile
20 25 30
Tyr Asp Gly Cys Cys Ser Leu Ala Tyr Thr Gln Ala Leu Gly Asp Leu
35 40 45
Ala Glu Ala Glu Tyr Tyr Gly Ala Asp Leu Ala Ala Ala Ala
50 55 60

<210> 1417
<211> 621
<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXN03041

<220>

<221> misc_feature

<222> (473)

<223> n = a, t, c, or g

<220>

<221> VARIANT

<222> (125)

<223> Xaa = Cys, Arg, Ser, or Gly

<400> 1417

accgaggaac tgaaggaaaa tgtaggtgtc ggggcttaga gaaacaaaaa aggctgctac 60

gcggacagca ttgtcacgtg ctgctgcgga gatcgcccttg atg gaa ggc cct gag 115
Met Glu Gly Pro Glu
1 5

gcg ttc acg gtt gcg gcc att gca gct gca gcc ggg gtc tcc ccc agg 163
Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Gly Val Ser Pro Arg
10 15 20

act ttt cat aac tac ttc cct tct cgg gaa gac gca ttg gtg caa ttt 211
Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp Ala Leu Val Gln Phe
25 30 35

gtg gtc att cgc gtt cag gaa ctc acg gat cag cta tac gag ttt cct 259
Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln Leu Tyr Glu Phe Pro
40 45 50

aca agc gtg ccc cca cga gat gcc att gaa caa ttg gtg ata aac caa 307
Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln Leu Val Ile Asn Gln
55 60 65

ttg cgg gat ggc gat gac gct atg gat tct ttc agc gca atg ttt cga 355
Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe Ser Ala Met Phe Arg
70 75 80 85

atc ggt gag atc ctt gaa aat ctt gac ccc atc aag tgt gtt atc gat 403
Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile Lys Cys Val Ile Asp
90 95 100

aag gag cga ctc att gct ccg ttg ctt gag ttc atg gtt gaa cgt gac 451
Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe Met Val Glu Arg Asp
105 110 115

aaa gac ctt gac aag ttc gat ngc ggc aac tct gat cca ttt gca tgc 499
Lys Asp Leu Asp Lys Phe Asp Xaa Gly Asn Ser Asp Pro Phe Ala Cys
120 125 130

agc ggc aat tgc aac ctc gct gca tac gtt tta cca agc ttc cga gcc 547
Ser Gly Asn Cys Asn Leu Ala Ala Tyr Val Leu Pro Ser Phe Arg Ala
135 140 145

ccg gga cat aga aga tgg agt cgc att gat ccg tcg ggc atg cgc ctg 595

Pro Gly His Arg Arg Trp Ser Arg Ile Asp Pro Ser Gly Met Arg Leu
150 155 160 165

gat taagaaanta aaaatctstg aca
Asp

621

<210> 1418

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<220>

<221> VARIANT

<222> (125)

<223> Xaa = Cys, Arg, Ser, or Gly

<400> 1418

Met Glu Gly Pro Glu Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala
1 5 10 15

Gly Val Ser Pro Arg Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp
20 25 30

Ala Leu Val Gln Phe Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln
35 40 45

Leu Tyr Glu Phe Pro Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln
50 55 60

Leu Val Ile Asn Gln Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe
65 70 75 80

Ser Ala Met Phe Arg Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile
85 90 95

Lys Cys Val Ile Asp Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe
100 105 110

Met Val Glu Arg Asp Lys Asp Leu Asp Lys Phe Asp Xaa Gly Asn Ser
115 120 125

Asp Pro Phe Ala Cys Ser Gly Asn Cys Asn Leu Ala Ala Tyr Val Leu
130 135 140

Pro Ser Phe Arg Ala Pro Gly His Arg Arg Trp Ser Arg Ile Asp Pro
145 150 155 160

Ser Gly Met Arg Leu Asp
165

<210> 1419

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> FRXA02892

<400> 1419

accgaggaac tgaaggaaaa tgtaggtgtc ggggcttaga gaaacaaaaa aggctgctac 60

gcggacagca ttgtcacgtg ctgctgcgga gatcgcccttg atg gaa ggc cct gag 115
Met Glu Gly Pro Glu
1 5

gcg ttc acg gtt gcg gcc att gca gct gca gcc ggg gtc tcc ccc agg 163
Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Gly Val Ser Pro Arg
10 15 20

act ttt cat aac tac ttc cct tct cgg gaa gac gca ttg gtg caa ttt 211
Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp Ala Leu Val Gln Phe
25 30 35

gtg gtc att cgc gtt cag gaa ctc acg gat cag cta tac gag ttt cct 259
Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln Leu Tyr Glu Phe Pro
40 45 50

aca agc gtg ccc cca cga gat gcc att gaa caa ttg gtg ata aac caa 307
Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln Leu Val Ile Asn Gln
55 60 65

ttg cgg gat ggc gat gac gct atg gat tct ttc agc gca atg ttt cga 355
Leu Arg Asp Gly Asp Ala Met Asp Ser Phe Ser Ala Met Phe Arg
70 75 80 85

atc ggt gag atc ctt gaa aat ctt gac ccc atc aag tgt gtt atc gat 403
Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile Lys Cys Val Ile Asp
90 95 100

aag gag cga ctc att gct ccg ttg ctt gag ttc atg gtt gaa cgt gac 451
Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe Met Val Glu Arg Asp
105 110 115

aaa gac ctt gac aag ttc gat gcg gca act ctg atc cat ttg cat gca 499
Lys Asp Leu Asp Lys Phe Asp Ala Ala Thr Leu Ile His Leu His Ala
120 125 130

gcg gca att gca acc tcg ctg cat acg ttt tac caa gct tcc gag ccc 547
Ala Ala Ile Ala Thr Ser Leu His Thr Phe Tyr Gln Ala Ser Glu Pro
135 140 145

cgg gac ata gaa gat gga gtc gca ttg atc cgt cgg gca tgc gcc tgg 595
Arg Asp Ile Glu Asp Gly Val Ala Leu Ile Arg Arg Ala Cys Ala Trp
150 155 160 165

att aag aaa taaaaattgt ggcgtgtgaa cct 627
Ile Lys Lys

<210> 1420

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 1420

Met Glu Gly Pro Glu Ala Phe Thr Val Ala Ala Ile Ala Ala Ala Ala

1	5	10	15
Gly Val Ser Pro Arg Thr Phe His Asn Tyr Phe Pro Ser Arg Glu Asp	20	25	30
Ala Leu Val Gln Phe Val Val Ile Arg Val Gln Glu Leu Thr Asp Gln	35	40	45
Leu Tyr Glu Phe Pro Thr Ser Val Pro Pro Arg Asp Ala Ile Glu Gln	50	55	60
Leu Val Ile Asn Gln Leu Arg Asp Gly Asp Asp Ala Met Asp Ser Phe	65	70	75
Ser Ala Met Phe Arg Ile Gly Glu Ile Leu Glu Asn Leu Asp Pro Ile	85	90	95
Lys Cys Val Ile Asp Lys Glu Arg Leu Ile Ala Pro Leu Leu Glu Phe	100	105	110
Met Val Glu Arg Asp Lys Asp Leu Asp Lys Phe Asp Ala Ala Thr Leu	115	120	125
Ile His Leu His Ala Ala Ala Ile Ala Thr Ser Leu His Thr Phe Tyr	130	135	140
Gln Ala Ser Glu Pro Arg Asp Ile Glu Asp Gly Val Ala Leu Ile Arg	145	150	155
Arg Ala Cys Ala Trp Ile Lys Lys	165		

<210> 1421

<211> 1096

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1096)

<223> RXN03045

<400> 1421

agctttttcta tttcgaaaaa tagccttgta ttcgaaaatt tgatcgggta tgggtggttg 60

tatttagcaca gggaactaaa cgggaaaggg ggaagacacc atg agc atc acc aca	115
Met Ser Ile Thr Thr	5
1	

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg	163
His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu	20
10	15

gcc agc atg ctt gac cat ggt gtc acc cca gac caa tac aag gcc atc	211
Ala Ser Met Leu Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile	35
25	30

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc	259
Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr	50
40	45

atc gcc gcc caa acc acc gcc ctc gcc gaa cgc acc aat gct gcg cag Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg Thr Asn Ala Ala Gln 55 60 65	307
tcg att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc ggc Ser Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly 70 75 80 85	355
cta tct aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu 90 95 100	403
tac ccc ata ccg aag cca aac tct gga tct ggc aac ggc ggt aat ggt Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly Gly Asn Gly 105 110 115	451
ggc aat ccc gac ggt ggt cct gat ggt ggc gac tcg ggt gat gac gac Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp 120 125 130	499
tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly 135 140 145	547
aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc gcg gaa aaa Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser Ala Glu Lys 150 155 160 165	595
cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr 170 175 180	643
ccc agc gcc gag gaa ctg cgc aac caa gcc ctg agt cag gcg atc tgg Pro Ser Ala Glu Leu Arg Asn Gln Ala Leu Ser Gln Ala Ile Trp 185 190 195	691
cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag gtc acc acc Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln Val Thr Thr 200 205 210	739
gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr 215 220 225	787
ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly 230 235 240 245	835
ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro 250 255 260	883
tta acc aaa cgc ggc aac ctc gtg gat cta cca gca gca gaa gat atg Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met 265 270 275	931
cgc acc cgc ggg caa cgc cat gcg gac gcg ttg cat cac atc atg gag Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu 280 285 290	979

atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc 1027
 Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
 295 300 305

atc atc atc tcc atg acc acc gat gat ctt gac gag atc aac cac gcc 1075
 Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile Asn His Ala
 310 315 320 325

aac agc agt ggt gaa agt ctg 1096
 Asn Ser Ser Gly Glu Ser Leu
 330

<210> 1422

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 1422

Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
 1 5 10 15

Ile Asp Asn His Leu Ala Ser Met Leu Asp His Gly Val Thr Pro Asp
 20 25 30

Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
 35 40 45

Asn His His Ala Thr Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg
 50 55 60

Thr Asn Ala Ala Gln Ser Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65 70 75 80

Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
 85 90 95

Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly
 100 105 110

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
 115 120 125

Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
 130 135 140

Lys Pro Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg
 145 150 155 160

Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
 165 170 175

Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Asn Gln Ala Leu
 180 185 190

Ser Gln Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
 195 200 205

His Gln Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
 210 215 220

Met Lys Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met
 225 230 235 240

Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
 245 250 255

Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
 260 265 270

Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
 275 280 285

His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
 290 295 300

Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
 305 310 315 320

Glu Ile Asn His Ala Asn Ser Ser Gly Glu Ser Leu
 325 330

<210> 1423

<211> 359

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(336)

<223> RXN03046

<400> 1423

gcc tca att gct aat tcc acc ctg aat att cca gtg gga ttg ggc ggc 48
 Ala Ser Ile Ala Asn Ser Thr Leu Asn Ile Pro Val Gly Leu Gly Gly
 1 5 10 15

tcc aat ttg ctg ctc aag gcg caa acc gcg acc cca tct gag cct gcg 96
 Ser Asn Leu Leu Leu Lys Ala Gln Thr Ala Thr Pro Ser Glu Pro Ala
 20 25 30

aat gct cag gac aaa ctg tac cgt ttc tgc atc gcc aat ggt aag agg 144
 Asn Ala Gln Asp Lys Leu Tyr Arg Phe Cys Ile Ala Asn Gly Lys Arg
 35 40 45

gca ttt tcc gat gcg cag cga ttc ttg ctc aac gcc gac gag ctc gcg 192
 Ala Phe Ser Asp Ala Gln Arg Phe Leu Leu Asn Ala Asp Glu Leu Ala
 50 55 60

gag ctt tct gat tat gag cgt ctg gct tat gcc atc acc ttg ctt gat 240
 Glu Leu Ser Asp Tyr Glu Arg Leu Ala Tyr Ala Ile Thr Leu Leu Asp
 65 70 75 80

cag cct gga aaa gaa gca gaa gga cgc gaa ctt ttt cct ttc gga gct 288
 Gln Pro Gly Lys Glu Ala Glu Gly Arg Glu Leu Phe Pro Phe Gly Ala
 85 90 95

tcg ccg cca ggg cta ccg cgc tgt cga ttt ctt gga atc cca gac tgt 336
 Ser Pro Pro Gly Leu Pro Arg Cys Arg Phe Leu Gly Ile Pro Asp Cys
 100 105 110

tgaccagctg aataaccccg atg

359

<210> 1424

<211> 112

<212> PRT

<213> Corynebacterium glutamicum

<400> 1424

Ala	Ser	Ile	Ala	Asn	Ser	Thr	Leu	Asn	Ile	Pro	Val	Gly	Leu	Gly	Gly
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Ser	Asn	Leu	Leu	Leu	Lys	Ala	Gln	Thr	Ala	Thr	Pro	Ser	Glu	Pro	Ala
		20						25					30		

Asn	Ala	Gln	Asp	Lys	Leu	Tyr	Arg	Phe	Cys	Ile	Ala	Asn	Gly	Lys	Arg
	35						40					45			

Ala	Phe	Ser	Asp	Ala	Gln	Arg	Phe	Leu	Leu	Asn	Ala	Asp	Glu	Leu	Ala
	50					55					60				

Glu	Leu	Ser	Asp	Tyr	Glu	Arg	Leu	Ala	Tyr	Ala	Ile	Thr	Leu	Leu	Asp
65					70				75						80

Gln	Pro	Gly	Lys	Glu	Ala	Glu	Gly	Arg	Glu	Leu	Phe	Pro	Phe	Gly	Ala
			85					90						95	

Ser	Pro	Pro	Gly	Leu	Pro	Arg	Cys	Arg	Phe	Leu	Gly	Ile	Pro	Asp	Cys
			100					105					110		

<210> 1425

<211> 1539

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1516)

<223> RXN03047

<400> 1425

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ttaactcaac	gtttactaaa	cagaatcgga	attaggagcc	atg	ctt	gaa	cgc	aca		115
				Met	Leu	Glu	Arg	Thr		
				1				5		

cag	gta	ttc	gtg	gat	acg	tcc	tac	ctg	ctc	gca	agc	ttt	tac	aac	tct	163
Gln	Val	Phe	Val	Asp	Thr	Ser	Tyr	Leu	Leu	Ala	Ser	Phe	Tyr	Asn	Ser	
			10					15					20			

tgg	gag	aca	ggg	gca	cgt	gcc	caa	tta	gaa	atc	gac	ctc	ccc	gaa	gta	211
Trp	Glu	Thr	Gly	Ala	Arg	Ala	Gln	Leu	Glu	Ile	Asp	Leu	Pro	Glu	Val	
		25					30					35				

gtc	ggg	gta	tta	gga	agg	atg	att	gaa	caa	caa	ctt	aaa	cag	cca	gta	259
Val	Gly	Val	Leu	Gly	Arg	Met	Ile	Glu	Gln	Gln	Leu	Lys	Gln	Pro	Val	
		40					45					50				

caa	cgc	caa	atg	tgg	tac	gac	gga	atc	ccc	gat	tcc	ggc	ccc	cac	cgc	307
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Gln	Arg	Gln	Met	Trp	Tyr	Asp	Gly	Ile	Pro	Asp	Ser	Gly	Pro	His	Arg		
55						60					65						
tat	caa	cga	gca	cta	cgc	acc	tgc	gat	ggg	gtg	caa	ctt	cgt	gct	ggc	355	
Tyr	Gln	Arg	Ala	Leu	Arg	Thr	Cys	Asp	Gly	Val	Gln	Leu	Arg	Ala	Gly	85	
70					75					80							
caa	tta	att	gaa	tgg	ggc	gaa	cgc	cgc	aca	caa	aag	gca	gta	gat	acc	403	
Gln	Leu	Ile	Glu	Trp	Gly	Glu	Arg	Arg	Thr	Gln	Lys	Ala	Val	Asp	Thr	100	
				90					95								
cgc	ctt	gtt	gca	gac	ctc	gtt	ctc	gca	ggg	gtt	cgc	gga	caa	tgc	tcc	451	
Arg	Leu	Val	Ala	Asp	Leu	Val	Leu	Ala	Gly	Val	Arg	Gly	Gln	Cys	Ser	115	
			105					110									
gat	atc	gtg	ctc	gtc	agt	ggc	gac	gcc	gac	atg	atc	ccc	ggg	gtt	caa	499	
Asp	Ile	Val	Leu	Val	Ser	Gly	Asp	Ala	Asp	Met	Ile	Pro	Gly	Val	Gln	130	
		120					125										
gaa	gct	gcc	aat	gca	ggc	ctt	cgc	gtt	cac	ctc	tac	ggc	ttc	ggc	tgg	547	
Glu	Ala	Ala	Asn	Ala	Gly	Leu	Arg	Val	His	Leu	Tyr	Gly	Phe	Gly	Trp	145	
	135					140											
gat	tcc	atg	tcc	tcc	caa	ctg	cgc	cac	tgc	tgt	gac	acc	acc	acc	att	595	
Asp	Ser	Met	Ser	Ser	Gln	Leu	Arg	His	Cys	Cys	Asp	Thr	Thr	Thr	Ile	165	
					155					160							
ttg	gat	cct	cga	gaa	gat	ttt	gct	gaa	tgc	atg	cag	ctg	cag	gtt	ctc	643	
Leu	Asp	Pro	Arg	Glu	Asp	Phe	Ala	Glu	Cys	Met	Gln	Leu	Gln	Val	Leu	180	
				170					175								
gaa	ggg	cca	cta	ccc	cct	gtc	gtt	cgg	gta	aag	ccc	atc	aac	gat	gca	691	
Glu	Gly	Pro	Leu	Pro	Pro	Val	Val	Arg	Val	Lys	Pro	Ile	Asn	Asp	Ala	195	
			185					190									
gaa	ccc	atc	gag	gat	ttg	gat	ttc	act	cca	gtt	cca	ggc	gtc	gcc	tca	739	
Glu	Pro	Ile	Glu	Asp	Leu	Asp	Phe	Thr	Pro	Val	Pro	Gly	Val	Ala	Ser	210	
		200					205						210				
cca	ttt	gaa	gag	gtc	agc	gcg	aaa	gat	gag	aaa	ttc	tct	cca	cgc	cca	787	
Pro	Phe	Glu	Glu	Val	Ser	Ala	Lys	Asp	Glu	Lys	Phe	Ser	Pro	Arg	Pro	225	
	215					220											
agt	gaa	cct	gcc	gaa	gct	ttg	tcg	gaa	cag	gtc	tgt	gaa	gcg	cag	tat	835	
Ser	Glu	Pro	Ala	Glu	Ala	Leu	Ser	Glu	Gln	Val	Cys	Glu	Ala	Gln	Tyr	245	
				235						240							
gag	atc	tcc	aaa	cac	gaa	ggg	caa	acc	gct	gat	tca	gga	gaa	atc	acc	883	
Glu	Ile	Ser	Lys	His	Glu	Gly	Gln	Thr	Ala	Asp	Ser	Gly	Glu	Ile	Thr	260	
				250					255								
gag	tct	ttc	gag	gcc	gct	gaa	atc	aag	gta	act	gag	ttt	ttt	gga	gaa	931	
Glu	Ser	Phe	Glu	Ala	Ala	Glu	Ile	Lys	Val	Thr	Glu	Phe	Phe	Gly	Glu	275	
			265					270									
cca	gct	gct	cca	gta	gcg	gaa	tca	ggc	gta	gaa	gct	ccc	act	ccg	gaa	979	
Pro	Ala	Ala	Pro	Val	Ala	Glu	Ser	Gly	Val	Glu	Ala	Pro	Thr	Pro	Glu	290	
			280					285									
gct	ccc	acg	gtt	cct	gaa	gca	gct	aag	ccc	act	ccg	gcg	aaa	cct	aag	1027	
Ala	Pro	Thr	Val	Pro	Glu	Ala	Ala	Lys	Pro	Thr	Pro	Ala	Lys	Pro	Lys		

295	300	305	
act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act			1075
Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr			
310	315	320	325
cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca			1123
Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro			
	330	335	340
gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca			1171
Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser			
	345	350	355
cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt			1219
Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu			
	360	365	370
cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga			1267
Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly			
	375	380	385
ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt			1315
Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe			
	390	395	400
gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct			1363
Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser			
	410	415	420
ggg ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct			1411
Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala			
	425	430	435
tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct			1459
Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala			
	440	445	450
tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag			1507
Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln			
	455	460	465
cga gat agc tagaatcaca aaaaactggg gct			1539
Arg Asp Ser			
470			

<210> 1426

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 1426

Met	Leu	Glu	Arg	Thr	Gln	Val	Phe	Val	Asp	Thr	Ser	Tyr	Leu	Leu	Ala
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Ser	Phe	Tyr	Asn	Ser	Trp	Glu	Thr	Gly	Ala	Arg	Ala	Gln	Leu	Glu	Ile
			20					25					30		

Asp	Leu	Pro	Glu	Val	Val	Gly	Val	Leu	Gly	Arg	Met	Ile	Glu	Gln	Gln
		35					40					45			

Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
50 55 60

Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
65 70 75 80

Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
85 90 95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
100 105 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
115 120 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
130 135 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145 150 155 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
165 170 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
180 185 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
195 200 205

Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
210 215 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225 230 235 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
245 250 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
260 265 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
275 280 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
290 295 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305 310 315 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
325 330 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
340 345 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
355 360 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
 370 375 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
 385 390 395 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
 405 410 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
 420 425 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
 435 440 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
 450 455 460

Val Leu Leu Asn Gln Arg Asp Ser
 465 470

<210> 1427

<211> 1539

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1516)

<223> FRXA00036

<400> 1427

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ttaactcaac gtttactaaa cagaatcgga attaggagcc atg ctt gaa cgc aca 115
 Met Leu Glu Arg Thr 5
 1

cag gta ttc gtg gat acg tcc tac ctg ctc gca agc ttt tac aac tct 163
 Gln Val Phe Val Asp Thr Ser Tyr Leu Leu Ala Ser Phe Tyr Asn Ser 20
 10 15

tgg gag aca ggg gca cgt gcc caa tta gaa atc gac ctc ccc gaa gta 211
 Trp Glu Thr Gly Ala Arg Ala Gln Leu Glu Ile Asp Leu Pro Glu Val 35
 25 30

gtc ggg gta tta gga agg atg att gaa caa caa ctt aaa cag cca gta 259
 Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln Leu Lys Gln Pro Val 50
 40 45

caa cgc caa atg tgg tac gac gga atc ccc gat tcc ggc ccc cac cgc 307
 Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp Ser Gly Pro His Arg 65
 55 60

tat caa cga gca cta cgc acc tgc gat ggt gtg caa ctt cgt gct ggc 355
 Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val Gln Leu Arg Ala Gly 85
 70 75 80

caa tta att gaa tgg ggc gaa cgc cgc aca caa aag gca gta gat acc 403
 Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln Lys Ala Val Asp Thr

90	95	100	
cgc ctt gtt gca gac ctc gtt ctc gca ggt gtt cgc gga caa tgc tcc Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val Arg Gly Gln Cys Ser 105 110 115			451
gat atc gtg ctc gtc agt ggc gac gcc gac atg atc ccc ggt gtt caa Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met Ile Pro Gly Val Gln 120 125 130			499
gaa gct gcc aat gca ggc ctt cgc gtt cac ctc tac ggc ttc ggc tgg Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu Tyr Gly Phe Gly Trp 135 140 145			547
gat tcc atg tcc tcc caa ctg cgc cac tgc tgt gac acc acc acc att Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys Asp Thr Thr Thr Ile 150 155 160 165			595
ttg gat cct cga gaa gat ttt gct gaa tgc atg cag ctg cag gtt ctc Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met Gln Leu Gln Val Leu 170 175 180			643
gaa ggt cca cta ccc cct gtc gtt cgg gta aag ccc atc aac gat gca Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys Pro Ile Asn Asp Ala 185 190 195			691
gaa ccc atc gag gat ttg gat ttc act cca gtt cca ggc gtc gcc tca Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val Pro Gly Val Ala Ser 200 205 210			739
cca ttt gaa gag gtc agc gcg aaa gat gag aaa ttc tct cca cgc cca Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys Phe Ser Pro Arg Pro 215 220 225			787
agt gaa cct gcc gaa gct ttg tcg gaa cag gtc tgt gaa gcg cag tat Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val Cys Glu Ala Gln Tyr 230 235 240 245			835
gag atc tcc aaa cac gaa ggt caa acc gct gat tca gga gaa atc acc Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp Ser Gly Glu Ile Thr 250 255 260			883
gag tct ttc gag gcc gct gaa atc aag gta act gag ttt ttt gga gaa Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr Glu Phe Phe Gly Glu 265 270 275			931
cca gct gct cca gta gcg gaa tca ggc gta gaa gct ccc act ccg gaa Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu Ala Pro Thr Pro Glu 280 285 290			979
gct ccc acg gtt cct gaa gca gct aag ccc act ccg gcg aaa cct aag Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr Pro Ala Lys Pro Lys 295 300 305			1027
act cca aag gca gag ccc caa aag caa gaa tcc ccc aag ccg gga act Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser Pro Lys Pro Gly Thr 310 315 320 325			1075
cca aaa cca aaa gct cca agc cct gcg gat att cca ccg aaa gcc cca Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile Pro Pro Lys Ala Pro 330 335 340			1123

gct gac act gag gaa cat tcg gaa gtc gaa gct gaa atc gag gac tca 1171
 Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala Glu Ile Glu Asp Ser
 345 350 355
 cgt cca aag atc ccc agc cct tcg atg atg gct ccc cgc cgc aag ctt 1219
 Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala Pro Arg Arg Lys Leu
 360 365 370
 cgt tcc cgc tac gtt ccg ctt ccc aac gaa gtg tgg gca aca gca gga 1267
 Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val Trp Ala Thr Ala Gly
 375 380 385
 ttc caa act cct tac gat gtc ggg caa cag tac gca tcg tgg tgg ttt 1315
 Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr Ala Ser Trp Trp Phe
 390 395 400 405
 gaa aac gca gct acc agc act caa aga gat cag gct cat cta ttg tct 1363
 Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln Ala His Leu Leu Ser
 410 415 420
 ggt ggc gga ctt cca cca gag atc gat cgc ccg ctt ctg cag ttt gct 1411
 Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro Leu Leu Gln Phe Ala
 425 430 435
 tgt gaa act ctc cac gaa tac acc ctg act gaa gcg cag cgc gta gct 1459
 Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu Ala Gln Arg Val Ala
 440 445 450
 tta cgc gat ggc ttt cac tcc gga atc cgt ggt gta ttg ctc aac cag 1507
 Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly Val Leu Leu Asn Gln
 455 460 465
 cga gat agc tagaatcaca aaaaactggg gct 1539
 Arg Asp Ser
 470

<210> 1428

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 1428

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 Asp Leu Pro Glu Val Val Gly Val Leu Gly Arg Met Ile Glu Gln Gln
 35 40 45
 Leu Lys Gln Pro Val Gln Arg Gln Met Trp Tyr Asp Gly Ile Pro Asp
 50 55 60
 Ser Gly Pro His Arg Tyr Gln Arg Ala Leu Arg Thr Cys Asp Gly Val
 65 70 75 80
 Gln Leu Arg Ala Gly Gln Leu Ile Glu Trp Gly Glu Arg Arg Thr Gln
 85 90 95

Lys Ala Val Asp Thr Arg Leu Val Ala Asp Leu Val Leu Ala Gly Val
100 105 110

Arg Gly Gln Cys Ser Asp Ile Val Leu Val Ser Gly Asp Ala Asp Met
115 120 125

Ile Pro Gly Val Gln Glu Ala Ala Asn Ala Gly Leu Arg Val His Leu
130 135 140

Tyr Gly Phe Gly Trp Asp Ser Met Ser Ser Gln Leu Arg His Cys Cys
145 150 155 160

Asp Thr Thr Thr Ile Leu Asp Pro Arg Glu Asp Phe Ala Glu Cys Met
165 170 175

Gln Leu Gln Val Leu Glu Gly Pro Leu Pro Pro Val Val Arg Val Lys
180 185 190

Pro Ile Asn Asp Ala Glu Pro Ile Glu Asp Leu Asp Phe Thr Pro Val
195 200 205

Pro Gly Val Ala Ser Pro Phe Glu Glu Val Ser Ala Lys Asp Glu Lys
210 215 220

Phe Ser Pro Arg Pro Ser Glu Pro Ala Glu Ala Leu Ser Glu Gln Val
225 230 235 240

Cys Glu Ala Gln Tyr Glu Ile Ser Lys His Glu Gly Gln Thr Ala Asp
245 250 255

Ser Gly Glu Ile Thr Glu Ser Phe Glu Ala Ala Glu Ile Lys Val Thr
260 265 270

Glu Phe Phe Gly Glu Pro Ala Ala Pro Val Ala Glu Ser Gly Val Glu
275 280 285

Ala Pro Thr Pro Glu Ala Pro Thr Val Pro Glu Ala Ala Lys Pro Thr
290 295 300

Pro Ala Lys Pro Lys Thr Pro Lys Ala Glu Pro Gln Lys Gln Glu Ser
305 310 315 320

Pro Lys Pro Gly Thr Pro Lys Pro Lys Ala Pro Ser Pro Ala Asp Ile
325 330 335

Pro Pro Lys Ala Pro Ala Asp Thr Glu Glu His Ser Glu Val Glu Ala
340 345 350

Glu Ile Glu Asp Ser Arg Pro Lys Ile Pro Ser Pro Ser Met Met Ala
355 360 365

Pro Arg Arg Lys Leu Arg Ser Arg Tyr Val Pro Leu Pro Asn Glu Val
370 375 380

Trp Ala Thr Ala Gly Phe Gln Thr Pro Tyr Asp Val Gly Gln Gln Tyr
385 390 395 400

Ala Ser Trp Trp Phe Glu Asn Ala Ala Thr Ser Thr Gln Arg Asp Gln
405 410 415

Ala His Leu Leu Ser Gly Gly Gly Leu Pro Pro Glu Ile Asp Arg Pro
 420 425 430

Leu Leu Gln Phe Ala Cys Glu Thr Leu His Glu Tyr Thr Leu Thr Glu
 435 440 445

Ala Gln Arg Val Ala Leu Arg Asp Gly Phe His Ser Gly Ile Arg Gly
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Val Leu Leu Asn Gln Arg Asp Ser
 465 470

<210> 1429
 <211> 996
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(973)
 <223> RXN03048

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 ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg ctc 115
 Met Ala Asn Pro Leu
 1 5

agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat 163
 Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp
 10 15 20

gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc 211
 Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala
 25 30 35

cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt 259
 Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly
 40 45 50

cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc 307
 Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg
 55 60 65

gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag 355
 Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys
 70 75 80 85

tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act 403
 Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr
 90 95 100

gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag 451
 Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu
 105 110 115

cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct 499
 Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala
 120 125 130

gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct 547
 Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser
 135 140 145

 cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa 595
 Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu
 150 155 160 165

 agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat 643
 Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp
 170 175 180

 tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga 691
 Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg
 185 190 195

 tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt 739
 Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser
 200 205 210

 gat cgc atg gct gag att gcg cag tcc ggc acc gat atg cgg gcg tca 787
 Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser
 215 220 225

 gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg ggc acg tcc gca acg 835
 Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr
 230 235 240 245

 cct aag ggc cag cta gag gca ggt gtc gag gat gcg gaa gaa ctt atc 883
 Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp Ala Glu Glu Leu Ile
 250 255 260

 gac gaa acc tcc acc cct tca gct acc cca gaa acc gca agc cca gaa 931
 Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu Thr Ala Ser Pro Glu
 265 270 275

 gct gat gct cca gaa gca tcc gca gac gag tcc gag aag aaa 973
 Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser Glu Lys Lys
 280 285 290

 taacctaacc acaaaaaact ggg 996

<210> 1430

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 1430

Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe
 1 5 10 15

Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln
 20 25 30

Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala
 35 40 45

Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg
 50 55 60

Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile
65 70 75 80

Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln
85 90 95

Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val
100 105 110

Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val
115 120 125

Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu
130 135 140

Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln
145 150 155 160

Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln
165 170 175

Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu
180 185 190

Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr
195 200 205

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
210 215 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
225 230 235 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
245 250 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
260 265 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
275 280 285

Glu Lys Lys
290

<210> 1431

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(973)

<223> FRXA00037

<400> 1431

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ttagacacac gtaactaaaa cctcagggaa gtgactgata atg gct aat ccg etc 115

	Met	Ala	Asn	Pro	Leu	
	1				5	
agc aag ggc tgg aag tat ctc atg gca tcg ttc gac aac aag atc gat						163
Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe Asp Asn Lys Ile Asp						
	10				20	
gag aat gca gat cca aag atc caa att cag caa gct aca gaa gct gcc						211
Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln Ala Thr Glu Ala Ala						
	25				35	
cag aag cag cac cag cag att atg cag cac gct tct cag att atc ggt						259
Gln Lys Gln His Gln Gln Ile Met Gln His Ala Ser Gln Ile Ile Gly						
	40				50	
cag cag aag cag ctt gag atg aaa ttg aac cgc ttg gtt act gac cgc						307
Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg Leu Val Thr Asp Arg						
	55				65	
gat aag ttg cag gaa cag gct cgt cag gca att cag ttg gca gat aag						355
Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile Gln Leu Ala Asp Lys						
	70				80	85
tcc gca aac gaa ggc gac agt gtt aag gct cag gag ttc aac aac act						403
Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln Glu Phe Asn Asn Thr						
	90				95	100
gct gag gtt ttt gct tcc cag ttg gta gct gtg gaa cag cag ttg gag						451
Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val Glu Gln Gln Leu Glu						
	105				110	115
cag act act gcg ctt cat cag cag gct gag gtt gcg gcg aag gat gct						499
Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val Ala Ala Lys Asp Ala						
	120				125	130
gtt gcg aag tct aaa gag tct gag atg cgc ctg aaa gag cag atg tct						547
Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu Lys Glu Gln Met Ser						
	135				140	145
cag att gat gct cta cgt gcg cag gct gat cag gcg aag atg cag gaa						595
Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln Ala Lys Met Gln Glu						
	150				155	160
agt gtc act aag tct atg gat tct ttg aat cag ttt ggc act cag gat						643
Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln Phe Gly Thr Gln Asp						
	170				175	180
tct tct gtt cct acc ctt gat gcg gtg cgt gag aag atc gag cgt cga						691
Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu Lys Ile Glu Arg Arg						
	185				190	195
tac gca gat gct ttg ggc gcg cag gaa ctt acc cag aac act gtt agt						739
Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr Gln Asn Thr Val Ser						
	200				205	210
gat gcg atg gct gag att gcg cag tcc gcc acc gat atg cgg gcg tca						787
Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr Asp Met Arg Ala Ser						
	215				220	225
gct cgt ttg gct gaa ctt cgc gcg gag gcg ctg gcc acg tcc gca acg						835
Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu Gly Thr Ser Ala Thr						

230	235	240	245	
cct aag ggc cag cta gag gca ggt gtc	gag gat gcg gaa gaa ctt atc	883		
Pro Lys Gly Gln Leu Glu Ala Gly Val	Glu Asp Ala Glu Glu Leu Ile			
250	255	260		
gac gaa acc tcc acc cct tca gct acc	cca gaa acc gca agc cca gaa	931		
Asp Glu Thr Ser Thr Pro Ser Ala Thr	Pro Glu Thr Ala Ser Pro Glu			
265	270	275		
gct gat gct cca gaa gca tcc gca gac	gag tcc gag aag aaa	973		
Ala Asp Ala Pro Glu Ala Ser Ala Asp	Glu Ser Glu Lys Lys			
280	285	290		
taacctaaac acaaaaaact ggg		996		

<210> 1432

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 1432

Met Ala Asn Pro Leu Ser Lys Gly Trp Lys Tyr Leu Met Ala Ser Phe	
1 5 10 15	
Asp Asn Lys Ile Asp Glu Asn Ala Asp Pro Lys Ile Gln Ile Gln Gln	
20 25 30	
Ala Thr Glu Ala Ala Gln Lys Gln His Gln Gln Ile Met Gln His Ala	
35 40 45	
Ser Gln Ile Ile Gly Gln Gln Lys Gln Leu Glu Met Lys Leu Asn Arg	
50 55 60	
Leu Val Thr Asp Arg Asp Lys Leu Gln Glu Gln Ala Arg Gln Ala Ile	
65 70 75 80	
Gln Leu Ala Asp Lys Ser Ala Asn Glu Gly Asp Ser Val Lys Ala Gln	
85 90 95	
Glu Phe Asn Asn Thr Ala Glu Val Phe Ala Ser Gln Leu Val Ala Val	
100 105 110	
Glu Gln Gln Leu Glu Gln Thr Thr Ala Leu His Gln Gln Ala Glu Val	
115 120 125	
Ala Ala Lys Asp Ala Val Ala Lys Ser Lys Glu Ser Glu Met Arg Leu	
130 135 140	
Lys Glu Gln Met Ser Gln Ile Asp Ala Leu Arg Ala Gln Ala Asp Gln	
145 150 155 160	
Ala Lys Met Gln Glu Ser Val Thr Lys Ser Met Asp Ser Leu Asn Gln	
165 170 175	
Phe Gly Thr Gln Asp Ser Ser Val Pro Thr Leu Asp Ala Val Arg Glu	
180 185 190	
Lys Ile Glu Arg Arg Tyr Ala Asp Ala Leu Gly Ala Gln Glu Leu Thr	
195 200 205	

Gln Asn Thr Val Ser Asp Arg Met Ala Glu Ile Ala Gln Ser Gly Thr
 210 215 220

Asp Met Arg Ala Ser Ala Arg Leu Ala Glu Leu Arg Ala Glu Ala Leu
 225 230 235 240

Gly Thr Ser Ala Thr Pro Lys Gly Gln Leu Glu Ala Gly Val Glu Asp
 245 250 255

Ala Glu Glu Leu Ile Asp Glu Thr Ser Thr Pro Ser Ala Thr Pro Glu
 260 265 270

Thr Ala Ser Pro Glu Ala Asp Ala Pro Glu Ala Ser Ala Asp Glu Ser
 275 280 285

Glu Lys Lys
 290

<210> 1433
 <211> 1066
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1066)
 <223> RXN03050

<400> 1433
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agagtgggtg gtaacaacac ggggaaaggg ggaagacacc atg agc atc acc aca 115
 Met Ser Ile Thr Thr
 1 5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg 163
 His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
 10 15 20

gcc agc atg ctc gac cat ggt gtc acc cca gac caa tac aag gcc atc 211
 Ala Ser Met Leu Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile
 25 30 35

gag ccc gac ctc atc gcc cta gaa cac acc atc aac cac cac gcc acc 259
 Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile Asn His His Ala Thr
 40 45 50

atc gcc gcc caa acc aca gcc ctc gcc gaa cgc acc aac gcc gcc cac 307
 Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg Thr Asn Ala Ala His
 55 60 65

acc att ggc tcc acc cac ctc atc gac tac ctc acc acc acc ttc gga 355
 Thr Ile Gly Ser Thr His Leu Ile Asp Tyr Leu Thr Thr Thr Phe Gly
 70 75 80 85

cta tcc aaa gca cgc gcc cac cac cgc atc aat ctc gcc cac tcc ctc 403
 Leu Ser Lys Ala Arg Ala His His Arg Ile Asn Leu Ala His Ser Leu
 90 95 100

tac ccc ata ccg aag cca aac cct gga tct ggc aac ggc ggt aat ggt	451
Tyr Pro Ile Pro Lys Pro Asn Pro Gly Ser Gly Asn Gly Gly Asn Gly	
105 110 115	
ggc aat ccc gac ggc ggt cct gat ggt ggc gac tcg ggt gat gac gac	499
Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly Asp Asp Asp	
120 125 130	
tcc ggc gac gat gac ccc gac ccc gaa ccg gac aag cct gaa gac ggc	547
Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro Glu Asp Gly	
135 140 145	
aaa cct gat ggt gat aag cct cgt ggg cca ccg atc agc gcg gaa aaa	595
Lys Pro Asp Gly Asp Lys Pro Arg Gly Pro Arg Ile Ser Ala Glu Lys	
150 155 160 165	
cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg aat acc aca	643
His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro Asn Thr Thr	
170 175 180	
ccc agc gcc gag gag cta cgc acc caa gcc ctg agt caa gcg atc tgg	691
Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln Ala Ile Trp	
185 190 195	
cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cac gtc acc acc	739
Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His His Val Thr Thr	
200 205 210	
gcc aat aaa aac aac ccc aac ccc atc acc gcc atg aaa agg cgc tac	787
Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys Arg Arg Tyr	
215 220 225	
ctc gct gta ggt aaa ccc gat gcc gac aac atg gtc cgc atc agc ggc	835
Leu Ala Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg Ile Ser Gly	
230 235 240 245	
ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac acc gca ccg	883
Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn Thr Ala Pro	
250 255 260	
tta acc aaa cgc ggc aac ctc gtg gat cta ccc gca gca gaa gat atg	931
Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala Glu Asp Met	
265 270 275	
cgc acc cgc ggc caa cgc cat gcg gac gcg ttg cat cac atc atg gag	979
Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu	
280 285 290	
atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc	1027
Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser	
295 300 305	
atc atc atc tcc atg acc acc gat gat ctt gat gag atc	1066
Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile	
310 315 320	

<210> 1434

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 1434

Met Ser Ile Thr Thr His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala
 1 5 10 15
 Ile Asp Asn His Leu Ala Ser Met Leu Asp His Gly Val Thr Pro Asp
 20 25 30
 Gln Tyr Lys Ala Ile Glu Pro Asp Leu Ile Ala Leu Glu His Thr Ile
 35 40 45
 Asn His His Ala Thr Ile Ala Ala Gln Thr Thr Ala Leu Ala Glu Arg
 50 55 60
 Thr Asn Ala Ala His Thr Ile Gly Ser Thr His Leu Ile Asp Tyr Leu
 65 70 75 80
 Thr Thr Thr Phe Gly Leu Ser Lys Ala Arg Ala His His Arg Ile Asn
 85 90 95
 Leu Ala His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Pro Gly Ser Gly
 100 105 110
 Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
 115 120 125
 Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
 130 135 140
 Lys Pro Glu Asp Gly Lys Pro Asp Gly Asp Lys Pro Arg Gly Pro Arg
 145 150 155 160
 Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
 165 170 175
 Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu
 180 185 190
 Ser Gln Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
 195 200 205
 His His Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
 210 215 220
 Met Lys Arg Arg Tyr Leu Ala Val Gly Lys Pro Asp Ala Asp Asn Met
 225 230 235 240
 Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
 245 250 255
 Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
 260 265 270
 Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
 275 280 285
 His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
 290 295 300
 Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
 305 310 315 320

Glu Ile

<210> 1435

<211> 1558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (12)..(1535)

<223> RXN03053

<400> 1435

gaggtaaagg a ttc cac ttc acc tcg act gag ttt gcc ggt tct tat tct 50
 Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr Ser
 1 5 10

ttg gtc acc aat ggt ctt aac gat gtt gct ggc gaa tac gtc ggt gtc 98
 Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly Val
 15 20 25

atg cgt ggc gat gtc aac aac tcc gct gtg ctt ttt gat gtg gat cgc 146
 Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp Arg
 30 35 40 45

tgg tcg gga cat gtc gta tgc gca gat agc tcg att aat aca tca cca 194
 Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser Pro
 50 55 60

cta ctt aag cgt ccc cgt gtc gtt gac atg tgg ggg tcg aag att tct 242
 Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile Ser
 65 70 75

cag gca gcg cta ctg aat aac cgt cgc gta gtg cac ctg gtg ctc aat 290
 Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu Asn
 80 85 90

ggt gcc aag ctc gat gaa atg gga cca aag cta gaa tcc atg acc gct 338
 Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr Ala
 95 100 105

cat gtg gat atg act agc gga gat ctc aac atg ttc gag ctg ttt ggt 386
 His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe Gly
 110 115 120 125

aag caa gaa gat gag ctg tcg ctg tat tcc aca cac atg gac aaa atc 434
 Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys Ile
 130 135 140

gtg ttt atg acc gag cag gca ttg ggc gat aag acc tct gag ctg gcg 482
 Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu Ala
 145 150 155

cta ttg cgc gga aag ctc aaa gaa att att aca gcc ttt tat gtg gat 530
 Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val Asp
 160 165 170

atg aaa atg tgg gct ctt aat gcc ggt gaa aac cgt gac aag ctg cgt 578

Met	Lys	Met	Trp	Ala	Leu	Asn	Ala	Gly	Glu	Asn	Arg	Asp	Lys	Leu	Arg		
175						180					185						
ctt	gtt	ggt	gtg	cct	cat	gag	cag	atc	ccg	ttg	ctc	tct	gtc	ttc	gtg	626	
Leu	Val	Gly	Val	Pro	His	Glu	Gln	Ile	Pro	Leu	Leu	Ser	Val	Phe	Val		
190					195					200					205		
tcc	tat	ttg	gat	caa	gaa	tat	gag	cgc	cag	aaa	tat	gag	gga	acc	aaa	674	
Ser	Tyr	Leu	Asp	Gln	Glu	Tyr	Glu	Arg	Gln	Lys	Tyr	Glu	Gly	Thr	Lys		
				210					215					220			
gac	cct	gaa	atg	ttt	cgt	gcc	att	tct	gtg	ctg	cga	ctg	acc	tat	aag	722	
Asp	Pro	Glu	Met	Phe	Arg	Ala	Ile	Ser	Val	Leu	Arg	Leu	Thr	Tyr	Lys		
			225					230					235				
gat	ttg	ctc	gat	act	cat	ggc	gat	ctg	ttt	aat	cag	cac	acg	gca	gat	770	
Asp	Leu	Leu	Asp	Thr	His	Gly	Asp	Leu	Phe	Asn	Gln	His	Thr	Ala	Asp		
	240						245					250					
ggc	att	gat	tct	gtg	aac	tct	gca	cgc	cgc	gtg	atc	tat	gat	ttt	tct	818	
Gly	Ile	Asp	Ser	Val	Asn	Ser	Ala	Arg	Arg	Val	Ile	Tyr	Asp	Phe	Ser		
	255					260					265						
gga	gtg	ctg	cga	cgt	ggc	gca	ggt	gtc	gcg	atg	gca	cag	ctg	gtt	aac	866	
Gly	Val	Leu	Arg	Arg	Gly	Ala	Gly	Val	Ala	Met	Ala	Gln	Leu	Val	Asn		
270					275					280					285		
gtg	att	ggt	ttt	gct	gtg	gag	acg	ctt	ggt	caa	ggc	gat	gtg	gtc	atc	914	
Val	Ile	Gly	Phe	Ala	Val	Glu	Thr	Leu	Gly	Gln	Gly	Asp	Val	Val	Ile		
				290					295					300			
att	cac	ggt	gct	gat	ggc	att	gtc	gat	gtt	gat	gtt	cag	gat	tat	ttg	962	
Ile	His	Gly	Ala	Asp	Gly	Ile	Val	Asp	Val	Asp	Val	Gln	Asp	Tyr	Leu		
			305					310					315				
gct	aat	cag	ttc	gca	tat	atg	gct	gag	cgt	ggt	ggg	cga	gtg	gcg	tat	1010	
Ala	Asn	Gln	Phe	Ala	Tyr	Met	Ala	Glu	Arg	Gly	Gly	Arg	Val	Ala	Tyr		
		320					325					330					
ctc	tac	agc	tcg	atg	gac	gcg	atg	ctt	ggc	act	gtt	ggc	ttc	aat	caa	1058	
Leu	Tyr	Ser	Ser	Met	Asp	Ala	Met	Leu	Gly	Thr	Val	Gly	Phe	Asn	Gln		
						340					345						
ttc	caa	cgt	gct	gcg	tac	acc	att	ttg	ggc	ccg	atg	aac	gtt	gac	tcg	1106	
Phe	Gln	Arg	Ala	Ala	Tyr	Thr	Ile	Leu	Gly	Pro	Met	Asn	Val	Asp	Ser		
350					355					360					365		
gtg	gat	act	tat	caa	tct	ctg	att	aat	agt	cag	atc	ccg	atg	gac	ttg	1154	
Val	Asp	Thr	Tyr	Gln	Ser	Leu	Ile	Asn	Ser	Gln	Ile	Pro	Met	Asp	Leu		
				370				375						380			
gca	cgg	ttg	gtg	aca	acg	cag	aat	tct	ggt	gcg	agc	tat	ttg	cgc	cga	1202	
Ala	Arg	Leu	Val	Thr	Thr	Gln	Asn	Ser	Gly	Ala	Ser	Tyr	Leu	Arg	Arg		
			385					390					395				
gga	tct	acc	aat	gtg	gtg	ttt	gaa	acc	aac	ctt	gcg	ttg	ggc	gtt	aat	1250	
Gly	Ser	Thr	Asn	Val	Val	Phe	Glu	Thr	Asn	Leu	Ala	Leu	Gly	Val	Asn		
		400					405					410					
cct	tat	atg	gag	cag	cgt	cgc	aag	att	gaa	gca	cag	cga	ggt	cag	cga	1298	
Pro	Tyr	Met	Glu	Gln	Arg	Arg	Lys	Ile	Glu	Ala	Gln	Arg	Gly	Gln	Arg		

415	420	425	
cga tcc aag cga gac aag cac tac ggt ggt ggc acg acg atg gtg ggc			1346
Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val Gly			
430	435	440	445
aca gcg gat ctt gat gtt gtc gca att cag gcg aag gcc gag cac cgc			1394
Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His Arg			
	450	455	460
gaa gag cgc ttt gat gag aaa tct gcg cgc aag atg aag gag ctt gat			1442
Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu Asp			
	465	470	475
gat gta gaa gcg aaa gaa cta gct ttg aaa act ggg ccg aag aat ctt			1490
Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn Leu			
	480	485	490
gat gat gcg ctt gca cag gtg gag aag aag cgc ctg gcg aag cgg			1535
Asp Asp Ala Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg			
	495	500	505
tagttgttgg ctgtggtgaa taa			1558

<210> 1436

<211> 508

<212> PRT

<213> Corynebacterium glutamicum

<400> 1436

Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr Ser Leu Val Thr
1 5 10 15

Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly Val Met Arg Gly
20 25 30

Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp Arg Trp Ser Gly
35 40 45

His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser Pro Leu Leu Lys
50 55 60

Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile Ser Gln Ala Ala
65 70 75 80

Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu Asn Gly Ala Lys
85 90 95

Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr Ala His Val Asp
100 105 110

Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe Gly Lys Gln Glu
115 120 125

Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys Ile Val Phe Met
130 135 140

Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu Ala Leu Leu Arg
145 150 155 160

Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val Asp Met Lys Met
165 170 175

Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu Arg Leu Val Gly
180 185 190

Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe Val Ser Tyr Leu
195 200 205

Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr Lys Asp Pro Glu
210 215 220

Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr Lys Asp Leu Leu
225 230 235 240

Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala Asp Gly Ile Asp
245 250 255

Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe Ser Gly Val Leu
260 265 270

Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val Asn Val Ile Gly
275 280 285

Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val Ile Ile His Gly
290 295 300

Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr Leu Ala Asn Gln
305 310 315 320

Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala Tyr Leu Tyr Ser
325 330 335

Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn Gln Phe Gln Arg
340 345 350

Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp Ser Val Asp Thr
355 360 365

Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp Leu Ala Arg Leu
370 375 380

Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg Arg Gly Ser Thr
385 390 395 400

Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn Pro Tyr Met
405 410 415

Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln Arg Arg Ser Lys
420 425 430

Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val Gly Thr Ala Asp
435 440 445

Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His Arg Glu Glu Arg
450 455 460

Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu Asp Asp Val Glu
465 470 475 480

Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn Leu Asp Asp Ala

485

490

495

Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
 500 505

<210> 1437

<211> 1559

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1536)

<223> FRXA02885

<400> 1437

cga ggt aaa gga ttc cac ttc acc tcg act gag ttt gcc ggt tct tat 48
 Arg Gly Lys Gly Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr
 1 5 10 15

tct ttg gtc acc aat ggt ctt aac gat gtt gct ggc gaa tac gtc ggt 96
 Ser Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly
 20 25 30

gtc atg cgt ggc gat gtc aac aac tcc gct gtg ctt ttt gat gtg gat 144
 Val Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp
 35 40 45

cgc tgg tcg gga cat gtc gta tgc gca gat agc tcg att aat aca tca 192
 Arg Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser
 50 55 60

cca cta ctt aag cgt ccc cgt gtc gtt gac atg tgg ggg tcg aag att 240
 Pro Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile
 65 70 75 80

tct cag gca gcg cta ctg aat aac cgt cgc gta gtg cac ctg gtg ctc 288
 Ser Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu
 85 90 95

aat ggt gcc aag ctc gat gaa atg gga cca aag cta gaa tcc atg acc 336
 Asn Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr
 100 105 110

gct cat gtg gat atg act agc gga gat ctc aac atg ttc gag ctg ttt 384
 Ala His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe
 115 120 125

ggt aag caa gaa gat gag ctg tcg ctg tat tcc aca cac atg gac aaa 432
 Gly Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys
 130 135 140

atc gtg ttt atg acc gag cag gca ttg ggc gat aag acc tct gag ctg 480
 Ile Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu
 145 150 155 160

gcg cta ttg cgc gga aag ctc aaa gaa att att aca gcc ttt tat gtg 528
 Ala Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val
 165 170 175

gat atg aaa atg.tgg gct ctt aat gcc ggt gaa aac cgt gac aag ctg	576
Asp Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu	
180 185 190	
cgt ctt gtt ggt gtg cct cat gag cag atc ccg ttg ctc tct gtc ttc	624
Arg Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe	
195 200 205	
gtg tcc tat ttg gat caa gaa tat gag cgc cag aaa tat gag gga acc	672
Val Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr	
210 215 220	
aaa gac cct gaa atg ttt cgt gcc att tct gtg ctg cga ctg acc tat	720
Lys Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr	
225 230 235 240	
aag gat ttg ctc gat act cat ggc gat ctg ttt aat cag cac acg gca	768
Lys Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala	
245 250 255	
gat ggc att gat tct gtg aac tct gca cgc cgc gtg atc tat gat ttt	816
Asp Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe	
260 265 270	
tct gga gtg ctg cga cgt ggc gca ggt gtc gcg atg gca cag ctg gtt	864
Ser Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val	
275 280 285	
aac gtg att ggt ttt gct gtg gag acg ctt ggt caa ggc gat gtg gtc	912
Asn Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val	
290 295 300	
atc att cac ggt gct gat ggc att gtc gat gtt gat gtt cag gat tat	960
Ile Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr	
305 310 315 320	
ttg gct aat cag ttc gca tat atg gct gag cgt ggt ggg cga gtg gcg	1008
Leu Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala	
325 330 335	
tat ctc tac agc tcg atg gac gcg atg ctt ggc act gtt ggc ttc aat	1056
Tyr Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn	
340 345 350	
caa ttc caa cgt gct gcg tac acc att ttg ggc ccg atg aac gtt gac	1104
Gln Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp	
355 360 365	
tcg gtg gat act tat caa tct ctg att aat agt cag atc ccg atg gac	1152
Ser Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp	
370 375 380	
ttg gca cgg ttg gtg aca acg cag aat tct ggt gcg agc tat ttg cgc	1200
Leu Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg	
385 390 395 400	
cga gga tct acc aat gtg gtg ttt gaa acc aac ctt gcg ttg ggc gtt	1248
Arg Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val	
405 410 415	
aat cct tat atg gag cag cgt cgc aag att gaa gca cag cga ggt cag	1296

Asn Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln
 420 425 430
 cga cga tcc aag cga gac aag cac tac ggt ggt ggc acg acg atg gtg 1344
 Arg Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val
 435 440 445
 ggc aca gcg gat ctt gat gtt gtc gca att cag gcg aag gcc gag cac 1392
 Gly Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His
 450 455 460
 cgc gaa gag cgc ttt gat gag aaa tct gcg cgc aag atg aag gag ctt 1440
 Arg Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu
 465 470 475 480
 gat gat gta gaa gcg aaa gaa cta gct ttg aaa act ggg ccg aag aat 1488
 Asp Asp Val Glu Ala Lys Glu Leu Ala Leu Lys Thr Gly Pro Lys Asn
 485 490 495
 ctt gat gat gcg ctt gca cag gtg gag aag aag cgc ctg gcg aag cgg 1536
 Leu Asp Asp Ala Leu Ala Gln Val Glu Lys Lys Arg Leu Ala Lys Arg
 500 505 510
 tagttgttgg ctgtggtgaa taa 1559

<210> 1438

<211> 512

<212> PRT

<213> Corynebacterium glutamicum

<400> 1438

Arg Gly Lys Gly Phe His Phe Thr Ser Thr Glu Phe Ala Gly Ser Tyr
 1 5 10 15
 Ser Leu Val Thr Asn Gly Leu Asn Asp Val Ala Gly Glu Tyr Val Gly
 20 25 30
 Val Met Arg Gly Asp Val Asn Asn Ser Ala Val Leu Phe Asp Val Asp
 35 40 45
 Arg Trp Ser Gly His Val Val Cys Ala Asp Ser Ser Ile Asn Thr Ser
 50 55 60
 Pro Leu Leu Lys Arg Pro Arg Val Val Asp Met Trp Gly Ser Lys Ile
 65 70 75 80
 Ser Gln Ala Ala Leu Leu Asn Asn Arg Arg Val Val His Leu Val Leu
 85 90 95
 Asn Gly Ala Lys Leu Asp Glu Met Gly Pro Lys Leu Glu Ser Met Thr
 100 105 110
 Ala His Val Asp Met Thr Ser Gly Asp Leu Asn Met Phe Glu Leu Phe
 115 120 125
 Gly Lys Gln Glu Asp Glu Leu Ser Leu Tyr Ser Thr His Met Asp Lys
 130 135 140
 Ile Val Phe Met Thr Glu Gln Ala Leu Gly Asp Lys Thr Ser Glu Leu
 145 150 155 160

Ala Leu Leu Arg Gly Lys Leu Lys Glu Ile Ile Thr Ala Phe Tyr Val
165 170 175

Asp Met Lys Met Trp Ala Leu Asn Ala Gly Glu Asn Arg Asp Lys Leu
180 185 190

Arg Leu Val Gly Val Pro His Glu Gln Ile Pro Leu Leu Ser Val Phe
195 200 205

Val Ser Tyr Leu Asp Gln Glu Tyr Glu Arg Gln Lys Tyr Glu Gly Thr
210 215 220

Lys Asp Pro Glu Met Phe Arg Ala Ile Ser Val Leu Arg Leu Thr Tyr
225 230 235 240

Lys Asp Leu Leu Asp Thr His Gly Asp Leu Phe Asn Gln His Thr Ala
245 250 255

Asp Gly Ile Asp Ser Val Asn Ser Ala Arg Arg Val Ile Tyr Asp Phe
260 265 270

Ser Gly Val Leu Arg Arg Gly Ala Gly Val Ala Met Ala Gln Leu Val
275 280 285

Asn Val Ile Gly Phe Ala Val Glu Thr Leu Gly Gln Gly Asp Val Val
290 295 300

Ile Ile His Gly Ala Asp Gly Ile Val Asp Val Asp Val Gln Asp Tyr
305 310 315 320

Leu Ala Asn Gln Phe Ala Tyr Met Ala Glu Arg Gly Gly Arg Val Ala
325 330 335

Tyr Leu Tyr Ser Ser Met Asp Ala Met Leu Gly Thr Val Gly Phe Asn
340 345 350

Gln Phe Gln Arg Ala Ala Tyr Thr Ile Leu Gly Pro Met Asn Val Asp
355 360 365

Ser Val Asp Thr Tyr Gln Ser Leu Ile Asn Ser Gln Ile Pro Met Asp
370 375 380

Leu Ala Arg Leu Val Thr Thr Gln Asn Ser Gly Ala Ser Tyr Leu Arg
385 390 395 400

Arg Gly Ser Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val
405 410 415

Asn Pro Tyr Met Glu Gln Arg Arg Lys Ile Glu Ala Gln Arg Gly Gln
420 425 430

Arg Arg Ser Lys Arg Asp Lys His Tyr Gly Gly Gly Thr Thr Met Val
435 440 445

Gly Thr Ala Asp Leu Asp Val Val Ala Ile Gln Ala Lys Ala Glu His
450 455 460

Arg Glu Glu Arg Phe Asp Glu Lys Ser Ala Arg Lys Met Lys Glu Leu
465 470 475 480

cgg 552

<210> 1440

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 1440

Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
 1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
 20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
 35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
 50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
 65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
 85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
 100 105 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
 115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 130 135 140

<210> 1441

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> FRXA00261

<400> 1441

aaggtcagcc gtatttcggt cagtcagcaa ctaattacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag 115
 Met Tyr Ser Asp Lys
 1 5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc 163
 Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
 10 15 20

gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt 211
 Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
 25 30 35

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 130 135 140

<210> 1443

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> FRXA02888

<400> 1443

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accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag 115
 Met Tyr Ser Asp Lys
 1 5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc 163
 Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
 10 15 20

gta ggt tta tta gat ggc tca gat gga cgt gat tat att gaa aag ctt 211
 Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp Tyr Ile Glu Lys Leu
 25 30 35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att 259
 Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
 40 45 50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg 307
 Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
 55 60 65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt 355
 His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
 70 75 80 85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt 403
 Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
 90 95 100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg 451
 Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
 105 110 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag 499
 Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
 120 125 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc 549
 Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 135 140

cgg 552

<210> 1444

<211> 143

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1444

Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser
 1 5 10 15

Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Arg Asp
 20 25 30

Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu
 35 40 45

Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr
 50 55 60

Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro
 65 70 75 80

Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr
 85 90 95

Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser
 100 105 110

Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val
 115 120 125

Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 130 135 140

<210> 1445

<211> 603

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(580)

<223> RXN03059

<400> 1445

gtgtcatttt cttggcggac ggtcgtatcg tgaaccagtt gtttgatccc accatcgagg 60

aaatcttggc cacgatgaac ggaattgagg atattgccta atg aat tcc ggt tcc 115
 Met Asn Ser Gly Ser
 1 5

aca atg cgc aga atc agt ctg cgc aat att ggc gcg cac aag gtc agg 163
 Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly Ala His Lys Val Arg
 10 15 20

ctg ttt ttg aca gtt ctg gca gtg gtg ctc ggc acg tct ttt gtt tcc 211
 Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly Thr Ser Phe Val Ser
 25 30 35

ggc gcg atg atg ttt acc aac gcg ctg tcc tcc act ttt gat gag gct 259
 Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser Thr Phe Asp Glu Ala
 40 45 50

att gcc agc agc ttt gac ggc gtg gat gtg gtg gtt tca cca aac ggt 307
 Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val Val Ser Pro Asn Gly
 55 60 65
 gca tca gag gtg cag ggt gtt cct gtt gag acg gtt gaa tct ttg cgt 355
 Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr Val Glu Ser Leu Arg
 70 75 80 85
 gag gat tcc cgc atc aac cat ctc aac atc aac ggt tcc cag act gtc 403
 Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn Gly Ser Gln Thr Val
 90 95 100
 gtt ctg gcg gat gct gat tcc aag gca att caa acg act ggg gga tcg 451
 Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln Thr Thr Gly Gly Ser
 105 110 115
 tcg tta agc att tat tac agc gcg gac gac gcg gtt gcc cag gca cct 499
 Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala Val Ala Gln Ala Pro
 120 125 130
 gaa ttg gct gag gga gag gca ccg act ggc acc gaa gag gtg ctt gcc 547
 Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr Glu Glu Val Leu Ala
 135 140 145
 tcg aag gcg ggc gct gag gcg aat ggc ctg gag taggggacca gatcttggtc 600
 Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
 150 155 160
 gtg 603

<210> 1446

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1446

Met Asn Ser Gly Ser Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly
 1 5 10 15
 Ala His Lys Val Arg Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly
 20 25 30
 Thr Ser Phe Val Ser Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser
 35 40 45
 Thr Phe Asp Glu Ala Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val
 50 55 60
 Val Ser Pro Asn Gly Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr
 65 70 75 80
 Val Glu Ser Leu Arg Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn
 85 90 95
 Gly Ser Gln Thr Val Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln
 100 105 110
 Thr Thr Gly Gly Ser Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala
 115 120 125

Val Ala Gln Ala Pro Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr
130 135 140

Glu Glu Val Leu Ala Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
145 150 155 160

<210> 1447

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02899

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aaatcttggc cacgatgaac ggaattgagg atattgccta atg aat tcc ggt tcc 115
Met Asn Ser Gly Ser
1 5

aca atg cgc aga atc agt ctg cgc aat att ggc gcg cac aag gtc agg 163
Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly Ala His Lys Val Arg
10 15 20

ctg ttt ttg aca gtt ctg gca gtg gtg ctc ggc acg tct ttt gtt tcc 211
Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly Thr Ser Phe Val Ser
25 30 35

ggc gcg atg atg ttt acc aac gcg ctg tcc tcc act ttt gat gag gct 259
Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser Thr Phe Asp Glu Ala
40 45 50

att gcc agc agc ttt gac ggc gtg gat gtg gtg gtt tca cca aac ggt 307
Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val Val Ser Pro Asn Gly
55 60 65

gca tca gag gtg cag ggt gtt cct gtt gag acg gtt gaa tct ttg cgt 355
Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr Val Glu Ser Leu Arg
70 75 80 85

gag gat tcc cgc atc aac cat ctc aac atc aac ggt tcc cag act gtc 403
Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn Gly Ser Gln Thr Val
90 95 100

gtt ctg gcg gat gct gat tcc aag gca att caa acg act ggg gga tcg 451
Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln Thr Thr Gly Gly Ser
105 110 115

tcg tta agc att tat tac agc gcg gac gac gcg gtt gcc cag gca cct 499
Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala Val Ala Gln Ala Pro
120 125 130

gaa ttg gct gag gga gag gca ccg act ggc acc gaa gag gtg ctt gcc 547
Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr Glu Glu Val Leu Ala
135 140 145

tcg aag gcg ggc gct gag gcg aat ggc ctg gag taggggacca gatcttggtc 600
 Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
 150 155 160

gtg

603

<210> 1448

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1448

Met Asn Ser Gly Ser Thr Met Arg Arg Ile Ser Leu Arg Asn Ile Gly
 1 5 10 15

Ala His Lys Val Arg Leu Phe Leu Thr Val Leu Ala Val Val Leu Gly
 20 25 30

Thr Ser Phe Val Ser Gly Ala Met Met Phe Thr Asn Ala Leu Ser Ser
 35 40 45

Thr Phe Asp Glu Ala Ile Ala Ser Ser Phe Asp Gly Val Asp Val Val
 50 55 60

Val Ser Pro Asn Gly Ala Ser Glu Val Gln Gly Val Pro Val Glu Thr
 65 70 75 80

Val Glu Ser Leu Arg Glu Asp Ser Arg Ile Asn His Leu Asn Ile Asn
 85 90 95

Gly Ser Gln Thr Val Val Leu Ala Asp Ala Asp Ser Lys Ala Ile Gln
 100 105 110

Thr Thr Gly Gly Ser Ser Leu Ser Ile Tyr Tyr Ser Ala Asp Asp Ala
 115 120 125

Val Ala Gln Ala Pro Glu Leu Ala Glu Gly Glu Ala Pro Thr Gly Thr
 130 135 140

Glu Glu Val Leu Ala Ser Lys Ala Gly Ala Glu Ala Asn Gly Leu Glu
 145 150 155 160

<210> 1449

<211> 622

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXN03062

<400> 1449

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atatttggcc catatggata attgacagga gtttaacgcc atg gaa acc cca acc 115
 Met Glu Thr Pro Thr
 1 5

caa gac atg gat gtc cgc tgg tta tac acc caa agc cag ctc aaa ctc 163
 Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln Ser Gln Leu Lys Leu
 10 15 20
 cgc gaa att ctc ccc aca aac aaa acc ttc gat gtc atc caa atc agc 211
 Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp Val Ile Gln Ile Ser
 25 30 35
 gaa ctc gtt gac ccc acc gac ttc atc agg ccc aac agc gtg gtc tta 259
 Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro Asn Ser Val Val Leu
 40 45 50
 tcc gtt ggc atc gcc ttc gca gaa acg ccc gac ggg ctt cgc gat tgg 307
 Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp Gly Leu Arg Asp Trp
 55 60 65
 gca cac cga ctc gcc gac gca ggg gtc atc gcg atc ggg ttc ggc tcc 355
 Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala Ile Gly Phe Gly Ser
 70 75 80 85
 ggc ctc acc ttc cca cag gtt ccg cag gcg ctt atc gac gcc tcc ctc 403
 Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu Ile Asp Ala Ser Leu
 90 95 100
 cac ctt ggc ctc ggc ctc ttt gaa gtc ccc cgt gaa att cca ttt atc 451
 His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg Glu Ile Pro Phe Ile
 105 110 115
 tcg atc acc tcc agc gtg cgt gat gag caa acc cgc cgt gcc ggc cgc 499
 Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr Arg Arg Ala Gly Arg
 120 125 130
 ctg caa caa gaa ctc ctc ctg gaa cag gaa cgg ctt aac tcc atc gcc 547
 Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg Leu Asn Ser Ile Ala
 135 140 145
 atc tcc ggt ggc atc gaa gcc ctg tgc cgt gct gcc gcc gac tat ttg 595
 Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala Ala Ala Asp Tyr Leu
 150 155 160 165
 ggt ggt gca gta acc atc gtg gac agc 622
 Gly Gly Ala Val Thr Ile Val Asp Ser
 170

<210> 1450

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 1450

Met Glu Thr Pro Thr Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln
 1 5 10 15
 Ser Gln Leu Lys Leu Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp
 20 25 30
 Val Ile Gln Ile Ser Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro
 35 40 45
 Asn Ser Val Val Leu Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp

50	55	60
Gly Leu Arg Asp Trp Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala		
65	70	75 80
Ile Gly Phe Gly Ser Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu		
	85	90 95
Ile Asp Ala Ser Leu His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg		
	100	105 110
Glu Ile Pro Phe Ile Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr		
	115	120 125
Arg Arg Ala Gly Arg Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg		
	130	135 140
Leu Asn Ser Ile Ala Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala		
145	150	155 160
Ala Ala Asp Tyr Leu Gly Gly Ala Val Thr Ile Val Asp Ser		
	165	170

<210> 1451

<211> 786

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(763)

<223> RXN03066

<400> 1451

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cgaaatcacc gggcgtaat agcaccagct taaaaacctt atg aca tca gac aaa	115
	Met Thr Ser Asp Lys
	1 5

gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc	163
Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg	
	10 15 20

cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc	211
Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu	
	25 30 35

acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg	259
Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr	
	40 45 50

ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac	307
Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr	
	55 60 65

caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg	355
Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val	
	70 75 80 85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt 403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
90 95 100
cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg 451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
105 110 115
gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc 499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
120 125 130
atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa 547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Thr Glu Lys
135 140 145
gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt 595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
150 155 160 165
gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg 643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
170 175 180
gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa 691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
185 190 195
gag gat ttc gac agc atc gtg gaa gaa ata aaa cga atg ctg att tct 739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
200 205 210
tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgttcca ccg 786
Tyr Leu Phe Ser Val Ala Thr Gly
215 220

<210> 1452

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 1452

Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
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Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
20 25 30
Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
35 40 45
Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
50 55 60
Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
65 70 75 80
Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
85 90 95

Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
 100 105 110
 Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
 115 120 125
 Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
 130 135 140
 Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
 145 150 155 160
 Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
 165 170 175
 Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
 180 185 190
 Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
 195 200 205
 Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
 210 215 220

<210> 1453

<211> 786

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(763)

<223> FRXA02876

<400> 1453

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 Met Thr Ser Asp Lys
 1 5
 gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc 163
 Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
 10 15 20
 cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
 Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
 25 30 35
 acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg 259
 Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
 40 45 50
 ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac 307
 Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
 55 60 65
 caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg 355
 Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
 70 75 80 85

gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt 403
Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
90 95 100
cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg 451
Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
105 110 115
gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc 499
Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
120 125 130
atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa 547
Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Thr Glu Lys
135 140 145
gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt 595
Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
150 155 160 165
gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg 643
Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
170 175 180
gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa 691
Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
185 190 195
gag gat ttc gac agc atc gtg gaa gaa atc aaa cga atg ctg att tct 739
Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
200 205 210
tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgtcgcc acc 786
Tyr Leu Phe Ser Val Ala Thr Gly
215 220

<210> 1454

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 1454

Met Thr Ser Asp Lys Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu
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Ile Leu Met Pro Arg Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg
20 25 30
Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
35 40 45
Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
50 55 60
Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
65 70 75 80
Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
85 90 95

Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
100 105 110

Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
115 120 125

Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
130 135 140

Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
145 150 155 160

Pro Leu Ala Arg Gly Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly
165 170 175

Leu Leu Val His Thr Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp
180 185 190

Val Asn Ser Ser Glu Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys
195 200 205

Arg Met Leu Ile Ser Tyr Leu Phe Ser Val Ala Thr Gly
210 215 220

<210> 1455

<211> 294

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(271)

<223> RXN03067

<400> 1455

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tgagctgaac ttccctcttc tttccgatga ggacaagtct gtg atg act gcg tgg 115
Val Met Thr Ala Trp
1 5

ggt gcg ttt ggt gag aag aag aat tac ggc aag att gtt cag ggt gta 163
Gly Ala Phe Gly Glu Lys Lys Asn Tyr Gly Lys Ile Val Gln Gly Val
10 15 20

att cgt tcc aca ttc ctc atc aat gct gac gga act gtt ggc atg gcg 211
Ile Arg Ser Thr Phe Leu Ile Asn Ala Asp Gly Thr Val Gly Met Ala
25 30 35

aag tac aat gtt cgt gca act ggt cac gtg gag cgc atc gtc cgc gaa 259
Lys Tyr Asn Val Arg Ala Thr Gly His Val Glu Arg Ile Val Arg Glu
40 45 50

atc acc gcg gcg taatagcacc agcttaaaaa cct 294
Ile Thr Ala Ala
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<210> 1456

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 1456

Val Met Thr Ala Trp Gly Ala Phe Gly Glu Lys Lys Asn Tyr Gly Lys
1 5 10 15

Ile Val Gln Gly Val Ile Arg Ser Thr Phe Leu Ile Asn Ala Asp Gly
20 25 30

Thr Val Gly Met Ala Lys Tyr Asn Val Arg Ala Thr Gly His Val Glu
35 40 45

Arg Ile Val Arg Glu Ile Thr Ala Ala
50 55

<210> 1457

<211> 143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(120)

<223> RXN03068

<400> 1457

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Thr Lys Glu Ala Cys Asp Phe Arg Asp Ser Leu Ser Asn Leu Asn Asp
1 5 10 15

ctc gac att gct gtt gtt ggc att tcc ccg gat ccg gtg gac aag ctg 96
Leu Asp Ile Ala Val Val Gly Ile Ser Pro Asp Pro Val Asp Lys Leu
20 25 30

gta agt tcc gtg agg acc atg agc tgaacttccc ttttttttcc gat 143
Val Ser Ser Val Arg Thr Met Ser
35 40

<210> 1458

<211> 40

<212> PRT

<213> Corynebacterium glutamicum

<400> 1458

Thr Lys Glu Ala Cys Asp Phe Arg Asp Ser Leu Ser Asn Leu Asn Asp
1 5 10 15

Leu Asp Ile Ala Val Val Gly Ile Ser Pro Asp Pro Val Asp Lys Leu
20 25 30

Val Ser Ser Val Arg Thr Met Ser
35 40

<210> 1459

<211> 753

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(730)

<223> RXN03073

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aaagggtgcc caattgtttc atgccgtgag ttttgcatta atg gac tcc gta aat 115
Met Asp Ser Val Asn
1 5

gtc ctg ctc att ggc ata atc gtc gcg att gct gct ttg ctg cct cgc 163
Val Leu Leu Ile Gly Ile Ile Val Ala Ile Ala Ala Leu Leu Pro Arg
10 15 20

aag ggt aaa tat ggg cca atc gcc acg cta ctg gtt gcc ggc gat tgg 211
Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu Val Ala Gly Asp Trp
25 30 35

ctt ggc gtt ttc ctc ctc agt att ttg gtg atg ctc gtt ttt gat gga 259
Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met Leu Val Phe Asp Gly
40 45 50

cta gag gat tta gtt cag ggc ttt ttg gat tca atc tgg ttc gga gtc 307
Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser Ile Trp Phe Gly Val
55 60 65

atc ctt ctt gta act ggc atc gtt tcc ttc gtt gcg aca ctg gtt tct 355
Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val Ala Thr Leu Val Ser
70 75 80 85

aaa acc gac agc act aga aag ctt gat gga ttc cta gcg cca gta aaa 403
Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe Leu Ala Pro Val Lys
90 95 100

act cct agt tgg aaa act gtt gga gcc gga ttg atc ctt gga atc gtt 451
Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu Ile Leu Gly Ile Val
105 110 115

cag tca gcg aca tct gta cct ttt tat gca ggg ctt gga tat ttg agc 499
Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly Leu Gly Tyr Leu Ser
120 125 130

gtt ggc aat ttc agt cca gaa att agg tat ggc gga ctt gtg gtc tat 547
Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly Gly Leu Val Val Tyr
135 140 145

gcg acc ttg gct ctg agt ctg ccg att atc gtg gca att ctc gtt gga 595
Ala Thr Leu Ala Leu Ser Leu Pro Ile Ile Val Ala Ile Leu Val Gly
150 155 160 165

atg gtt cgc aaa tac cct gaa agt cct gtt ggt agg ttg ttt gaa ctg 643
Met Val Arg Lys Tyr Pro Glu Ser Pro Val Gly Arg Leu Phe Glu Leu
170 175 180

att ggt caa aat aaa gag aga gtc acc aaa tgg tcg ggc tat ctc gtg 691
Ile Gly Gln Asn Lys Glu Arg Val Thr Lys Trp Ser Gly Tyr Leu Val
185 190 195

tca ctg gtt ctg tgc ata atg ggc att act tcg atc ctg taactagcgc 740
 Ser Leu Val Leu Cys Ile Met Gly Ile Thr Ser Ile Leu
 200 205 210

atgtactcat gag 753

<210> 1460
 <211> 210
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1460
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 Ala Leu Leu Pro Arg Lys Gly Lys Tyr Gly Pro Ile Ala Thr Leu Leu
 20 25 30
 Val Ala Gly Asp Trp Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met
 35 40 45
 Leu Val Phe Asp Gly Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser
 50 55 60
 Ile Trp Phe Gly Val Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val
 65 70 75 80
 Ala Thr Leu Val Ser Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe
 85 90 95
 Leu Ala Pro Val Lys Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu
 100 105 110
 Ile Leu Gly Ile Val Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly
 115 120 125
 Leu Gly Tyr Leu Ser Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly
 130 135 140
 Gly Leu Val Val Tyr Ala Thr Leu Ala Leu Ser Leu Pro Ile Ile Val
 145 150 155 160
 Ala Ile Leu Val Gly Met Val Arg Lys Tyr Pro Glu Ser Pro Val Gly
 165 170 175
 Arg Leu Phe Glu Leu Ile Gly Gln Asn Lys Glu Arg Val Thr Lys Trp
 180 185 190
 Ser Gly Tyr Leu Val Ser Leu Val Leu Cys Ile Met Gly Ile Thr Ser
 195 200 205
 Ile Leu
 210

<210> 1461
 <211> 574
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> FRXA02905

<400> 1461

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				Met	Asp	Ser	Val	Asn	
				1				5	

gtc	ctg	ctc	att	ggc	ata	atc	gtc	gcg	att	gct	gct	ttg	ctg	cct	cgc	163
Val	Leu	Leu	Ile	Gly	Ile	Ile	Val	Ala	Ile	Ala	Ala	Leu	Leu	Pro	Arg	
			10					15						20		

aag	ggt	aaa	tat	ggg	cca	atc	gcc	acg	cta	ctg	ggt	gcc	ggc	gat	tgg	211
Lys	Gly	Lys	Tyr	Gly	Pro	Ile	Ala	Thr	Leu	Leu	Val	Ala	Gly	Asp	Trp	
			25				30						35			

ctt	ggc	ggt	ttc	ctc	ctc	agt	att	ttg	gtg	atg	ctc	ggt	ttt	gat	gga	259
Leu	Gly	Val	Phe	Leu	Leu	Ser	Ile	Leu	Val	Met	Leu	Val	Phe	Asp	Gly	
		40					45					50				

cta	gag	gat	tta	ggt	cag	ggc	ttt	ttg	gat	tca	atc	tgg	ttc	gga	gtc	307
Leu	Glu	Asp	Leu	Val	Gln	Gly	Phe	Leu	Asp	Ser	Ile	Trp	Phe	Gly	Val	
	55					60					65					

atc	ctt	ctt	gta	act	ggc	atc	ggt	tcc	ttc	ggt	gcg	aca	ctg	ggt	tct	355
Ile	Leu	Leu	Val	Thr	Gly	Ile	Val	Ser	Phe	Val	Ala	Thr	Leu	Val	Ser	
	70				75					80					85	

aaa	acc	gac	agc	act	aga	aag	ctt	gat	gga	ttc	cta	gcg	cca	gta	aaa	403
Lys	Thr	Asp	Ser	Thr	Arg	Lys	Leu	Asp	Gly	Phe	Leu	Ala	Pro	Val	Lys	
				90					95					100		

act	cct	agt	tgg	aaa	act	ggt	gga	gcc	gga	ttg	atc	ctt	gga	atc	ggt	451
Thr	Pro	Ser	Trp	Lys	Thr	Val	Gly	Ala	Gly	Leu	Ile	Leu	Gly	Ile	Val	
		105						110					115			

cag	tca	gcg	aca	tct	gta	cct	ttt	tat	gca	ggg	ctt	gga	tat	ttg	agc	499
Gln	Ser	Ala	Thr	Ser	Val	Pro	Phe	Tyr	Ala	Gly	Leu	Gly	Tyr	Leu	Ser	
		120					125					130				

gtt	ggc	aat	ttc	agt	cca	gaa	att	agg	tat	ggc	gga	ctt	gtg	gtc	tat	547
Val	Gly	Asn	Phe	Ser	Pro	Glu	Ile	Arg	Tyr	Gly	Gly	Leu	Val	Val	Tyr	
	135					140					145					

gcg	acc	ttg	gct	ctg	agt	ctg	ccg	att								574
Ala	Thr	Leu	Ala	Leu	Ser	Leu	Pro	Ile								
150					155											

<210> 1462

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 1462

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Val Ala Gly Asp Trp Leu Gly Val Phe Leu Leu Ser Ile Leu Val Met	35	40	45
Leu Val Phe Asp Gly Leu Glu Asp Leu Val Gln Gly Phe Leu Asp Ser	50	55	60
Ile Trp Phe Gly Val Ile Leu Leu Val Thr Gly Ile Val Ser Phe Val	65	70	75
Ala Thr Leu Val Ser Lys Thr Asp Ser Thr Arg Lys Leu Asp Gly Phe	85	90	95
Leu Ala Pro Val Lys Thr Pro Ser Trp Lys Thr Val Gly Ala Gly Leu	100	105	110
Ile Leu Gly Ile Val Gln Ser Ala Thr Ser Val Pro Phe Tyr Ala Gly	115	120	125
Leu Gly Tyr Leu Ser Val Gly Asn Phe Ser Pro Glu Ile Arg Tyr Gly	130	135	140
Gly Leu Val Val Tyr Ala Thr Leu Ala Leu Ser Leu Pro Ile	145	150	155

<210> 1463

<211> 474

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(451)

<223> RXN03085

<400> 1463

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ccgtgagctc ggccgctcgca ttaagggaat caacgcgtaa atg agt att cac atc	115
Met Ser Ile His Ile	5
1	

gca aaa gtc cac gac gtc ctc aaa ggt gaa aaa acc tac gga acc acc	163
Ala Lys Val His Asp Val Leu Lys Gly Glu Lys Thr Tyr Gly Thr Thr	20
10	15

att ttg gtg gat cgg ctc tgg cca cgc ggt gtg aaa aaa gac gac ctt	211
Ile Leu Val Asp Arg Leu Trp Pro Arg Gly Val Lys Lys Asp Asp Leu	35
25	30

gag cca gac ctc tgg ctc aaa agc gtc gcc ccc aca acc gaa ctc cga	259
Glu Pro Asp Leu Trp Leu Lys Ser Val Ala Pro Thr Thr Glu Leu Arg	50
40	45

aaa tgg ttc ggc cac gac cca gct aaa ttc tcc gaa ttc agc acc cgt	307
Lys Trp Phe Gly His Asp Pro Ala Lys Phe Ser Glu Phe Ser Thr Arg	

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<400> 1465
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His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly
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1	5	10	15	
ggt aat ggt ggc aat ccc gat ggc ggt cct gat ggt ggc gac tcg ggt				96
Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly				
20		25	30	
gat gac gac tcc ggc gat gat gac ccc gac ccc gaa ccg gac aag cct				144
Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro				
35		40	45	
gaa gac ggc aaa cct gat agt gat aag ccc cgt agg cca cgg atc agc				192
Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser				
50		55	60	
gcg gaa aaa cac gcc atc atc acc gac gaa ctc gcc cgc ctc aac ccg				240
Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro				
65		70	75	80
aat acc aca ccc agc gcc gag gaa cta cgc acc caa gcc ctg agt caa				288
Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln				
85		90	95	
gcg atc tgg cgc acc cca gaa gac ctc cgc acg tgg cta cgc cac cag				336
Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln				
100		105	110	
gtc acc acc gcg aac aaa aac aac ccc aac ccc atc acc gcc atg aaa				384
Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys				
115		120	125	
agg cgc tac ctc tca gta ggt aaa ccc gat gcc gac aac atg gtc cgc				432
Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg				
130		135	140	
atc agc ggc ctc gtg ccc gca gcc acc gca gca ctg atc acc gcg aac				480
Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn				
145		150	155	160
acc gca ccg tta acc aaa cgt ggc aac ctc gtg gat cta cca gca gca				528
Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala				
165		170	175	
gaa gat atg cgc acc cgc ggg caa cgc cat gcg gat gcg ttg cat cac				576
Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His				
180		185	190	
atc atg gag atc tac aac cac ggt att gtc acc cca gct cgt ggt gga				624
Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly				
195		200	205	
aca gcc agc atc atc atc tcc atg acc acc gat gat ctt gac gag atc				672
Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile				
210		215	220	
aac cac ggt gat cat ggc gat ggc agt cta ctt aac aac ctg tac ccc				720
Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro				
225		230	235	240
acg aac acg ggt tac tca ttg aac ttg gcg gag atc atg aac ctc atc				768
Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile				
245		250	255	

gct gcg aaa tac gac ttc gct gtg ctc ctc gat ggt gag acg ggg cag 816
Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln
260 265 270

ccg ttg aac gtc aat agg atg cag cgc tca gcg aac ctg act caa cgc 864
Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg
275 280 285

atc gcg ttg ttt gct tct gag ttg gtg tgc tcg gca ccc aat tgt gac 912
Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp
290 295 300

agg ccg cag tta gag tgc gag gtt cat cat tta gat ccc tgg atg aga 960
Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg
305 310 315 320

ggt ggg ctg acc aac ctg gtc aat ctc acg cat cag tgc ttt aat cac 1008
Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His
325 330 335

cac cca cgc aac gat gat tcc agg agt ggg gtc aat ggt aaa ggg ttt 1056
His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe
340 345 350

atg gac cgc gat ccc gtc act ggc aga gta ggt cac tac tca gca agt 1104
Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser
355 360 365

ggt gag ggg ccg gtg ttt aac cgg tcg gct gct gct gat cgt tcc ggt 1152
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370 375 380

ggt gca tagtccagac gtaagcatta tgg 1181
Gly Ala
385

<210> 1466

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 1466

His Ser Leu Tyr Pro Ile Pro Lys Pro Asn Ser Gly Ser Gly Asn Gly
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Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp Ser Gly
20 25 30

Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp Lys Pro
35 40 45

Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg Ile Ser
50 55 60

Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu Asn Pro
65 70 75 80

Asn Thr Thr Pro Ser Ala Glu Glu Leu Arg Thr Gln Ala Leu Ser Gln
85 90 95

Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg His Gln
100 105 110

Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala Met Lys
115 120 125

Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met Val Arg
130 135 140

Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr Ala Asn
145 150 155 160

Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro Ala Ala
165 170 175

Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His
180 185 190

Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly
195 200 205

Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile
210 215 220

Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro
225 230 235 240

Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile
245 250 255

Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln
260 265 270

Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg
275 280 285

Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp
290 295 300

Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg
305 310 315 320

Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His
325 330 335

His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe
340 345 350

Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser
355 360 365

Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly
370 375 380

Gly Ala
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<210> 1467

<211> 1575

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1552)

<223> FRXA00071

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<223> Xaa = Gln or His

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<222> 189

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<222> 194

<223> Xaa = Gln

<400> 1467

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Met Ser Ile Thr Thr
1 5

cac gtc caa gca ctc acc aca gca ctc aac gcc atc gac aac cat ttg 163

His Val Gln Ala Leu Thr Thr Ala Leu Asn Ala Ile Asp Asn His Leu
10 15 20

gcc agc atg cty gac cat ggt gtc acc cca gac caa tac aag gcc atc 211

Ala Ser Met Xaa Asp His Gly Val Thr Pro Asp Gln Tyr Lys Ala Ile

25										30										35										
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Glu	Pro	Asp	Leu	Ile	Ala	Leu	Glu	His	Thr	Ile	Asn	His	His	Ala	Thr															
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Ile	Ala	Ala	Gln	Thr	Xaa	Ala	Leu	Ala	Glu	Arg	Thr	Xaa	Xaa	Xaa	Xaa															
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wcs	att	ggc	tcc	acc	cac	ctc	atc	gac	tac	ctc	acc	acc	acc	ttc	ggc	355														
Xaa	Ile	Gly	Ser	Thr	His	Leu	Ile	Asp	Tyr	Leu	Thr	Thr	Thr	Phe	Gly															
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cta	tct	aaa	gca	cgc	gcc	cac	cac	cgc	atc	aat	ctc	gcc	cac	tcc	ctc	403														
Leu	Ser	Lys	Ala	Arg	Ala	His	His	Arg	Ile	Asn	Leu	Ala	His	Ser	Leu															
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tac	ccc	ata	ccg	aag	cca	aac	tct	gga	tct	ggc	aac	ggc	ggt	aat	ggt	451														
Tyr	Pro	Ile	Pro	Lys	Pro	Asn	Ser	Gly	Ser	Gly	Asn	Gly	Gly	Asn	Gly															
105					110					115																				
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Gly	Asn	Pro	Asp	Gly	Gly	Pro	Asp	Gly	Gly	Asp	Ser	Gly	Asp	Asp	Asp															
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Ser	Gly	Asp	Asp	Asp	Pro	Asp	Pro	Glu	Pro	Asp	Lys	Pro	Glu	Asp	Gly															
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aaa	cct	gat	agt	gat	aag	ccc	cgt	agg	cca	cgg	atc	agc	gcg	gaa	aaa	595														
Lys	Pro	Asp	Ser	Asp	Lys	Pro	Arg	Arg	Pro	Arg	Ile	Ser	Ala	Glu	Lys															
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cac	gcc	atc	atc	acc	gac	gaa	ctc	gcc	cgc	ctc	aac	ccg	aat	acc	aca	643														
His	Ala	Ile	Ile	Thr	Asp	Glu	Leu	Ala	Arg	Leu	Asn	Pro	Asn	Thr	Thr															
170					175					180																				
ccc	agc	gcc	gag	gaa	ctr	cgc	amc	caa	gcc	ctg	agt	car	gcg	atc	tgg	691														
Pro	Ser	Ala	Glu	Glu	Xaa	Arg	Xaa	Gln	Ala	Leu	Ser	Xaa	Ala	Ile	Trp															
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cgc	acc	cca	gaa	gac	ctc	cgc	acg	tgg	cta	cgc	cac	cag	gtc	acc	acc	739														
Arg	Thr	Pro	Glu	Asp	Leu	Arg	Thr	Trp	Leu	Arg	His	Gln	Val	Thr	Thr															
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gcg	aac	aaa	aac	aac	ccc	aac	ccc	atc	acc	gcc	atg	aaa	agg	cgc	tac	787														
Ala	Asn	Lys	Asn	Asn	Pro	Asn	Pro	Ile	Thr	Ala	Met	Lys	Arg	Arg	Tyr															
215					220					225																				
ctc	tca	gta	ggt	aaa	ccc	gat	gcc	gac	aac	atg	gtc	cgc	atc	agc	ggc	835														
Leu	Ser	Val	Gly	Lys	Pro	Asp	Ala	Asp	Asn	Met	Val	Arg	Ile	Ser	Gly															
230					235					240					245															
ctc	gtg	ccc	gca	gcc	acc	gca	gca	ctg	atc	acc	gcg	aac	acc	gca	ccg	883														
Leu	Val	Pro	Ala	Ala	Thr	Ala	Ala	Leu	Ile	Thr	Ala	Asn	Thr	Ala	Pro															
250					255					260																				
tta	acc	aaa	cgt	ggc	aac	ctc	gtg	gat	cta	cca	gca	gca	gaa	gat	atg	931														
Leu	Thr	Lys	Arg	Gly	Asn	Leu	Val	Asp	Leu	Pro	Ala	Ala	Glu	Asp	Met															
265					270					275																				

cgc acc cgc ggg caa cgc cat gcg gat gcg ttg cat cac atc atg gag 979
 Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu His His Ile Met Glu
 280 285 290

atc tac aac cac ggt att gtc acc cca gct cgt ggt gga aca gcc agc 1027
 Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg Gly Gly Thr Ala Ser
 295 300 305

atc atc atc tcc atg acc acc gat gat ctt gac gag atc aac cac ggt 1075
 Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp Glu Ile Asn His Gly
 310 315 320 325

gat cat ggc gat ggc agt cta ctt aac aac ctg tac ccc acg aac acg 1123
 Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu Tyr Pro Thr Asn Thr
 330 335 340

ggt tac tca ttg aac ttg gcg gag atc atg aac ctc atc gct gcg aaa 1171
 Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn Leu Ile Ala Ala Lys
 345 350 355

tac gac ttc gct gtg ctc ctc gat ggt gag acg ggg cag ccg ttg aac 1219
 Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr Gly Gln Pro Leu Asn
 360 365 370

gtc aat agg atg cag cgc tca gcg aac ctg act caa cgc atc gcg ttg 1267
 Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr Gln Arg Ile Ala Leu
 375 380 385

ttt gct tct gag ttg gtg tgc tcg gca ccc aat tgt gac agg ccg cag 1315
 Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn Cys Asp Arg Pro Gln
 390 395 400 405

tta gag tgc gag gtt cat cat tta gat ccc tgg atg aga ggt ggg ctg 1363
 Leu Glu Cys Glu Val His His Leu Asp Pro Trp Met Arg Gly Gly Leu
 410 415 420

acc aac ctg gtc aat ctc acg cat cag tgc ttt aat cac cac cca cgc 1411
 Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe Asn His His Pro Arg
 425 430 435

aac gat gat tcc agg agt ggg gtc aat ggt aaa ggg ttt atg gac cgc 1459
 Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys Gly Phe Met Asp Arg
 440 445 450

gat ccc gtc act ggc aga gta ggt cac tac tca gca agt ggt gag ggg 1507
 Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser Ala Ser Gly Glu Gly
 455 460 465

ccg gtg ttt aac cgg tcg gct gct gct gat cgt tcc ggt ggt gca 1552
 Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg Ser Gly Gly Ala
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tagtcagac gtaagcatta tgg 1575

<210> 1468

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<220>

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<222> 25, 187

<223> Xaa = Leu

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<221> VARIANT

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<223> Xaa = Gln or His

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<223> Xaa = Thr or Ser

<220>

<221> VARIANT

<222> 189

<223> Xaa = Asn or Thr

<220>

<221> VARIANT

<222> 194

<223> Xaa = Gln

<400> 1468

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		20						25					30		

Gln	Tyr	Lys	Ala	Ile	Glu	Pro	Asp	Leu	Ile	Ala	Leu	Glu	His	Thr	Ile
		35					40					45			

Asn	His	His	Ala	Thr	Ile	Ala	Ala	Gln	Thr	Xaa	Ala	Leu	Ala	Glu	Arg
	50					55					60				

Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Gly	Ser	Thr	His	Leu	Ile	Asp	Tyr	Leu
65					70					75					80

Thr	Thr	Thr	Phe	Gly	Leu	Ser	Lys	Ala	Arg	Ala	His	His	Arg	Ile	Asn
			85						90					95	

Leu	Ala	His	Ser	Leu	Tyr	Pro	Ile	Pro	Lys	Pro	Asn	Ser	Gly	Ser	Gly
			100					105					110		

Asn Gly Gly Asn Gly Gly Asn Pro Asp Gly Gly Pro Asp Gly Gly Asp
 115 120 125
 Ser Gly Asp Asp Asp Ser Gly Asp Asp Asp Pro Asp Pro Glu Pro Asp
 130 135 140
 Lys Pro Glu Asp Gly Lys Pro Asp Ser Asp Lys Pro Arg Arg Pro Arg
 145 150 155 160
 Ile Ser Ala Glu Lys His Ala Ile Ile Thr Asp Glu Leu Ala Arg Leu
 165 170 175
 Asn Pro Asn Thr Thr Pro Ser Ala Glu Glu Xaa Arg Xaa Gln Ala Leu
 180 185 190
 Ser Xaa Ala Ile Trp Arg Thr Pro Glu Asp Leu Arg Thr Trp Leu Arg
 195 200 205
 His Gln Val Thr Thr Ala Asn Lys Asn Asn Pro Asn Pro Ile Thr Ala
 210 215 220
 Met Lys Arg Arg Tyr Leu Ser Val Gly Lys Pro Asp Ala Asp Asn Met
 225 230 235 240
 Val Arg Ile Ser Gly Leu Val Pro Ala Ala Thr Ala Ala Leu Ile Thr
 245 250 255
 Ala Asn Thr Ala Pro Leu Thr Lys Arg Gly Asn Leu Val Asp Leu Pro
 260 265 270
 Ala Ala Glu Asp Met Arg Thr Arg Gly Gln Arg His Ala Asp Ala Leu
 275 280 285
 His His Ile Met Glu Ile Tyr Asn His Gly Ile Val Thr Pro Ala Arg
 290 295 300
 Gly Gly Thr Ala Ser Ile Ile Ile Ser Met Thr Thr Asp Asp Leu Asp
 305 310 315 320
 Glu Ile Asn His Gly Asp His Gly Asp Gly Ser Leu Leu Asn Asn Leu
 325 330 335
 Tyr Pro Thr Asn Thr Gly Tyr Ser Leu Asn Leu Ala Glu Ile Met Asn
 340 345 350
 Leu Ile Ala Ala Lys Tyr Asp Phe Ala Val Leu Leu Asp Gly Glu Thr
 355 360 365
 Gly Gln Pro Leu Asn Val Asn Arg Met Gln Arg Ser Ala Asn Leu Thr
 370 375 380
 Gln Arg Ile Ala Leu Phe Ala Ser Glu Leu Val Cys Ser Ala Pro Asn
 385 390 395 400
 Cys Asp Arg Pro Gln Leu Glu Cys Glu Val His His Leu Asp Pro Trp
 405 410 415
 Met Arg Gly Gly Leu Thr Asn Leu Val Asn Leu Thr His Gln Cys Phe
 420 425 430

Asn His His Pro Arg Asn Asp Asp Ser Arg Ser Gly Val Asn Gly Lys
 435 440 445

Gly Phe Met Asp Arg Asp Pro Val Thr Gly Arg Val Gly His Tyr Ser
 450 455 460

Ala Ser Gly Glu Gly Pro Val Phe Asn Arg Ser Ala Ala Ala Asp Arg
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Ser Gly Gly Ala

<210> 1469

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(724)

<223> RXN03098

<400> 1469

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ttccgtcacc accctcttcg agggcgaggc ctaaaccacc atg ccc acc acg gac 115
 Met Pro Thr Thr Asp
 1 5

gtc ttc aac cgc gtc cgg ttg gca ttg gaa cct cta gct gat ccc gca 163
 Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro Leu Ala Asp Pro Ala
 10 15 20

cgt gcc acc gga atg gca agc tac atg cgg gat cag ttt tct ttt ctc 211
 Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp Gln Phe Ser Phe Leu
 25 30 35

ggc atc cca tcc acc ccc aga aaa gaa gcc tgc aaa ccc gtg ctg tcc 259
 Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys Lys Pro Val Leu Ser
 40 45 50

gcg cta aaa gag ttg gac act gac ttt gtc tca gac tgc ttt ggc gca 307
 Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser Asp Cys Phe Gly Ala
 55 60 65

gct gaa cgg gaa tac cag tat gtc gcc tgc gat cac atc aat cgc gtc 355
 Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp His Ile Asn Arg Val
 70 75 80 85

ggc atc acc gat tta ggt ttt gcc aaa gca tta gtg cag acc aaa tcc 403
 Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu Val Gln Thr Lys Ser
 90 95 100

tgg tgg gac acc gtc gat tcc cta gca aaa ccg atc ggc gcc aaa cac 451
 Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro Ile Gly Ala Lys His
 105 110 115

gat gat gat ctg atg aaa acg tgg gcg ctt gat gag gac ttc tgg gtg 499
 Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp Glu Asp Phe Trp Val
 120 125 130

cgc cgc atc gcg atc atc cac caa ctg ggc cgc aag aaa aac acc gac 547
 Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg Lys Lys Asn Thr Asp
 135 140 145
 gct gcc ctg ctg gcc tgg atc atc gag cag aac ctc ggc tcc agc gag 595
 Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn Leu Gly Ser Ser Glu
 150 155 160 165
 ttc ttc atc aac aaa gcg atc ggc tgg gca ctg cgg gat ttc gcc cgc 643
 Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu Arg Asp Phe Ala Arg
 170 175 180
 cac gac ccc agc tgg gtc cgg gct ttt gtc gac gcc acg gac ctt tcc 691
 His Asp Pro Ser Trp Val Arg Ala Phe Val Asp Ala Thr Asp Leu Ser
 185 190 195
 cca ctg agc cgg cga gaa gcc ctg aag aat att tagccctcag gcatcatctg 744
 Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile
 200 205
 agc 747

<210> 1470
 <211> 208
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1470

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 Gln Phe Ser Phe Leu Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys
 35 40 45
 Lys Pro Val Leu Ser Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser
 50 55 60
 Asp Cys Phe Gly Ala Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp
 65 70 75 80
 His Ile Asn Arg Val Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu
 85 90 95
 Val Gln Thr Lys Ser Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro
 100 105 110
 Ile Gly Ala Lys His Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp
 115 120 125
 Glu Asp Phe Trp Val Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg
 130 135 140
 Lys Lys Asn Thr Asp Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn
 145 150 155 160
 Leu Gly Ser Ser Glu Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu

gat gtc ggt ttc cgc acc aat gac cgg cgc gag agc gtc ctc cag gaa 595
Asp Val Gly Phe Arg Thr Asn Asp Arg Arg Glu Ser Val Leu Gln Glu
150 155 160 165

ggc acg cag gtc ggt gct ttc gga ttc ttc gaa gct gta ggc cag ctg 643
Gly Thr Gln Val Gly Ala Phe Gly Phe Phe Glu Ala Val Gly Gln Leu
170 175 180

tcc cag gtc gat cga tgc ggt acc aag gtt cat atc tac cag ttc gcg 691
Ser Gln Val Asp Arg Cys Gly Thr Lys Val His Ile Tyr Gln Phe Ala
185 190 195

caa aat atc caa gga gct ttc cag tgg aag ttc ctt gga tat gat gtg 739
Gln Asn Ile Gln Gly Ala Phe Gln Trp Lys Phe Leu Gly Tyr Asp Val
200 205 210

gcg ggc gta gcg gtg aga ctt gat gat atc gat gtc tgagacattc 785
Ala Gly Val Ala Val Arg Leu Asp Asp Ile Asp Val
215 220 225

acaaggagac gac 798

<210> 1472

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 1472

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Gly Glu Tyr Asn Leu Gly Asn Ala Leu Gly Leu Glu Val Leu Gly Gln
20 25 30

Ala Phe Ala Val Thr Pro Ala Ala Gly Val Val Tyr His Asp Gly Val
35 40 45

Ile Asp Ala Val Phe Gly Val Ile Asn Gly Gly Trp Val Ile Gly Val
50 55 60

Asp Asp Leu Asp Trp Gly Ala Val Gly Pro Asp Asp Val Val Val Ile
65 70 75 80

Ile Gly Gly Asp Gly Ala Ile Glu Ser Thr Val Asp Arg Ile Thr Thr
85 90 95

Gln Gln Gly Cys Ala Leu Asp Gln Val Phe Phe Thr Ile Phe Ala Asp
100 105 110

His Asp Gly Ala Gln Thr Ser Thr Val Ile Gln Cys Leu Ala Gly Asn
115 120 125

Gln Asp Ala Gly Gln Gln Ala Thr Asp Ala Ala Glu Thr Val Gln His
130 135 140

Asp Ile Ser Trp Val Asp Val Gly Phe Arg Thr Asn Asp Arg Arg Glu
145 150 155 160

Ser Val Leu Gln Glu Gly Thr Gln Val Gly Ala Phe Gly Phe Phe Glu

	165		170		175
Ala Val Gly Gln Leu Ser Gln Val Asp Arg Cys Gly Thr Lys Val His					
	180		185		190
Ile Tyr Gln Phe Ala Gln Asn Ile Gln Gly Ala Phe Gln Trp Lys Phe					
	195		200		205
Leu Gly Tyr Asp Val Ala Gly Val Ala Val Arg Leu Asp Asp Ile Asp					
	210		215		220
Val					
225					

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 <212> DNA
 <213> Corynebacterium glutamicum

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 Leu Glu Leu Asn Ala
 1 5
 tgg gag gac atc ctt gac ctt ctg agc tgg agt gga tcc gga aac gga 163
 Trp Glu Asp Ile Leu Asp Leu Leu Ser Trp Ser Gly Ser Gly Asn Gly
 10 15 20
 gca cag gat caa acc gtt atc caa gtc ctc gag ggt ttc aat gcg atc 211
 Ala Gln Asp Gln Thr Val Ile Gln Val Leu Glu Gly Phe Asn Ala Ile
 25 30 35
 gtc atc ttg gcg aac aag cag agc ctg gtg ggt aag cag gta tgg gcc 259
 Val Ile Leu Ala Asn Lys Gln Ser Leu Val Gly Lys Gln Val Trp Ala
 40 45 50
 acc gaa gtt gac gga ctc tgaacggcca gcgttgatgg agt 300
 Thr Glu Val Asp Gly Leu
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<210> 1474
 <211> 59
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1474
 Leu Glu Leu Asn Ala Trp Glu Asp Ile Leu Asp Leu Leu Ser Trp Ser
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 Gly Ser Gly Asn Gly Ala Gln Asp Gln Thr Val Ile Gln Val Leu Glu
 20 25 30

Gly Phe Asn Ala Ile Val Ile Leu Ala Asn Lys Gln Ser Leu Val Gly
 35 40 45
 Lys Gln Val Trp Ala Thr Glu Val Asp Gly Leu
 50 55

<210> 1475
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(292)
 <223> RXN03106

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 Met Ser Ala Ser Phe
 1 5
 gat gac ccc aac ctc atc tcg ctt gct gga ctg gtt cca acc atg cac 163
 Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu Val Pro Thr Met His
 10 15 20
 tta gcc gat gct gcc agc ctg tcc acc ttg gcc cag gac cgg ttg agc 211
 Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala Gln Asp Arg Leu Ser
 25 30 35
 atc acc ggt gat aaa ggt gcc aat gct ggt gcg aag atc gcc tcc cta 259
 Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala Lys Ile Ala Ser Leu
 40 45 50
 gtc gcg ggc atg gtc gcc ggt gct gat tcc atc 292
 Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
 55 60

<210> 1476
 <211> 64
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1476
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 Val Pro Thr Met His Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala
 20 25 30
 Gln Asp Arg Leu Ser Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala
 35 40 45
 Lys Ile Ala Ser Leu Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile
 50 55 60

<210> 1477

<211> 324
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(301)
<223> RXN03107

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Met Ser Asp Phe Ser
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Asn Lys Ala Glu Asp Leu Thr Gly Lys Ala Lys Glu Gly Phe Gly Glu
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gca act gat aac gag tcc ctc gct gat gag ggc cgt gcg gat cag gct 211
Ala Thr Asp Asn Glu Ser Leu Ala Asp Glu Gly Arg Ala Asp Gln Ala
25 30 35
aag gca gac atc aag gat gct gtc gaa aac gcc ggt gaa aag gta aag 259
Lys Ala Asp Ile Lys Asp Ala Val Glu Asn Ala Gly Glu Lys Val Lys
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gac gca gct aac aag gtt ctg ggt gcg ttc aag aag gac gac 301
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<212> PRT
<213> Corynebacterium glutamicum

<400> 1478
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Gly Glu Lys Val Lys Asp Ala Ala Asn Lys Val Leu Gly Ala Phe Lys
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Lys Asp Asp
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<223> RXN03113

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Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile Leu Ala Val Gly Leu
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Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser Leu Gly Ala Ala Ala
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Val Leu Phe Val Ala Leu Val Val Ser Thr Ala Asn Thr Asp Ile Val
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Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala Met Phe Val Tyr Val
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Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu Leu Ala Thr Leu Ile
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Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly Leu Asp Ala Ala Ile
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Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser Thr Pro Gly Met Ala
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Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro Ser Leu Ala Ser Glu
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cct gtt att ggt tat tcc ttg gca tat ccg gga gcc gtg ctg gga tcc 595
Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly Ala Val Leu Gly Ser
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att gtg gtg gcc gcg gtt gga gcg aaa ctg ctc aaa gta aat cac cgg 643
Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu Lys Val Asn His Arg
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gaa gat gct cga aaa gaa ggc atg atc acc gca ccg ctg gtg tgg aag 691
Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala Pro Leu Val Trp Lys
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Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg Val Gly Asp Leu Pro	
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cgc ctt gca ggt gaa agt atc atc gca acc cgc att gtg gat gat cca	787
Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg Ile Val Asp Asp Pro	
215 220 225	
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His Thr His Arg Leu Ala Asp Pro Asp Leu Pro Ile Thr Glu Gly Met	
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Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val Asp Arg Ala Ile Lys	
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Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu Asp Thr Glu Leu Ile	
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Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val Ala Gly Arg Thr Val	
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Ala Glu Leu Asp Thr Val Ala His Gly Phe Met Ile Ala Arg Ile Arg	
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Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp Thr Val Ile Asn Tyr	
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Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly Arg Val Ala Glu Val	
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Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu Ala Asp Val Asn Leu	
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Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu Leu Leu Gly Ala Ile	
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Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser Leu Gly Phe Gly Gly	
375 380 385	
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Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala Leu Lys His Thr Gly	
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Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn Arg Thr Ile Ser Thr	
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Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly Thr Ser Ala Gly Ala	
425 430 435	
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Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser Ser Leu Ile Tyr Met Ala
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Gly Gly Leu Val Ile Thr Leu Ala Ser Ala Leu Leu Cys Ala Val Ile
455 460 465

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Gly Met Trp Val Leu Arg Leu Arg Trp Asp Glu Ala Met Gly Val Ala
470 475 480 485

gct ggc acc acc aca aat cct gca att att tcc tat ctg aat ggg caa 1603
Ala Gly Thr Thr Thr Asn Pro Ala Ile Ile Ser Tyr Leu Asn Gly Gln
490 495 500

acc gga acg gat ctt gcc aac agg gga tat gcc act gtg tac ccc acg 1651
Thr Gly Thr Asp Leu Ala Asn Arg Gly Tyr Ala Thr Val Tyr Pro Thr
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<210> 1480

<211> 533

<212> PRT

<213> Corynebacterium glutamicum

<400> 1480

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Leu Gly Ala Ala Ala Val Leu Phe Val Ala Leu Val Val Ser Thr Ala
35 40 45

Asn Thr Asp Ile Val Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala
50 55 60

Met Phe Val Tyr Val Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser
65 70 75 80

Glu Phe Ala Lys Lys Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu
85 90 95

Leu Ala Thr Leu Ile Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly
100 105 110

Leu Asp Ala Ala Ile Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser
115 120 125

Thr Pro Gly Met Ala Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro
130 135 140

Ser Leu Ala Ser Glu Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly
145 150 155 160

Ala Val Leu Gly Ser Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu
 165 170 175
 Lys Val Asn His Arg Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala
 180 185 190
 Pro Leu Val Trp Lys Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg
 195 200 205
 Val Gly Asp Leu Pro Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg
 210 215 220
 Ile Val Asp Asp Pro His Thr His Arg Leu Ala Asp Pro Asp Leu Pro
 225 230 235 240
 Ile Thr Glu Gly Met Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val
 245 250 255
 Asp Arg Ala Ile Lys Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu
 260 265 270
 Asp Thr Glu Leu Ile Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val
 275 280 285
 Ala Gly Arg Thr Val Ala Glu Leu Asp Thr Val Ala His Gly Phe Met
 290 295 300
 Ile Ala Arg Ile Arg Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp
 305 310 315 320
 Thr Val Ile Asn Tyr Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly
 325 330 335
 Arg Val Ala Glu Val Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu
 340 345 350
 Ala Asp Val Asn Leu Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu
 355 360 365
 Leu Leu Gly Ala Ile Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser
 370 375 380
 Leu Gly Phe Gly Gly Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala
 385 390 395 400
 Leu Lys His Thr Gly Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn
 405 410 415
 Arg Thr Ile Ser Thr Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly
 420 425 430
 Thr Ser Ala Gly Ala Gly Phe Arg Ala Ala Leu Thr Asp Ser Ser Ser
 435 440 445
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Val Leu Asp Phe Leu																5
1																
gct gcg aac ccg ctg att gcg ctg gtg gtt att ttg gcc gtt ggt tta																163
Ala Ala Asn Pro Leu Ile Ala Leu Val Val Ile Leu Ala Val Gly Leu																20
10 15																
gca att ggt cag att agg gtc ttt ggc ctt tct tta ggt gcc gcc gcg																211
Ala Ile Gly Gln Ile Arg Val Phe Gly Leu Ser Leu Gly Ala Ala Ala																35
25 30																
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Val Leu Phe Val Ala Leu Val Val Ser Thr Ala Asn Thr Asp Ile Val																50
40 45																
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Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala Met Phe Val Tyr Val																65
55 60																
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Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu Leu Ala Thr Leu Ile																100
90 95																
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Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly Leu Asp Ala Ala Ile																115
105 110																
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Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser Thr Pro Gly Met Ala																125
120 125 130																

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Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro Ser Leu Ala Ser Glu	
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Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly Ala Val Leu Gly Ser	
150 155 160 165	
att gtg gtg gcc gcg gtt gga gcg aaa ctg ctc aaa gta aat cac cgg	643
Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu Lys Val Asn His Arg	
170 175 180	
gaa gat gct cga aaa gaa ggc atg atc acc gca ccg ctg gtg tgg aag	691
Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala Pro Leu Val Trp Lys	
185 190 195	
ggt gtg cag ctc aaa cct gga atc aca ggc agg gtg gga gat ctt cca	739
Gly Val Gln Leu Lys Pro Gly Ile Thr Gly Arg Val Gly Asp Leu Pro	
200 205 210	
cgc ctt gca ggt gaa agt atc atc gca acc cgc att gtg gat gat cca	787
Arg Leu Ala Gly Glu Ser Ile Ile Ala Thr Arg Ile Val Asp Asp Pro	
215 220 225	
cat aca cac cgc ctc gcg gat cca gat ctg ccg att act gaa ggc atg	835
His Thr His Arg Leu Ala Asp Pro Asp Leu Pro Ile Thr Glu Gly Met	
230 235 240 245	
gaa ctg ttg atc aac ggc act gaa gaa gcc gtg gat cgg gca att aag	883
Glu Leu Leu Ile Asn Gly Thr Glu Glu Ala Val Asp Arg Ala Ile Lys	
250 255 260	
gcg ttg ggt gaa gaa cgc gaa acc aaa att gag gac aca gag ctg atc	931
Ala Leu Gly Glu Glu Arg Glu Thr Lys Ile Glu Asp Thr Glu Leu Ile	
265 270 275	
tac acc cgc ctg acg gta tct agc cct gag gtt gca ggt aga acc gtt	979
Tyr Thr Arg Leu Thr Val Ser Ser Pro Glu Val Ala Gly Arg Thr Val	
280 285 290	
gct gag ctt gat act gta gct cac gga ttc atg att gcc cgt atc cgc	1027
Ala Glu Leu Asp Thr Val Ala His Gly Phe Met Ile Ala Arg Ile Arg	
295 300 305	
cag ggc gat tct gag gta gtg cct aaa cct gac acc gtg atc aac tac	1075
Gln Gly Asp Ser Glu Val Val Pro Lys Pro Asp Thr Val Ile Asn Tyr	
310 315 320 325	
tct gac cgc atc cgc gtg gtg gtt gct cct ggt cgt gtg gct gaa gtg	1123
Ser Asp Arg Ile Arg Val Val Val Ala Pro Gly Arg Val Ala Glu Val	
330 335 340	
cga cga ttc tta ggg gac tct gaa aag tcc ctt gct gat gtt aat ctg	1171
Arg Arg Phe Leu Gly Asp Ser Glu Lys Ser Leu Ala Asp Val Asn Leu	
345 350 355	
ctg cct tta gcc atc gga tta tct ctt ggc ctg ttg ttg ggc gcg atc	1219
Leu Pro Leu Ala Ile Gly Leu Ser Leu Gly Leu Leu Leu Gly Ala Ile	
360 365 370	

ccg att cct ctt cca ggc ggc acc acg atg tcc ctt ggc ttt ggt ggc 1267
 Pro Ile Pro Leu Pro Gly Gly Thr Thr Met Ser Leu Gly Phe Gly Gly
 375 380 385

ggc ccg att att gcc ggc ctg att ttg gga gca ctc aag cac aca gga 1315
 Gly Pro Ile Ile Ala Gly Leu Ile Leu Gly Ala Leu Lys His Thr Gly
 390 395 400 405

ccg ctg acg tgg cag atg ccg ttc cac gcc aac cgc acg atc tcc acc 1363
 Pro Leu Thr Trp Gln Met Pro Phe His Ala Asn Arg Thr Ile Ser Thr
 410 415 420

ttg ggc ctg gcg ctg .ttt ttg gct ggt gtg ggt acc tct gca ggt gca 1411
 Leu Gly Leu Ala Leu Phe Leu Ala Gly Val Gly Thr Ser Ala Gly Ala
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<210> 1482

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 1482

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Leu Gly Ala Ala Ala Val Leu Phe Val Ala Leu Val Val Ser Thr Ala
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Asn Thr Asp Ile Val Ile Pro Met Ile Val Tyr Gln Leu Gly Leu Ala
 50 55 60

Met Phe Val Tyr Val Ile Gly Leu Ser Ala Gly Pro Ala Phe Phe Ser
 65 70 75 80

Glu Phe Ala Lys Lys Gly Trp Lys Leu Thr Ile Phe Met Leu Leu Leu
 85 90 95

Leu Ala Thr Leu Ile Gly Leu Ala Trp Val Leu Ile Lys Ser Leu Gly
 100 105 110

Leu Asp Ala Ala Ile Gly Thr Gly Met Phe Thr Gly Ala Leu Thr Ser
 115 120 125

Thr Pro Gly Met Ala Ala Val Val Glu Leu Ile Glu Gly Ile Asp Pro
 130 135 140

Ser Leu Ala Ser Glu Pro Val Ile Gly Tyr Ser Leu Ala Tyr Pro Gly
 145 150 155 160

Ala Val Leu Gly Ser Ile Val Val Ala Ala Val Gly Ala Lys Leu Leu
 165 170 175

Lys Val Asn His Arg Glu Asp Ala Arg Lys Glu Gly Met Ile Thr Ala

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Val	Gly	Asp	Leu	Pro	Arg	Leu	Ala	Gly	Glu	Ser	Ile	Ile	Ala	Thr	Arg
	210					215					220				
Ile	Val	Asp	Asp	Pro	His	Thr	His	Arg	Leu	Ala	Asp	Pro	Asp	Leu	Pro
225					230					235					240
Ile	Thr	Glu	Gly	Met	Glu	Leu	Leu	Ile	Asn	Gly	Thr	Glu	Glu	Ala	Val
				245					250					255	
Asp	Arg	Ala	Ile	Lys	Ala	Leu	Gly	Glu	Glu	Arg	Glu	Thr	Lys	Ile	Glu
		260						265					270		
Asp	Thr	Glu	Leu	Ile	Tyr	Thr	Arg	Leu	Thr	Val	Ser	Ser	Pro	Glu	Val
	275						280					285			
Ala	Gly	Arg	Thr	Val	Ala	Glu	Leu	Asp	Thr	Val	Ala	His	Gly	Phe	Met
	290					295					300				
Ile	Ala	Arg	Ile	Arg	Gln	Gly	Asp	Ser	Glu	Val	Val	Pro	Lys	Pro	Asp
305					310					315					320
Thr	Val	Ile	Asn	Tyr	Ser	Asp	Arg	Ile	Arg	Val	Val	Val	Ala	Pro	Gly
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Arg	Val	Ala	Glu	Val	Arg	Arg	Phe	Leu	Gly	Asp	Ser	Glu	Lys	Ser	Leu
		340						345					350		
Ala	Asp	Val	Asn	Leu	Leu	Pro	Leu	Ala	Ile	Gly	Leu	Ser	Leu	Gly	Leu
		355					360					365			
Leu	Leu	Gly	Ala	Ile	Pro	Ile	Pro	Leu	Pro	Gly	Gly	Thr	Thr	Met	Ser
	370					375					380				
Leu	Gly	Phe	Gly	Gly	Gly	Pro	Ile	Ile	Ala	Gly	Leu	Ile	Leu	Gly	Ala
385					390					395					400
Leu	Lys	His	Thr	Gly	Pro	Leu	Thr	Trp	Gln	Met	Pro	Phe	His	Ala	Asn
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Arg	Thr	Ile	Ser	Thr	Leu	Gly	Leu	Ala	Leu	Phe	Leu	Ala	Gly	Val	Gly
		420						425					430		
Thr	Ser	Ala	Gly	Ala	Gly	Phe	Arg	Ala	Ala	Leu	Thr	Asp	Ser	Ser	
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<213> Corynebacterium glutamicum

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<222> (101)..(499)

<223> RXN03115

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Ala Asp His Val Arg	Ala Gln Leu Glu Thr Leu Gly Leu His Val Glu					
	85		90		95	
Ala Pro Met Ser Glu Met Leu Thr Val Asn Ile Ala Pro Asp Ser Pro						
	100		105		110	
Ser His Gly Leu Glu Ile Leu Leu Asp Asp Leu His Ala Gln Gly Val						
	115		120		125	
Ile Phe Arg Ala Leu						
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<210> 1485

<211> 270

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(247)

<223> RXN03122

<400> 1485

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gccagggca cccgaggctg cccggctcta ccttgagcag	atg acc gcc cac cat	115
	Met Thr Ala His His	
	1 5	

gag ggc gcg gtc gat atg gcc cgc gat gag gtc act gat ggc cag aac	163
Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn	
	10 15 20

ccg cag gcc atc gct ctg gct gag cag gtc att gaa gat cag gag gcc	211
Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala	
	25 30 35

gag atc gcc gag atg gag cat atg ctc aac gag ctc tgaacaagga	257
Glu Ile Ala Glu Met Glu His Met Leu Asn Glu Leu	
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<210> 1486

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1486

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Glu Asp Gln Glu Ala Glu Ile Ala Glu Met Glu His Met Leu Asn Glu	
35 40 45	

Leu

<210> 1487
 <211> 474
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(451)
 <223> RXN03134

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 Val Ala Trp Arg Val
 1 5
 ggc cca ggt tcc cat gag cat gac ata gtt ggg tcc tcc ggc ttt gga 163
 Gly Pro Gly Ser His Glu His Asp Ile Val Gly Ser Ser Gly Phe Gly
 10 15 20
 tcc gag gcc gac gga gga ttt ttt cca gcc tcc gaa gga ttg gcg ttg 211
 Ser Glu Ala Asp Gly Gly Phe Phe Pro Ala Ser Glu Gly Leu Ala Leu
 25 30 35
 gac aat ggc gcc ggt gat gcc gcg gtt gac gta ggc gtt tcc gac atc 259
 Asp Asn Gly Ala Gly Asp Ala Ala Val Asp Val Gly Val Ser Asp Ile
 40 45 50
 gac gtg gtc aag cca ggt gcg gac ttc gtc ggc gtc gag gga ttg gag 307
 Asp Val Val Lys Pro Gly Ala Asp Phe Val Gly Val Glu Gly Leu Glu
 55 60 65
 tcc gcc ggt gag tcc gaa gtc gtt gcc gtt ttg gaa ttc gat ggc ttc 355
 Ser Ala Gly Glu Ser Glu Val Val Ala Val Leu Glu Phe Asp Gly Phe
 70 75 80 85
 att gag gtc ggt ggc ttt cat cag gcc gag gac tgg tcc gaa tac ttc 403
 Ile Glu Val Gly Gly Phe His Gln Ala Glu Asp Trp Ser Glu Tyr Phe
 90 95 100
 tgt gag gtg gaa gaa ggt tcc tgg ttt gac gcc ttc ttt gat gcc ggg 451
 Cys Glu Val Glu Glu Gly Ser Trp Phe Asp Ala Phe Phe Asp Ala Gly
 105 110 115
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<210> 1488
 <211> 117
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1488
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 1 5 10 15

Ser Ser Gly Phe Gly Ser Glu Ala Asp Gly Gly Phe Phe Pro Ala Ser
 20 25 30

Glu Gly Leu Ala Leu Asp Asn Gly Ala Gly Asp Ala Ala Val Asp Val
 35 40 45

Gly Val Ser Asp Ile Asp Val Val Lys Pro Gly Ala Asp Phe Val Gly
 50 55 60

Val Glu Gly Leu Glu Ser Ala Gly Glu Ser Glu Val Val Ala Val Leu
 65 70 75 80

Glu Phe Asp Gly Phe Ile Glu Val Gly Gly Phe His Gln Ala Glu Asp
 85 90 95

Trp Ser Glu Tyr Phe Cys Glu Val Glu Glu Gly Ser Trp Phe Asp Ala
 100 105 110

Phe Phe Asp Ala Gly
 115

<210> 1489

<211> 852

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(829)

<223> RXN03135

<400> 1489

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cgggctctgc tgcggtggcg acggcttttg tggccactg ttg gtt ttg gat gag 115
 Leu Val Leu Asp Glu
 1 5

cgc tgg gtt ggt gtc ggg ctc gtt gat aaa tgg gac gag ggg ggc gtc 163
 Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp Asp Glu Gly Gly Val
 10 15 20

gag aag cgt ctc ttt gct gcg gtc ttg tgt gtg gtt ggg gcc ggg cgc 211
 Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val Val Gly Ala Gly Arg
 25 30 35

ggg cac gtc gat gag cgt ggc gag gtc aga tat gga ggc gcg gaa gcg 259
 Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr Gly Gly Ala Glu Ala
 40 45 50

gct ctc ctc tcg ctt gaa gga cgg gtt gtc ggc gtc gag gtc gaa gat 307
 Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly Val Glu Val Glu Asp
 55 60 65

ggc gga cat gaa gtt ttc gct cgc ggc gtt ttc ctc gag gcg gcg cac 355
 Gly Gly His Glu Val Phe Ala Arg Gly Val Phe Leu Glu Ala Ala His
 70 75 80 85

gag gta aga aat ggc cac gtc gaa ttc ttg tgg gcg cac ggc tgg tac 403

Glu Val Arg Asn Gly His Val Glu Phe Leu Trp Ala His Gly Trp Tyr
 90 95 100
 gta aag cag cag ctc acc gac gtc aac gct gac ggc gcg cgc ctg atc 451
 Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp Gly Ala Arg Leu Ile
 105 110 115
 gga cgc cat gcc ctg cag cat ttc gaa ctc cac acg gtc cgc tac ccc 499
 Gly Arg His Ala Leu Gln His Phe Glu Leu His Thr Val Arg Tyr Pro
 120 125 130
 acg ctc cac aga gag caa atg tgc gaa tgc tat gtc gaa aag gtt gtg 547
 Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr Val Glu Lys Val Val
 135 140 145
 gcc ggc aac gcc cag gcg cag gcc ctc cat gtt ttc ttt gcg cat cgt 595
 Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val Phe Phe Ala His Arg
 150 155 160 165
 cca ata gag gac gcg ctt gta att ggc atc ggt ggc ttg ttt gga agg 643
 Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly Gly Leu Phe Gly Arg
 170 175 180
 ttc tgt ggc aac tgg cca gcc ggt gat ctg cgc gtg gac gtg ctc cat 691
 Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg Val Asp Val Leu His
 185 190 195
 agg caa att agc acc ctt gac cag gcg aac ctt aac gcc cgc ccc gcc 739
 Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu Asn Ala Arg Pro Ala
 200 205 210
 tgt gtt gac gcg ctc gcg gcc gaa ctg cgc caa gtc ctg gat tgc acc 787
 Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln Val Leu Asp Cys Thr
 215 220 225
 gag ggc atc ggg aag gta cgc ctg caa cac aat tcc ggc ttc 829
 Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn Ser Gly Phe
 230 235 240
 tagttcatgc agctctggat tgg 852

<210> 1490

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 1490

Leu Val Leu Asp Glu Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp
 1 5 10 15

Asp Glu Gly Gly Val Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val
 20 25 30

Val Gly Ala Gly Arg Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr
 35 40 45

Gly Gly Ala Glu Ala Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly
 50 55 60

Val Glu Val Glu Asp Gly Gly His Glu Val Phe Ala Arg Gly Val Phe

65		70		75		80									
Leu	Glu	Ala	Ala	His	Glu	Val	Arg	Asn	Gly	His	Val	Glu	Phe	Leu	Trp
				85					90					95	
Ala	His	Gly	Trp	Tyr	Val	Lys	Gln	Gln	Leu	Thr	Asp	Val	Asn	Ala	Asp
		100						105					110		
Gly	Ala	Arg	Leu	Ile	Gly	Arg	His	Ala	Leu	Gln	His	Phe	Glu	Leu	His
		115					120					125			
Thr	Val	Arg	Tyr	Pro	Thr	Leu	His	Arg	Glu	Gln	Met	Cys	Glu	Cys	Tyr
	130					135					140				
Val	Glu	Lys	Val	Val	Ala	Gly	Asn	Ala	Gln	Ala	Gln	Ala	Leu	His	Val
145					150				155						160
Phe	Phe	Ala	His	Arg	Pro	Ile	Glu	Asp	Ala	Leu	Val	Ile	Gly	Ile	Gly
			165						170					175	
Gly	Leu	Phe	Gly	Arg	Phe	Cys	Gly	Asn	Trp	Pro	Ala	Gly	Asp	Leu	Arg
		180						185					190		
Val	Asp	Val	Leu	His	Arg	Gln	Ile	Ser	Thr	Leu	Asp	Gln	Ala	Asn	Leu
	195						200					205			
Asn	Ala	Arg	Pro	Ala	Cys	Val	Asp	Ala	Leu	Ala	Ala	Glu	Leu	Arg	Gln
	210					215					220				
Val	Leu	Asp	Cys	Thr	Glu	Gly	Ile	Gly	Lys	Val	Arg	Leu	Gln	His	Asn
225					230				235						240

Ser Gly Phe

<210> 1491
 <211> 852
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(829)
 <223> FRXA02285

<400> 1491
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 cgggctctgc tgcggtggcg acggcttttg tggccactg ttg gtt ttg gat gag 115
 Leu Val Leu Asp Glu
 1 5
 cgc tgg gtt ggt gtc ggg ctc gtt gat aaa tgg gac gag ggg ggc gtc 163
 Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp Asp Glu Gly Gly Val
 10 15 20
 gag aag cgt ctc ttt gct gcg gtc ttg tgt gtg gtt ggg gcc ggg cgc 211
 Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val Val Gly Ala Gly Arg
 25 30 35

ggg cac gtc gat gag cgt ggc gag gtc aga tat gga ggc gcg gaa gcg 259
 Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr Gly Gly Ala Glu Ala
 40 45 50

gct ctc ctc tcg ctt gaa gga cgg gtt gtc ggc gtc gag gtc gaa gat 307
 Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly Val Glu Val Glu Asp
 55 60 65

ggc gga cat gaa gtt ttc gct cgc ggc gtt ttc ctc gag gcg gcg cac 355
 Gly Gly His Glu Val Phe Ala Arg Gly Val Phe Leu Glu Ala Ala His
 70 75 80 85

gag gta aga aat ggc cac gtc gaa ttc ttg tgg gcg cac ggc tgg tac 403
 Glu Val Arg Asn Gly His Val Glu Phe Leu Trp Ala His Gly Trp Tyr
 90 95 100

gta aag cag cag ctc acc gac gtc aac gct gac ggc gcg cgc ctg atc 451
 Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp Gly Ala Arg Leu Ile
 105 110 115

gga cgc cat gcc ctg cag cat ttc gaa ctc cac acg gtc cgc tac ccc 499
 Gly Arg His Ala Leu Gln His Phe Glu Leu His Thr Val Arg Tyr Pro
 120 125 130

acg ctc cac aga gag caa atg tgc gaa tgc tat gtc gaa aag gtt gtg 547
 Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr Val Glu Lys Val Val
 135 140 145

gcc ggc aac gcc cag gcg cag gcc ctc cat gtt ttc ttt gcg cat cgt 595
 Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val Phe Phe Ala His Arg
 150 155 160 165

cca ata gag gac gcg ctt gta att ggc atc ggt ggc ttg ttt gga agg 643
 Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly Gly Leu Phe Gly Arg
 170 175 180

ttc tgt ggc aac tgg cca gcc ggt gat ctg cgc gtg gac gtg ctc cat 691
 Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg Val Asp Val Leu His
 185 190 195

agg caa att agc acc ctt gac cag gcg aac ctt aac gcc cgc ccc gcc 739
 Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu Asn Ala Arg Pro Ala
 200 205 210

tgt gtt gac gcg ctc gcg gcc gaa ctg cgc caa gtc ctg gat tgc acc 787
 Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln Val Leu Asp Cys Thr
 215 220 225

gag ggc atc ggg aag gta cgc ctg caa cac aat tcc ggc ttc 829
 Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn Ser Gly Phe
 230 235 240

tagttcatgc agctctggat tgg 852

<210> 1492

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 1492

Leu Val Leu Asp Glu Arg Trp Val Gly Val Gly Leu Val Asp Lys Trp
1 5 10 15
Asp Glu Gly Gly Val Glu Lys Arg Leu Phe Ala Ala Val Leu Cys Val
20 25 30
Val Gly Ala Gly Arg Gly His Val Asp Glu Arg Gly Glu Val Arg Tyr
35 40 45
Gly Gly Ala Glu Ala Ala Leu Leu Ser Leu Glu Gly Arg Val Val Gly
50 55 60
Val Glu Val Glu Asp Gly Gly His Glu Val Phe Ala Arg Gly Val Phe
65 70 75 80
Leu Glu Ala Ala His Glu Val Arg Asn Gly His Val Glu Phe Leu Trp
85 90 95
Ala His Gly Trp Tyr Val Lys Gln Gln Leu Thr Asp Val Asn Ala Asp
100 105 110
Gly Ala Arg Leu Ile Gly Arg His Ala Leu Gln His Phe Glu Leu His
115 120 125
Thr Val Arg Tyr Pro Thr Leu His Arg Glu Gln Met Cys Glu Cys Tyr
130 135 140
Val Glu Lys Val Val Ala Gly Asn Ala Gln Ala Gln Ala Leu His Val
145 150 155 160
Phe Phe Ala His Arg Pro Ile Glu Asp Ala Leu Val Ile Gly Ile Gly
165 170 175
Gly Leu Phe Gly Arg Phe Cys Gly Asn Trp Pro Ala Gly Asp Leu Arg
180 185 190
Val Asp Val Leu His Arg Gln Ile Ser Thr Leu Asp Gln Ala Asn Leu
195 200 205
Asn Ala Arg Pro Ala Cys Val Asp Ala Leu Ala Ala Glu Leu Arg Gln
210 215 220
Val Leu Asp Cys Thr Glu Gly Ile Gly Lys Val Arg Leu Gln His Asn
225 230 235 240
Ser Gly Phe

<210> 1493

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXN03138

<400> 1493

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Val His Ser Ile Asp Gly Gly Ser Asp Phe Gly Gly Ser Val Trp Gly
35 40 45

70	75	80	85	
gtc ttc gga tgg gag ggt gta ctg gac tgc ctt ttg aac gcc agg gat				403
Val Phe Gly Trp Glu Gly Val Leu Asp Cys Leu Leu Asn Ala Arg Asp				
	90	95	100	
gcg tcg caa agc atc gga gtg gcc ctg tgacaaacct gggccccaga				450
Ala Ser Gln Ser Ile Gly Val Ala Leu				
	105	110		
agg				453

<210> 1498

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 1498

Val Val Glu Ala Thr Gly Val Ala Gly Gly Asn His Val Ala Thr Val
1 5 10 15

Trp His Ala Gly Val Leu Gly Val Glu Gly Cys Phe Val Asp Glu Val
20 25 30

Asp Phe Asp Phe Val Ala Asn Glu Val Ile Arg His Gly Ala Asp Val
35 40 45

Val Phe Asp Ala Leu Val Ile Gly Arg Val Gly Asn His Glu Ala Leu
50 55 60

Ala Leu Val Gly Leu Leu Ser Gly Lys Val Ala Gly Phe Ala Ala Ala
65 70 75 80

Gly Leu Phe Gln Gly Val Phe Gly Trp Glu Gly Val Leu Asp Cys Leu
85 90 95

Leu Asn Ala Arg Asp Ala Ser Gln Ser Ile Gly Val Ala Leu
100 105 110

<210> 1499

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXN03146

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acgatacgcc catccacggc gcatgtctga aaggttcccc atg aat ccc cgc atc	115
Met Asn Pro Arg Ile	
1 5	

ctc atg ctg ctt cgc atc att ttc ggc gcg gcc ttc ctc gca ctg ttg	163
Leu Met Leu Leu Arg Ile Ile Phe Gly Ala Ala Phe Leu Ala Leu Leu	
10 15 20	

gtg ctg caa gtc ctg ctc gcc atc aaa atc gtg cgc gat ggc ctc aac 211
Val Leu Gln Val Leu Leu Ala Ile Lys Ile Val Arg Asp Gly Leu Asn
25 30 35

tcc ggc gag ctc tcc ccc atc ccg ctc acc att ctc gcg agc ttc gtg 259
Ser Gly Glu Leu Ser Pro Ile Pro Leu Thr Ile Leu Ala Ser Phe Val
40 45 50

atc atc ggt ttc ggg ctc gtg cag ttc atc atc gtc tgt ctg ttc gcg 307
Ile Ile Gly Phe Gly Leu Val Gln Phe Ile Ile Val Cys Leu Phe Ala
55 60 65

cta ctg cgt ctc gtg gaa gac gat gaa atc ttc gac gcc cac tcg ctc 355
Leu Leu Arg Leu Val Glu Asp Asp Glu Ile Phe Asp Ala His Ser Leu
70 75 80 85

gcc tgg gtt gat cga att gcc atc acc atc gca gcc ggc gcc gtt tta 403
Ala Trp Val Asp Arg Ile Ala Ile Thr Ile Ala Ala Gly Ala Val Leu
90 95 100

ctc ctc cca atg gcc tac atc gtc gca gaa gtc gac gac gcc ccc gga 451
Leu Leu Pro Met Ala Tyr Ile Val Ala Glu Val Asp Asp Ala Pro Gly
105 110 115

gcc atc gtc ttc ggt ctc atc ctc gcg atg ctc atc acg ggc gta tcc 499
Ala Ile Val Phe Gly Leu Ile Leu Ala Met Leu Ile Thr Gly Val Ser
120 125 130

ctg ctg gta aaa atc atg cgc gca ctc ctg gcc cgc gcc atc gga ttc 547
Leu Leu Val Lys Ile Met Arg Ala Leu Leu Ala Arg Ala Ile Gly Phe
135 140 145

tcc acg gaa ctg gaa tcg gtg atc taaatggcca tcacgtcga cat 594
Ser Thr Glu Leu Glu Ser Val Ile
150 155

<210> 1500

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1500

Met Asn Pro Arg Ile Leu Met Leu Leu Arg Ile Ile Phe Gly Ala Ala
1 5 10 15

Phe Leu Ala Leu Leu Val Leu Gln Val Leu Leu Ala Ile Lys Ile Val
20 25 30

Arg Asp Gly Leu Asn Ser Gly Glu Leu Ser Pro Ile Pro Leu Thr Ile
35 40 45

Leu Ala Ser Phe Val Ile Ile Gly Phe Gly Leu Val Gln Phe Ile Ile
50 55 60

Val Cys Leu Phe Ala Leu Leu Arg Leu Val Glu Asp Asp Glu Ile Phe
65 70 75 80

Asp Ala His Ser Leu Ala Trp Val Asp Arg Ile Ala Ile Thr Ile Ala
85 90 95

Ala Gly Ala Val Leu Leu Leu Pro Met Ala Tyr Ile Val Ala Glu Val
 100 105 110
 Asp Asp Ala Pro Gly Ala Ile Val Phe Gly Leu Ile Leu Ala Met Leu
 115 120 125
 Ile Thr Gly Val Ser Leu Leu Val Lys Ile Met Arg Ala Leu Leu Ala
 130 135 140
 Arg Ala Ile Gly Phe Ser Thr Glu Leu Glu Ser Val Ile
 145 150 155

<210> 1501

<211> 375

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(352)

<223> RXN03147

<400> 1501

ccctgatccc gaggacgatg accgccaaag cgatggcgcc tccaatcagg atgtactgca 60

gtgggattgg gcgggcgctca tcgatggcat cgatgcagtt ttg gaa atc ctc ttt 115
 Leu Glu Ile Leu Phe
 1 5

aag agc ggt ttg gga ttc gtt gta atc atc ggt gcg gtc ggc gaa tac 163
 Lys Ser Gly Leu Gly Phe Val Val Ile Ile Gly Ala Val Gly Glu Tyr
 10 15 20

ttc ggc gcg gat ttc tgc ggt gcg ggt gcc ggt ggt ggc ggc ttg ttg 211
 Phe Gly Ala Asp Phe Cys Gly Ala Gly Ala Gly Gly Gly Gly Leu Leu
 25 30 35

aag ttg gct gag tac atc gct ggc tgg atc gct gga gaa tcc gct gat 259
 Lys Leu Ala Glu Tyr Ile Ala Gly Trp Ile Ala Gly Glu Ser Ala Asp
 40 45 50

gat gtc ttt ggc ttc gtc gta tgt gta ctc cgt ttt gaa act ttc ctc 307
 Asp Val Phe Gly Phe Val Val Cys Val Leu Arg Phe Glu Thr Phe Leu
 55 60 65

ggc gtt ggg gtc tgc cag cgt ggg atc gtc tgg gag gag cat ggc 352
 Gly Val Gly Val Cys Gln Arg Gly Ile Val Trp Glu Glu His Gly
 70 75 80

taggccttcg ccggattcga tgg 375

<210> 1502

<211> 84

<212> PRT

<213> Corynebacterium glutamicum

<400> 1502

Leu Glu Ile Leu Phe Lys Ser Gly Leu Gly Phe Val Val Ile Ile Gly

<210> 1504

<211> 89

<212> PRT

<213> Corynebacterium glutamicum

<400> 1504

Val Val Ile Gly Glu Leu Leu Pro Lys Ser Tyr Ser Ile Val Asn Thr
 1 5 10 15

Glu Lys Val Val Leu Phe Val Val Lys Pro Leu His Tyr Phe Tyr Lys
 20 25 30

Val Met Phe Pro Phe Ile Trp Val Leu Asn His Ser Ala Ala Gly Leu
 35 40 45

Gly Lys Leu Leu Gly Val Arg Leu Val Ser Glu Gly Glu Glu Thr Leu
 50 55 60

Ser Gln Glu Glu Leu Thr Leu Val Ala Leu Asn Ser Tyr Glu Lys Gly
 65 70 75 80

Glu Leu Pro Lys Lys Asn Ile Ile Ile
 85

<210> 1505

<211> 396

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(373)

<223> RXN03152

<400> 1505

gc aaaat atc agctttgacc tgcacatata gttgcacaat ggtgaaagtg cacataaagt 60

aa ctttcgta tt cgaatatt taaacctaag gggtttagca atg aag cta ttt tct 115
 Met Lys Leu Phe Ser
 1 5

cgt act ccc ctc gtc gca ctc ggc aca gct gct gca atg gca gca acc 163
 Arg Thr Pro Leu Val Ala Leu Gly Thr Ala Ala Ala Met Ala Ala Thr
 10 15 20

tcc atc tcc gtt cct gca cag gct gaa gaa gtc gca cca gca cag gtt 211
 Ser Ile Ser Val Pro Ala Gln Ala Glu Glu Val Ala Pro Ala Gln Val
 25 30 35

gtg tac gtg gct gac acc gta gaa gaa gaa acg ggt agc tcc aac gga 259
 Val Tyr Val Ala Asp Thr Val Glu Glu Glu Thr Gly Ser Ser Asn Gly
 40 45 50

tct tct gac att gac tct gac acc att ttg gat tac gtc gtc gtt att 307
 Ser Ser Asp Ile Asp Ser Asp Thr Ile Leu Asp Tyr Val Val Val Ile
 55 60 65

act ggc atc gtt ggc gtc ctc agc gct ggt ttg acc ttc gct act gct 355
 Thr Gly Ile Val Gly Val Leu Ser Ala Gly Leu Thr Phe Ala Thr Ala
 70 75 80 85

ttc cag cgt tca ttg cag taaatttcag cggttaatcac caa
 Phe Gln Arg Ser Leu Gln
 90

396

<210> 1506
 <211> 91
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1506
 Met Lys Leu Phe Ser Arg Thr Pro Leu Val Ala Leu Gly Thr Ala Ala
 1 5 10 15
 Ala Met Ala Ala Thr Ser Ile Ser Val Pro Ala Gln Ala Glu Glu Val
 20 25 30
 Ala Pro Ala Gln Val Val Tyr Val Ala Asp Thr Val Glu Glu Glu Thr
 35 40 45
 Gly Ser Ser Asn Gly Ser Ser Asp Ile Asp Ser Asp Thr Ile Leu Asp
 50 55 60
 Tyr Val Val Val Ile Thr Gly Ile Val Gly Val Leu Ser Ala Gly Leu
 65 70 75 80
 Thr Phe Ala Thr Ala Phe Gln Arg Ser Leu Gln
 85 90

<210> 1507
 <211> 687
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(664)
 <223> RXN03153

<400> 1507
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 ttcacggccc tcgttacgac tacaaagatc ggggtatttt atg cga cga atc tgg 115
 Met Arg Arg Ile Trp
 1 5
 ctg ctc gta tgc ggc atc gca ttg act gtc gcc ggc tgc acg agt gga 163
 Leu Leu Val Cys Gly Ile Ala Leu Thr Val Ala Gly Cys Thr Ser Gly
 10 15 20
 tcc acc act ccc aca acc gtc acg gta acc gca acg cca acg tcg gag 211
 Ser Thr Thr Pro Thr Thr Val Thr Val Thr Ala Thr Pro Thr Ser Glu
 25 30 35
 gag gct gca tcc acg gag ccg acc aac gac ata ctt gcc agc caa ttt 259
 Glu Ala Ala Ser Thr Glu Pro Thr Asn Asp Ile Leu Ala Ser Gln Phe
 40 45 50
 cat ccg tgt gaa gta ctc acg cag gaa cag ttc gaa gaa gtc gga ttg 307
 His Pro Cys Glu Val Leu Thr Gln Glu Gln Phe Glu Glu Val Gly Leu

55	60	65	
gga gtc ttg att gtt gaa gac gct tac ctc ggc tcg aca ggt tta ggt			355
Gly Val Leu Ile Val Glu Asp Ala Tyr Leu Gly Ser Thr Gly Leu Gly			
70	75	80	85
tgc agt ttc ggg aaa gca gac aga gag gat ttt tca ggt acg tgg ctc			403
Cys Ser Phe Gly Lys Ala Asp Arg Glu Asp Phe Ser Gly Thr Trp Leu			
	90	95	100
att tca act gac caa gca aac cga caa ttt gtt gaa aac caa gat cta			451
Ile Ser Thr Asp Gln Ala Asn Arg Gln Phe Val Glu Asn Gln Asp Leu			
	105	110	115
gag aca ttg gat tgg gga tcc aat gac aat cca gat ctg tat gtg cat			499
Glu Thr Leu Asp Trp Gly Ser Asn Asp Asn Pro Asp Leu Tyr Val His			
	120	125	130
caa atg tcc gag acg ggt cgt caa tgt gag gca gca gtt gac tat gac			547
Gln Met Ser Glu Thr Gly Arg Gln Cys Glu Ala Ala Val Asp Tyr Asp			
	135	140	145
tgg ggc cgg ctt acg gtt gac tat ctc gaa tta ggt gag ggc tgg gag			595
Trp Gly Arg Leu Thr Val Asp Tyr Leu Glu Leu Gly Glu Gly Trp Glu			
	150	155	160
cca gaa att ttg tgc tct gat gct gtt gaa att tta gaa aat ctc atc			643
Pro Glu Ile Leu Cys Ser Asp Ala Val Glu Ile Leu Glu Asn Leu Ile			
	170	175	180
aag gaa cta agg gga att cca tgacattgaa aattgatccc tcg			687
Lys Glu Leu Arg Gly Ile Pro			
	185		

<210> 1508

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 1508

Met Arg Arg Ile Trp Leu Leu Val Cys Gly Ile Ala Leu Thr Val Ala
1 5 10 15

Gly Cys Thr Ser Gly Ser Thr Thr Pro Thr Thr Val Thr Val Thr Ala
20 25 30

Thr Pro Thr Ser Glu Glu Ala Ala Ser Thr Glu Pro Thr Asn Asp Ile
35 40 45

Leu Ala Ser Gln Phe His Pro Cys Glu Val Leu Thr Gln Glu Gln Phe
50 55 60

Glu Glu Val Gly Leu Gly Val Leu Ile Val Glu Asp Ala Tyr Leu Gly
65 70 75 80

Ser Thr Gly Leu Gly Cys Ser Phe Gly Lys Ala Asp Arg Glu Asp Phe
85 90 95

Ser Gly Thr Trp Leu Ile Ser Thr Asp Gln Ala Asn Arg Gln Phe Val
100 105 110

Glu Asn Gln Asp Leu Glu Thr Leu Asp Trp Gly Ser Asn Asp Asn Pro
 115 120 125
 Asp Leu Tyr Val His Gln Met Ser Glu Thr Gly Arg Gln Cys Glu Ala
 130 135 140
 Ala Val Asp Tyr Asp Trp Gly Arg Leu Thr Val Asp Tyr Leu Glu Leu
 145 150 155 160
 Gly Glu Gly Trp Glu Pro Glu Ile Leu Cys Ser Asp Ala Val Glu Ile
 165 170 175
 Leu Glu Asn Leu Ile Lys Glu Leu Arg Gly Ile Pro
 180 185

<210> 1509

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1012)

<223> RXN03154

<400> 1509

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cattctgaaa attcagtcgc ttaaatgggc gcagcgggaa atg ctg aaa act aca 115
 Met Leu Lys Thr Thr
 1 5

tta atc acc gat acc cta ggg cac gtg acc tct act gaa ccc acc acc 163
 Leu Ile Thr Asp Thr Leu Gly His Val Thr Ser Thr Glu Pro Thr Thr
 10 15 20

aca gcc cat gtt cca cta cct gat gga tct tcc act cca gtc caa att 211
 Thr Ala His Val Pro Leu Pro Asp Gly Ser Ser Thr Pro Val Gln Ile
 25 30 35

tgg gcg tca gat aac aaa gac tcc caa ctg gtg atg ctg tgg cca ggt 259
 Trp Ala Ser Asp Asn Lys Asp Ser Gln Leu Val Met Leu Trp Pro Gly
 40 45 50

ttc ggc atg ggt ggc tat tac tat cgt ccg ctt gcg gca gcg cta aat 307
 Phe Gly Met Gly Gly Tyr Tyr Tyr Arg Pro Leu Ala Ala Ala Leu Asn
 55 60 65

aaa gct gga ttc cat gtg gcg att ggt gaa ctt cgt ggt cag ggg caa 355
 Lys Ala Gly Phe His Val Ala Ile Gly Glu Leu Arg Gly Gln Gly Gln
 70 75 80 85

agt tcc gcg aag gct tct cgg aaa agt cag tgg gga tac cat gat ctc 403
 Ser Ser Ala Lys Ala Ser Arg Lys Ser Gln Trp Gly Tyr His Asp Leu
 90 95 100

gca tcg gta gat ttt ccg ctg cag att gcc gct gcg aaa aag gcg ctt 451
 Ala Ser Val Asp Phe Pro Leu Gln Ile Ala Ala Ala Lys Lys Ala Leu
 105 110 115

gac ctg gag gaa ggc cat ccc atg agg ttt ttg tcg cat tcg atg ggt 499
 Asp Leu Glu Glu Gly His Pro Met Arg Phe Leu Ser His Ser Met Gly
 120 125 130

ggg cag att tct tgt ctt ttc gca gcg agg ccg gag gct gag aaa tat 547
 Gly Gln Ile Ser Cys Leu Phe Ala Ala Arg Pro Glu Ala Glu Lys Tyr
 135 140 145

aat ctt cgg gcg att ttc ggg gtg ggt gca ggg tcg ccg ttt agg cct 595
 Asn Leu Arg Ala Ile Phe Gly Val Gly Ala Gly Ser Pro Phe Arg Pro
 150 155 160 165

acg ttt agt ccg aaa atg ggg aag cgt ttg gga ttg ggt gcg gtg ctg 643
 Thr Phe Ser Pro Lys Met Gly Lys Arg Leu Gly Leu Gly Ala Val Leu
 170 175 180

ctt ggt ggg att ggt ggc cac att gtg gga ttt tgg ccc ggc aaa gtt 691
 Leu Gly Gly Ile Gly Gly His Ile Val Gly Phe Trp Pro Gly Lys Val
 185 190 195

tta gga aaa gac ctg gtg ggt tat ggc cga caa tcg gga act cac atg 739
 Leu Gly Lys Asp Leu Val Gly Tyr Gly Arg Gln Ser Gly Thr His Met
 200 205 210

agg gaa tgg cgt cga ttc cat aag cac aat tct ttg gac gat ctc acc 787
 Arg Glu Trp Arg Arg Phe His Lys His Asn Ser Leu Asp Asp Leu Thr
 215 220 225

gcg cag gac atc aac tat gtg gag gtg atg aag aag gtg agc att cct 835
 Ala Gln Asp Ile Asn Tyr Val Glu Val Met Lys Lys Val Ser Ile Pro
 230 235 240 245

att act ttt agt cgt tgt cct gat gat gag gac tgc ccg cag gca tcg 883
 Ile Thr Phe Ser Arg Cys Pro Asp Asp Glu Asp Cys Pro Gln Ala Ser
 250 255 260

att gat ggg ttg gcg agt ttt gtt ccc gca gcg cag atc aaa atg ata 931
 Ile Asp Gly Leu Ala Ser Phe Val Pro Ala Ala Gln Ile Lys Met Ile
 265 270 275

gaa att cca gaa gcc ctg gga cat aac cgg tgg gct cgg gaa cct gaa 979
 Glu Ile Pro Glu Ala Leu Gly His Asn Arg Trp Ala Arg Glu Pro Glu
 280 285 290

tca aca gtg aaa ctc ttc ctg gaa caa gct ctt tagtgaccga tggagcggag 1032
 Ser Thr Val Lys Leu Phe Leu Glu Gln Ala Leu
 295 300

gta 1035

<210> 1510

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 1510

Met Leu Lys Thr Thr Leu Ile Thr Asp Thr Leu Gly His Val Thr Ser
 1 5 10 15

Thr Glu Pro Thr Thr Thr Ala His Val Pro Leu Pro Asp Gly Ser Ser
 20 25 30
 Thr Pro Val Gln Ile Trp Ala Ser Asp Asn Lys Asp Ser Gln Leu Val
 35 40 45
 Met Leu Trp Pro Gly Phe Gly Met Gly Gly Tyr Tyr Tyr Arg Pro Leu
 50 55 60
 Ala Ala Ala Leu Asn Lys Ala Gly Phe His Val Ala Ile Gly Glu Leu
 65 70 75 80
 Arg Gly Gln Gly Gln Ser Ser Ala Lys Ala Ser Arg Lys Ser Gln Trp
 85 90 95
 Gly Tyr His Asp Leu Ala Ser Val Asp Phe Pro Leu Gln Ile Ala Ala
 100 105 110
 Ala Lys Lys Ala Leu Asp Leu Glu Glu Gly His Pro Met Arg Phe Leu
 115 120 125
 Ser His Ser Met Gly Gly Gln Ile Ser Cys Leu Phe Ala Ala Arg Pro
 130 135 140
 Glu Ala Glu Lys Tyr Asn Leu Arg Ala Ile Phe Gly Val Gly Ala Gly
 145 150 155 160
 Ser Pro Phe Arg Pro Thr Phe Ser Pro Lys Met Gly Lys Arg Leu Gly
 165 170 175
 Leu Gly Ala Val Leu Leu Gly Gly Ile Gly Gly His Ile Val Gly Phe
 180 185 190
 Trp Pro Gly Lys Val Leu Gly Lys Asp Leu Val Gly Tyr Gly Arg Gln
 195 200 205
 Ser Gly Thr His Met Arg Glu Trp Arg Arg Phe His Lys His Asn Ser
 210 215 220
 Leu Asp Asp Leu Thr Ala Gln Asp Ile Asn Tyr Val Glu Val Met Lys
 225 230 235 240
 Lys Val Ser Ile Pro Ile Thr Phe Ser Arg Cys Pro Asp Asp Glu Asp
 245 250 255
 Cys Pro Gln Ala Ser Ile Asp Gly Leu Ala Ser Phe Val Pro Ala Ala
 260 265 270
 Gln Ile Lys Met Ile Glu Ile Pro Glu Ala Leu Gly His Asn Arg Trp
 275 280 285
 Ala Arg Glu Pro Glu Ser Thr Val Lys Leu Phe Leu Glu Gln Ala Leu
 290 295 300

<210> 1511

<211> 303

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(280)
 <223> RXN03156

<400> 1511

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aagaaggata accaccacac cagaaaagaa gtacctcatt atg gct cga acc aca 115
                                     Met Ala Arg Thr Thr
                                     1 5
cct cca cca gct gat gta ctc gac atc atc att tcc acc gtg aag cag 163
Pro Pro Pro Ala Asp Val Leu Asp Ile Ile Ile Ser Thr Val Lys Gln
                10                15                20
acc atc ggc att gat ctt gct gaa ctg att cag ggc cgt gca ctc ggc 211
Thr Ile Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly
                25                30                35
cag gct caa ggt gag gca caa ggc aaa gct agt gca gca gcc ctt gag 259
Gln Ala Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu
                40                45                50
cag gca cct cat aat gag cag taaataacac acaccacatg tgc 303
Gln Ala Pro His Asn Glu Gln
                55                60
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<210> 1512
 <211> 60
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1512

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Met Ala Arg Thr Thr Pro Pro Pro Ala Asp Val Leu Asp Ile Ile Ile
 1 5 10 15
Ser Thr Val Lys Gln Thr Ile Gly Ile Asp Leu Ala Glu Leu Ile Gln
 20 25 30
Gly Arg Ala Leu Gly Gln Ala Gln Gly Glu Ala Gln Gly Lys Ala Ser
 35 40 45
Ala Ala Ala Leu Glu Gln Ala Pro His Asn Glu Gln
 50 55 60
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<210> 1513
 <211> 182
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(159)
 <223> FRXA00176

<400> 1513

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cag ctg atg tac tcg aca tca tca ttt acc acc gtg aag cag acc atc 48
Gln Leu Met Tyr Ser Thr Ser Ser Phe Thr Thr Val Lys Gln Thr Ile
 1 5 10 15
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ggc att gat ctt gct gaa ctg att cag ggc cgt gca ctc ggc cag gct 96
Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly Gln Ala
20 25 30

caa ggt gag gca caa ggc aaa gct agt gca gca gcc ctt gag cag gca 144
Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu Gln Ala
35 40 45

cct cat aat gag cag taaataacac acaccacatg tgc 182
Pro His Asn Glu Gln
50

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<210> 1514
<211> 53
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1514
Gln Leu Met Tyr Ser Thr Ser Ser Phe Thr Thr Val Lys Gln Thr Ile
1 5 10 15

Gly Ile Asp Leu Ala Glu Leu Ile Gln Gly Arg Ala Leu Gly Gln Ala
20 25 30

Gln Gly Glu Ala Gln Gly Lys Ala Ser Ala Ala Ala Leu Glu Gln Ala
35 40 45

Pro His Asn Glu Gln
50

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<210> 1515
<211> 519
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(496)
<223> RXN03162
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<400> 1515
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gggttgcgga gaagttgtcg cgccttctg ctggcttctt gtg cac gac gaa cac 115
Val His Asp Glu His
1 5

tgg	gtg	tgg	tcc	gac	gag	aag	gat	gcg	gat	ttc	gcc	ttc	gac	gat	gcg	163
Trp	Val	Trp	Ser	Asp	Glu	Lys	Asp	Ala	Asp	Phe	Ala	Phe	Asp	Asp	Ala	
				10					15					20		

tgg cat gaa acg cat atc aac gag cat gcc gtt gtc gcc gat gat gta 211
Trp His Glu Thr His Ile Asn Glu His Ala Val Val Ala Asp Asp Val

25 30 35

ctg gtc aca gaa atc cat gaa ctc gcc gag ctt gcg gac ttc agt gtg 259
Leu Val Thr Glu Ile His Glu Leu Ala Glu Leu Ala Asp Phe Ser Val
40 45 50

gtt gtc gac tgc ttc ggt gca ctt gat ttc agt gtc caa tgg cag tgc 307
 Val Val Asp Cys Phe Gly Ala Leu Asp Phe Ser Val Gln Trp Gln Cys
 55 60 65

ggt gcc tgg ctc gat gga tgc agc cag ttc ctt gtc tac caa ctg gac 355
 Gly Ala Trp Leu Asp Gly Cys Ser Gln Phe Leu Val Tyr Gln Leu Asp
 70 75 80 85

gcg cca aat gcc gga gcc ggt gga gcc acg gtt ttg ctt gag cac gcg 403
 Ala Pro Asn Ala Gly Ala Gly Gly Ala Thr Val Leu Leu Glu His Ala
 90 95 100

ctc acc gaa gga cag gga ggt tgg gaa aac ctt gtg gaa ggt ctc cac 451
 Leu Thr Glu Gly Gln Gly Gly Trp Glu Asn Leu Val Glu Gly Leu His
 105 110 115

gtc gta gta cgc ctc ggt gtc gga tgg cac cag gtc ggt ttg gga 496
 Val Val Val Arg Leu Gly Val Gly Trp His Gln Val Gly Leu Gly
 120 125 130

tagcttgacc agcgcatctt tcg 519

<210> 1516

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 1516

Val His Asp Glu His Trp Val Trp Ser Asp Glu Lys Asp Ala Asp Phe
 1 5 10 15

Ala Phe Asp Asp Ala Trp His Glu Thr His Ile Asn Glu His Ala Val
 20 25 30

Val Ala Asp Asp Val Leu Val Thr Glu Ile His Glu Leu Ala Glu Leu
 35 40 45

Ala Asp Phe Ser Val Val Val Asp Cys Phe Gly Ala Leu Asp Phe Ser
 50 55 60

Val Gln Trp Gln Cys Gly Ala Trp Leu Asp Gly Cys Ser Gln Phe Leu
 65 70 75 80

Val Tyr Gln Leu Asp Ala Pro Asn Ala Gly Ala Gly Gly Ala Thr Val
 85 90 95

Leu Leu Glu His Ala Leu Thr Glu Gly Gln Gly Gly Trp Glu Asn Leu
 100 105 110

Val Glu Gly Leu His Val Val Val Arg Leu Gly Val Gly Trp His Gln
 115 120 125

Val Gly Leu Gly
 130

<210> 1517

<211> 730

<212> DNA

ttt gcc ggc atc gct ggt gga att gtc tcc ggt att ttc ggc ttt gga 691
Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly Ile Phe Gly Phe Gly
185 190 195

tct gaa ttc ctc acc agt gtc atc atg att ttg gtg ctg
 Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu Val Leu
 200 205 210

730

<210> 1518
 <211> 210
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1518
 Met Asn Thr Asn Leu Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg
 1 5 10 15
 Ser Glu Ser Ser Glu Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu
 20 25 30
 Arg Leu Glu Gln Met Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln
 35 40 45
 Thr Val Gln Ala Phe Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr
 50 55 60
 Tyr Asp Ala Gln Leu Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile
 65 70 75 80
 Gln His Leu Gly Asn Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln
 85 90 95
 Pro Phe Ala Ala Pro Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln
 100 105 110
 Trp Asn Ser Gly Gln Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr
 115 120 125
 Gln Thr Gln Gln Ser Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser
 130 135 140
 Met Tyr Ala Gln Pro Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser
 145 150 155 160
 Asn Gln Val Phe Asn Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala
 165 170 175
 Ile Leu Asp Ser Ile Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly
 180 185 190
 Ile Phe Gly Phe Gly Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu
 195 200 205
 Val Leu
 210

<210> 1519
 <211> 736
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> FRXA02862

<400> 1519

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gccgcgactg cgggtgcttt tgcgctgttg cgtaaaaaat agtttttatt aagggcattc 60
cctgattccc aggtggtgcc acattgttta tgggtggagat atg aac acg aac ttg 115
                                         Met Asn Thr Asn Leu
                                         1 5
ccg aac cta tac acc gca ttt gac ctt gat cga agt gaa tcc tcc gaa 163
Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg Ser Glu Ser Ser Glu
              10              15              20
gct tta ggt gtt tcc ctt tct gcc cgc gat ctt cgc tta gaa caa atg 211
Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu Arg Leu Glu Gln Met
              25              30              35
gga att gcc cag gac gat cct cga cgt gcc caa acc gtc caa gct ttc 259
Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln Thr Val Gln Ala Phe
              40              45              50
gca gtg ctt gca gac cca gca aaa cgc gcc acc tac gat gct caa tta 307
Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr Tyr Asp Ala Gln Leu
              55              60              65
gaa gct gga gtt cca ctc acc tgg gcg cag att cag cat tta gga aac 355
Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile Gln His Leu Gly Asn
              70              75              80              85
ttc ggc acc ttg cct tcc acc cct act gcg cag ccg ttt gcg gca cct 403
Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln Pro Phe Ala Ala Pro
              90              95              100
cag ccg gag ccg tcg ccg gaa ccg caa cag cag tgg aat agc gga caa 451
Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln Trp Asn Ser Gly Gln
              105              110              115
aac tat gcg tat ggc aat ccg acc atg gat tac caa act cag cag agc 499
Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr Gln Thr Gln Gln Ser
              120              125              130
tac aac ccg atg cag gac caa acc caa gcg tcg atg tat gcg caa cct 547
Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser Met Tyr Ala Gln Pro
              135              140              145
ttc gcg aac acc cct gca ccg atg tac aac agc aat cag gtt ttt aac 595
Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser Asn Gln Val Phe Asn
              150              155              160              165
agg cct act gcg ggt acg cgt ttg tgg atg gcg atc ctc gac agt att 643
Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala Ile Leu Asp Ser Ile
              170              175              180
ttt gcc ggc atc gct ggt gga att gtc tcc ggt att ttc ggc ttt gga 691
Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly Ile Phe Gly Phe Gly
              185              190              195
tct gaa ttc ctc acc agt gtc atc atg att ttg gtg ctg atc gtc 736
Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu Val Leu Ile Val

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200

205

210

<210> 1520

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 1520

Met Asn Thr Asn Leu Pro Asn Leu Tyr Thr Ala Phe Asp Leu Asp Arg
1 5 10 15

Ser Glu Ser Ser Glu Ala Leu Gly Val Ser Leu Ser Ala Arg Asp Leu
20 25 30

Arg Leu Glu Gln Met Gly Ile Ala Gln Asp Asp Pro Arg Arg Ala Gln
35 40 45

Thr Val Gln Ala Phe Ala Val Leu Ala Asp Pro Ala Lys Arg Ala Thr
50 55 60

Tyr Asp Ala Gln Leu Glu Ala Gly Val Pro Leu Thr Trp Ala Gln Ile
65 70 75 80

Gln His Leu Gly Asn Phe Gly Thr Leu Pro Ser Thr Pro Thr Ala Gln
85 90 95

Pro Phe Ala Ala Pro Gln Pro Glu Pro Ser Pro Glu Pro Gln Gln Gln
100 105 110

Trp Asn Ser Gly Gln Asn Tyr Ala Tyr Gly Asn Pro Thr Met Asp Tyr
115 120 125

Gln Thr Gln Gln Ser Tyr Asn Pro Met Gln Asp Gln Thr Gln Ala Ser
130 135 140

Met Tyr Ala Gln Pro Phe Ala Asn Thr Pro Ala Pro Met Tyr Asn Ser
145 150 155 160

Asn Gln Val Phe Asn Arg Pro Thr Ala Gly Thr Arg Leu Trp Met Ala
165 170 175

Ile Leu Asp Ser Ile Phe Ala Gly Ile Ala Gly Gly Ile Val Ser Gly
180 185 190

Ile Phe Gly Phe Gly Ser Glu Phe Leu Thr Ser Val Ile Met Ile Leu
195 200 205

Val Leu Ile Val
210

<210> 1521

<211> 372

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(349)

<223> RXN03170

[illegible]

<213> Corynebacterium glutamicum

[illegible]

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(349)

<223> FRXA02856

<400> 1523

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aacggccact tttccagtcc aacaaagtat gaggattaat ttg ccc cac gcc aaa 115
                                   Leu Pro His Ala Lys
                                   1 5
gag ctc gcc cac gag ctg tgt ttg ttg ccc acc cct gct gtg ccc gcg 163
Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr Pro Ala Val Pro Ala
                                   10 15 20
ctt ccc act gat tct ggc gcg cag ttt gat atc cac cag gca cta tcc 211
Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile His Gln Ala Leu Ser
                                   25 30 35
gcc tcc ctt gcc acc tat gcc cgc aac ctc acc ttg ctg tcc cac acc 259
Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr Leu Leu Ser His Thr
                                   40 45 50
gcc gag aat tta gga aac cgc gcg ctg acg ggc ctc gct gaa atc gaa 307
Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly Leu Ala Glu Ile Glu
                                   55 60 65
gac acc gac gac caa ctc gca cac gca ttg gag cgc ctg aca 349
Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu Arg Leu Thr
                                   70 75 80
tgatcggtct gatcagcgcc ctt 372

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<210> 1524

<211> 83

<212> PRT

<213> Corynebacterium glutamicum

<400> 1524

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Leu Pro His Ala Lys Glu Leu Ala His Glu Leu Cys Leu Leu Pro Thr
 1 5 10 15
Pro Ala Val Pro Ala Leu Pro Thr Asp Ser Gly Ala Gln Phe Asp Ile
 20 25 30
His Gln Ala Leu Ser Ala Ser Leu Ala Thr Tyr Ala Arg Asn Leu Thr
 35 40 45
Leu Leu Ser His Thr Ala Glu Asn Leu Gly Asn Arg Ala Leu Thr Gly
 50 55 60
Leu Ala Glu Ile Glu Asp Thr Asp Asp Gln Leu Ala His Ala Leu Glu
 65 70 75 80
Arg Leu Thr

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<210> 1525

<211> 1049

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1026)

<223> RXN03172

<400> 1525

cca	gag	tgg	aag	aaa	ttc	aac	tcc	ggc	gac	gca	gcc	cgc	gtt	gtc	cca	48
Pro	Glu	Trp	Lys	Lys	Phe	Asn	Ser	Gly	Asp	Ala	Ala	Arg	Val	Val	Pro	
1				5				10					15			

gac	gcc	aac	gca	gag	ctc	gac	atc	atc	ggc	gca	cca	gca	ctt	ctt	gcc	96
Asp	Ala	Asn	Ala	Glu	Leu	Asp	Ile	Ile	Gly	Ala	Pro	Ala	Leu	Leu	Ala	
		20					25						30			

gat	cgc	ccc	tcc	tac	gca	aac	gtc	aaa	acc	ctc	tcc	cgc	atc	ttc	gct	144
Asp	Arg	Pro	Ser	Tyr	Ala	Asn	Val	Lys	Thr	Leu	Ser	Arg	Ile	Phe	Ala	
		35					40					45				

gtc	atg	cgc	agc	ctc	ggc	cac	gtc	acc	gct	gcc	tcc	cca	gtc	acc	gtg	192
Val	Met	Arg	Ser	Leu	Gly	His	Val	Thr	Ala	Ala	Ser	Pro	Val	Thr	Val	
	50					55					60					

ttc	ttc	tcc	tcc	cac	tcc	gtg	ctc	agc	aac	gtt	gac	cgc	gga	tcc	gag	240
Phe	Phe	Ser	Ser	His	Ser	Val	Leu	Ser	Asn	Val	Asp	Arg	Gly	Ser	Glu	
65					70					75					80	

cac	tac	tcc	gga	ccc	aac	ggc	ctg	ggc	gaa	tgg	acc	tcc	gtt	ggc	cgc	288
His	Tyr	Ser	Gly	Pro	Asn	Gly	Leu	Gly	Glu	Trp	Thr	Ser	Val	Gly	Arg	
			85						90					95		

gca	gta	gcc	acc	aac	tgg	aac	ggc	gtt	gtc	gac	gcc	ctc	gac	gaa	gcc	336
Ala	Val	Ala	Thr	Asn	Trp	Asn	Gly	Val	Val	Asp	Ala	Leu	Asp	Glu	Ala	
			100					105					110			

atc	acc	gtc	aag	gaa	gta	aac	agc	ctc	ttt	acc	gaa	gac	gcc	gca	acc	384
Ile	Thr	Val	Lys	Glu	Val	Asn	Ser	Leu	Phe	Thr	Glu	Asp	Ala	Ala	Thr	
		115					120					125				

cgc	att	caa	gaa	gca	caa	gca	gct	gtt	cag	gca	gct	cgc	gag	gct	gaa	432
Arg	Ile	Gln	Glu	Ala	Gln	Ala	Ala	Val	Gln	Ala	Ala	Arg	Glu	Ala	Glu	
	130					135					140					

gag	caa	atc	gcc	aag	gaa	gaa	gcc	gaa	aag	gtc	gac	cct	tac	gac	aac	480
Glu	Gln	Ile	Ala	Lys	Glu	Glu	Ala	Glu	Lys	Val	Asp	Pro	Tyr	Asp	Asn	
145					150				155						160	

tcc	cca	tgg	gct	gca	gca	ggc	atc	gac	ccc	atc	aag	gtc	tcc	atc	gac	528
Ser	Pro	Trp	Ala	Ala	Ala	Gly	Ile	Asp	Pro	Ile	Lys	Val	Ser	Ile	Asp	
			165						170					175		

gga	cgc	acc	atc	tac	acc	ctg	cgc	acc	tac	ctc	ggc	gga	cag	cca	gta	576
Gly	Arg	Thr	Ile	Tyr	Thr	Leu	Arg	Thr	Tyr	Leu	Gly	Gly	Gln	Pro	Val	
			180					185					190			

ttc	ctc	gga	aaa	ttc	ggc	gaa	atc	tcc	acc	ttc	aac	agc	caa	aaa	tcc	624
Phe	Leu	Gly	Lys	Phe	Gly	Glu	Ile	Ser	Thr	Phe	Asn	Ser	Gln	Lys	Ser	
		195					200					205				

ctc ctg cgc tgg ctc gtc gaa cac gat gac cac gac ctc gcc cgc gcc 672
 Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
 210 215 220
 tcc acc tgg agc gac ctc atg ctc ggc atc aac gcc ggt gaa acc gaa 720
 Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
 225 230 235 240
 ctc ctc gtc cac agc gac aac gtc tac tcc ttc aac ggc ctg gtc aaa 768
 Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
 245 250 255
 gaq atc aac acc tcc gtc gac gcc gta gac acc caa caa atg gcc cgc 816
 Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
 260 265 270
 gcc tac gaa ctc atg gca gac acc gcc gac tgg gcc gac gac gac tcc 864
 Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
 275 280 285
 atg aat tcc tac ttc ctg gcc aac cca cgc atg cag gac tac atc tcc 912
 Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
 290 295 300
 tac atg ctc ggc ggc agc gac acc tcc gga tat gtc cct cac gca cca 960
 Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
 305 310 315 320
 ttc aac gac cac tct gag agc tgg cgc gag ctg gag gag atg ctg atc 1008
 Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
 325 330 335
 aag cga ttc agc aag ttc taggtcgcct atttgggggtt cgt 1049
 Lys Arg Phe Ser Lys Phe
 340

<210> 1526

<211> 342

<212> PRT

<213> Corynebacterium glutamicum

<400> 1526

Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro
 1 5 10 15
 Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala
 20 25 30
 Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala
 35 40 45
 Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val
 50 55 60
 Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu
 65 70 75 80
 His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg
 85 90 95

Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala
100 105 110

Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr
115 120 125

Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu
130 135 140

Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
145 150 155 160

Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
165 170 175

Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
180 185 190

Phe Leu Gly Lys Phe Gly Glu Ile Ser Thr Phe Asn Ser Gln Lys Ser
195 200 205

Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
210 215 220

Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
225 230 235 240

Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
245 250 255

Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
260 265 270

Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Asp Ser
275 280 285

Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
290 295 300

Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
305 310 315 320

Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
325 330 335

Lys Arg Phe Ser Lys Phe
340

<210> 1527

<211> 1049

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1026)

<223> FRXA02858

<400> 1527

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Pro Glu Trp Lys Lys Phe Asn Ser Gly Asp Ala Ala Arg Val Val Pro	
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gac gcc aac gca gag ctc gac atc atc ggc gca cca gca ctt ctt gcc	96
Asp Ala Asn Ala Glu Leu Asp Ile Ile Gly Ala Pro Ala Leu Leu Ala	
20 25 30	
gat cgc ccc tcc tac gca aac gtc aaa acc ctc tcc cgc atc ttc gct	144
Asp Arg Pro Ser Tyr Ala Asn Val Lys Thr Leu Ser Arg Ile Phe Ala	
35 40 45	
gtc atg cgc agc ctc ggc cac gtc acc gct gcc tcc cca gtc acc gtg	192
Val Met Arg Ser Leu Gly His Val Thr Ala Ala Ser Pro Val Thr Val	
50 55 60	
ttc ttc tcc tcc cac tcc gtg ctc agc aac gtt gac cgc gga tcc gag	240
Phe Phe Ser Ser His Ser Val Leu Ser Asn Val Asp Arg Gly Ser Glu	
65 70 75 80	
cac tac tcc gga ccc aac ggc ctg ggc gaa tgg acc tcc gtt ggt cgc	288
His Tyr Ser Gly Pro Asn Gly Leu Gly Glu Trp Thr Ser Val Gly Arg	
85 90 95	
gca gta gcc acc aac tgg aac ggc gtt gtc gac gcc ctc gac gaa gcc	336
Ala Val Ala Thr Asn Trp Asn Gly Val Val Asp Ala Leu Asp Glu Ala	
100 105 110	
atc acc gtc aag gaa gta aac agc ctc ttt acc gaa gac gcc gca acc	384
Ile Thr Val Lys Glu Val Asn Ser Leu Phe Thr Glu Asp Ala Ala Thr	
115 120 125	
cgc att caa gaa gca caa gca gct gtt cag gca gct cgc gag gct gaa	432
Arg Ile Gln Glu Ala Gln Ala Ala Val Gln Ala Ala Arg Glu Ala Glu	
130 135 140	
gag caa atc gcc aag gaa gaa gcc gaa aag gtc gac cct tac gac aac	480
Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn	
145 150 155 160	
tcc cca tgg gct gca gca ggc atc gac ccc atc aag gtc tcc atc gac	528
Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp	
165 170 175	
gga cgc acc atc tac acc ctg cgc acc tac ctc ggc gga cag cca gta	576
Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val	
180 185 190	
ttc ctc gga aaa ttc ggc gaa atc ttc acc ttc aac agc caa aaa tcc	624
Phe Leu Gly Lys Phe Gly Glu Ile Phe Thr Phe Asn Ser Gln Lys Ser	
195 200 205	
ctc ctg cgc tgg ctc gtc gaa cac gat gac cac gac ctc gcc cgc gcc	672
Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala	
210 215 220	
tcc acc tgg agc gac ctc atg ctc ggc atc aac gcc ggt gaa acc gaa	720
Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu	
225 230 235 240	
ctc ctc gtc cac agc gac aac gtc tac tcc ttc aac ggc ctg gtc aaa	768

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<210> 1528
<211> 342
<212> PRT
<213> Corynebacterium glutamicum
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Asp	Ala	Asn	Ala	Glu	Leu	Asp	Ile	Ile	Gly	Ala	Pro	Ala	Leu	Leu	Ala
			20					25					30		
Asp	Arg	Pro	Ser	Tyr	Ala	Asn	Val	Lys	Thr	Leu	Ser	Arg	Ile	Phe	Ala
		35					40					45			
Val	Met	Arg	Ser	Leu	Gly	His	Val	Thr	Ala	Ala	Ser	Pro	Val	Thr	Val
	50					55					60				
Phe	Phe	Ser	Ser	His	Ser	Val	Leu	Ser	Asn	Val	Asp	Arg	Gly	Ser	Glu
65					70					75					80
His	Tyr	Ser	Gly	Pro	Asn	Gly	Leu	Gly	Glu	Trp	Thr	Ser	Val	Gly	Arg
				85					90					95	
Ala	Val	Ala	Thr	Asn	Trp	Asn	Gly	Val	Val	Asp	Ala	Leu	Asp	Glu	Ala
			100					105					110		
Ile	Thr	Val	Lys	Glu	Val	Asn	Ser	Leu	Phe	Thr	Glu	Asp	Ala	Ala	Thr
		115					120					125			
Arg	Ile	Gln	Glu	Ala	Gln	Ala	Ala	Val	Gln	Ala	Ala	Arg	Glu	Ala	Glu
	130					135					140				

Glu Gln Ile Ala Lys Glu Glu Ala Glu Lys Val Asp Pro Tyr Asp Asn
 145 150 155 160
 Ser Pro Trp Ala Ala Ala Gly Ile Asp Pro Ile Lys Val Ser Ile Asp
 165 170 175
 Gly Arg Thr Ile Tyr Thr Leu Arg Thr Tyr Leu Gly Gly Gln Pro Val
 180 185 190
 Phe Leu Gly Lys Phe Gly Glu Ile Phe Thr Phe Asn Ser Gln Lys Ser
 195 200 205
 Leu Leu Arg Trp Leu Val Glu His Asp Asp His Asp Leu Ala Arg Ala
 210 215 220
 Ser Thr Trp Ser Asp Leu Met Leu Gly Ile Asn Ala Gly Glu Thr Glu
 225 230 235 240
 Leu Leu Val His Ser Asp Asn Val Tyr Ser Phe Asn Gly Leu Val Lys
 245 250 255
 Asp Ile Asn Thr Ser Val Asp Ala Val Asp Thr Gln Gln Met Ala Arg
 260 265 270
 Ala Tyr Glu Leu Met Ala Asp Thr Ala Asp Trp Ala Asp Asp Ser
 275 280 285
 Met Asn Ser Tyr Phe Leu Ala Asn Pro Arg Met Gln Asp Tyr Ile Ser
 290 295 300
 Tyr Met Leu Gly Gly Ser Asp Thr Ser Gly Tyr Val Pro His Ala Pro
 305 310 315 320
 Phe Asn Asp His Ser Glu Ser Trp Arg Glu Leu Glu Glu Met Leu Ile
 325 330 335
 Lys Arg Phe Ser Lys Phe
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<210> 1529

<211> 1121

<212> DNA

<213> Corynebacterium glutamicum.

<220>

<221> CDS

<222> (1)..(1098)

<223> RXN03173

<400> 1529

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 1 5 10 15
 gac gac ttc gac gca gac tcc ttt acc acc gaa gtc atc cgg atc acc 96
 Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg Ile Thr
 20 25 30
 ggc tac tcc cgc cac gaa gtc aac aac ggc ctt aac gcc atg gcc gcg 144
 Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met Ala Ala

35	40	45	
atg acc aac ctc cca cac ctg cgc gcc atc caa gaa cgc tac tac ttc Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr Tyr Phe 50 55 60			192
ctg agc atc cgc tac ctc gcc tcc atc atg atc gcc gtg gcc aaa gca Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala Lys Ala 65 70 75 80			240
gac ccc acc ctg tgg gaa gaa ctc gac ctg cgc atc acc gac gcc tta Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp Ala Leu 85 90 95			288
aca cca gtc acc gca ggg gaa gtc atg atc caa tcc tcc acc ctg tcc Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr Leu Ser 100 105 110			336
aaa cgc atc gcc gcc tgg atc aaa gaa ctc gac ccc gaa ccc aca cca Lys Arg Ile Ala Ala Trp Ile Lys Glu Leu Asp Pro Glu Pro Thr Pro 115 120 125			384
gag ccc aca ccg aaa gag gac tat gtt cac gtc cac acc act gat gag Glu Pro Thr Pro Lys Glu Asp Tyr Val His Val His Thr Thr Asp Glu 130 135 140			432
gcg acc tat gtc cgc atc aaa atc agc ggc ccc aac cgc ctg atc ctc Ala Thr Tyr Val Arg Ile Lys Ile Ser Gly Pro Asn Arg Leu Ile Leu 145 150 155 160			480
aat gac atc atc acc caa ctc aaa gac aca gac acc gag gac agc ctg Asn Asp Ile Ile Thr Gln Leu Lys Asp Thr Asp Thr Glu Asp Ser Leu 165 170 175			528
cct gaa gcg ctc atg gcg ttc ctg aca gag aaa atc cag tta aag atc Pro Glu Ala Leu Met Ala Phe Leu Thr Glu Lys Ile Gln Leu Lys Ile 180 185 190			576
acc aaa tac ctc ttc acc cca cat aag cac cct gag cag gtg tgg tca Thr Lys Tyr Leu Phe Thr Pro His Lys His Pro Glu Gln Val Trp Ser 195 200 205			624
ccg gac tac ggt gac att gat ccc gaa gcc tat gcc aac gcc acc ctc Pro Asp Tyr Gly Asp Ile Asp Pro Glu Ala Tyr Ala Asn Ala Thr Leu 210 215 220			672
gtg tgc gcc aag gac tta gat gag ctc gct gga gcc acg gag aag agc Val Cys Ala Lys Asp Leu Asp Glu Leu Ala Gly Ala Thr Glu Lys Ser 225 230 235 240			720
tac acc ccg agt gag aag atg aaa gcc ctg atc aga gct cgg gat ggg Tyr Thr Pro Ser Glu Lys Met Lys Ala Leu Ile Arg Ala Arg Asp Gly 245 250 255			768
cat tgc cgc ttc cca ggg tgt tgc gtt ccg gcg agt aag tgc cag gtc His Cys Arg Phe Pro Gly Cys Cys Val Pro Ala Ser Lys Cys Gln Val 260 265 270			816
gat cac att atc ccg tgg gcg gag ggc ggc ccg aca gcg gcg tgg aac Asp His Ile Ile Pro Trp Ala Glu Gly Gly Pro Thr Ala Ala Trp Asn 275 280 285			864

ctg cag ttg ttg tgc cag cgg cat cac aat atg aaa acc gat ggt cgc 912
 Leu Gln Leu Leu Cys Gln Arg His His Asn Met Lys Thr Asp Gly Arg
 290 295 300
 ttt act gct gat gct aat gga ttg gcg gag att aga tgg att ggg ccg 960
 Phe Thr Ala Asp Ala Asn Gly Leu Ala Glu Ile Arg Trp Ile Gly Pro
 305 310 315 320
 atg gat gta cca gcg gtg acc agg ccg acg ggt ccg ttg gtg aaa gcg 1008
 Met Asp Val Pro Ala Val Thr Arg Pro Thr Gly Pro Leu Val Lys Ala
 325 330 335
 atg ccg cgg ggg att tgg ggt cag gtg ttg agg gat ccg atc cag gct 1056
 Met Pro Arg Gly Ile Trp Gly Gln Val Leu Arg Asp Arg Ile Gln Ala
 340 345 350
 agg ttt gag cgg atc cgc gac cgc gcc ctc aac aaa gaa gac 1098
 Arg Phe Glu Arg Ile Arg Asp Arg Ala Leu Asn Lys Glu Asp
 355 360 365
 tagaagcgca caggtttttg cat 1121

<210> 1530

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 1530

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 Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg Ile Thr
 20 25 30
 Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met Ala Ala
 35 40 45
 Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr Tyr Phe
 50 55 60
 Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala Lys Ala
 65 70 75 80
 Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp Ala Leu
 85 90 95
 Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr Leu Ser
 100 105 110
 Lys Arg Ile Ala Ala Trp Ile Lys Glu Leu Asp Pro Glu Pro Thr Pro
 115 120 125
 Glu Pro Thr Pro Lys Glu Asp Tyr Val His Val His Thr Thr Asp Glu
 130 135 140
 Ala Thr Tyr Val Arg Ile Lys Ile Ser Gly Pro Asn Arg Leu Ile Leu
 145 150 155 160
 Asn Asp Ile Ile Thr Gln Leu Lys Asp Thr Asp Thr Glu Asp Ser Leu

165										170					175				
Pro	Glu	Ala	Leu	Met	Ala	Phe	Leu	Thr	Glu	Lys	Ile	Gln	Leu	Lys	Ile				
			180					185					190						
Thr	Lys	Tyr	Leu	Phe	Thr	Pro	His	Lys	His	Pro	Glu	Gln	Val	Trp	Ser				
		195					200					205							
Pro	Asp	Tyr	Gly	Asp	Ile	Asp	Pro	Glu	Ala	Tyr	Ala	Asn	Ala	Thr	Leu				
	210					215					220								
Val	Cys	Ala	Lys	Asp	Leu	Asp	Glu	Leu	Ala	Gly	Ala	Thr	Glu	Lys	Ser				
225					230					235					240				
Tyr	Thr	Pro	Ser	Glu	Lys	Met	Lys	Ala	Leu	Ile	Arg	Ala	Arg	Asp	Gly				
				245					250					255					
His	Cys	Arg	Phe	Pro	Gly	Cys	Cys	Val	Pro	Ala	Ser	Lys	Cys	Gln	Val				
			260					265						270					
Asp	His	Ile	Ile	Pro	Trp	Ala	Glu	Gly	Gly	Pro	Thr	Ala	Ala	Trp	Asn				
		275					280					285							
Leu	Gln	Leu	Leu	Cys	Gln	Arg	His	His	Asn	Met	Lys	Thr	Asp	Gly	Arg				
	290					295					300								
Phe	Thr	Ala	Asp	Ala	Asn	Gly	Leu	Ala	Glu	Ile	Arg	Trp	Ile	Gly	Pro				
305					310					315					320				
Met	Asp	Val	Pro	Ala	Val	Thr	Arg	Pro	Thr	Gly	Pro	Leu	Val	Lys	Ala				
				325					330					335					
Met	Pro	Arg	Gly	Ile	Trp	Gly	Gln	Val	Leu	Arg	Asp	Arg	Ile	Gln	Ala				
			340					345					350						
Arg	Phe	Glu	Arg	Ile	Arg	Asp	Arg	Ala	Leu	Asn	Lys	Glu	Asp						
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<210> 1531

<211> 503

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(480)

<223> FRXA02874

<220>

<221> misc_feature

<222> (347, 356)

<223> n = a, c, t, or g

<220>

<221> VARIANT

<222> (116, 119)

<223> Xaa = Leu, Pro, Gln, or Arg

<400> 1531

acc gaa ctc aac cgc gac acc cat cac ctg tgg gtc gtc tta acc acc 48

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gac tcc gac gac ttc gac gca gac tcc ttt acc acc gaa gtc atc cgg 96
Asp Ser Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg
          20           25           30
atc acc ggc tac tcc cgc cac gaa gtc aac aac ggc ctt aac gcc atg 144
Ile Thr Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met
          35           40           45
gcc gcg atg acc aac ctc cca cac ctg cgc gcc atc caa gaa cgc tac 192
Ala Ala Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr
          50           55           60
tac ttc ctg agc atc cgc tac ctc gcc tcc atc atg atc gcc gtg gcc 240
Tyr Phe Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala
        65           70           75           80
aaa gca gac ccc acc ctg tgg gaa gaa ctc gac ctg cgc atc acc gac 288
Lys Ala Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp
          85           90           95
gcc tta aca cca gtc acc gca ggg gaa gtc atg atc caa tcc tcc acc 336
Ala Leu Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr
          100           105           110
ctg tcc aaa cng cat cgc cng cct gga tca aag aac tcg acc ccg aac 384
Leu Ser Lys Xaa His Arg Xaa Pro Gly Ser Lys Asn Ser Thr Pro Asn
          115           120           125
cca cac cag agc cca cac cga aag agg act atg ttc acg tcc aca cca 432
Pro His Gln Ser Pro His Arg Lys Arg Thr Met Phe Thr Ser Thr Pro
          130           135           140
ctg atg agg cga cct atg tcc gca tca aaa tca gcg gcc cca acc gcc 480
Leu Met Arg Arg Pro Met Ser Ala Ser Lys Ser Ala Ala Pro Thr Ala
        145           150           155           160
tgatcctcaa tgacatcatc acc 503

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<210> 1532

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<220>

<221> VARIANT

<222> (116, 119)

<223> Xaa = Leu, Pro, Gln, or Arg

<400> 1532

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Thr Glu Leu Asn Arg Asp Thr His His Leu Trp Val Val Leu Thr Thr
 1           5           10           15
Asp Ser Asp Asp Phe Asp Ala Asp Ser Phe Thr Thr Glu Val Ile Arg
          20           25           30
Ile Thr Gly Tyr Ser Arg His Glu Val Asn Asn Gly Leu Asn Ala Met
          35           40           45

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Ala Ala Met Thr Asn Leu Pro His Leu Arg Ala Ile Gln Glu Arg Tyr
 50 55 60

Tyr Phe Leu Ser Ile Arg Tyr Leu Ala Ser Ile Met Ile Ala Val Ala
 65 70 75 80

Lys Ala Asp Pro Thr Leu Trp Glu Glu Leu Asp Leu Arg Ile Thr Asp
 85 90 95

Ala Leu Thr Pro Val Thr Ala Gly Glu Val Met Ile Gln Ser Ser Thr
 100 105 110

Leu Ser Lys Xaa His Arg Xaa Pro Gly Ser Lys Asn Ser Thr Pro Asn
 115 120 125

Pro His Gln Ser Pro His Arg Lys Arg Thr Met Phe Thr Ser Thr Pro
 130 135 140

Leu Met Arg Arg Pro Met Ser Ala Ser Lys Ser Ala Ala Pro Thr Ala
 145 150 155 160

<210> 1533

<211> 556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXN03174

<400> 1533

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tggtcagatc actcaccact gaacgtgatc tactcctaaa atg ctg ctg aca att 115
 Met Leu Leu Thr Ile
 1 5

cta tgg gcc atc ggc atc acc gcc gaa ggc atg aca ggc gcg ctg gcc 163
 Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met Thr Gly Ala Leu Ala
 10 15 20

gca ggc cga caa aaa atg gat ctc ttc gga gta tcc gtc atc gca tgc 211
 Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val Ser Val Ile Ala Cys
 25 30 35

gtt acc gcg atc ggc ggc gga tcc atc cgc gac atg ctg ctg gga cat 259
 Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp Met Leu Leu Gly His
 40 45 50

tac ccg ctg gtg tgg gtg gaa aag cca ctg tat cta ctg ctg atc att 307
 Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr Leu Leu Leu Ile Ile
 55 60 65

ggc gca gcc att ttg aca gtg tcc att tcc ttc ctg atg gag cac ttc 355
 Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe Leu Met Glu His Phe
 70 75 80 85

cgt gtg ttg ttc ctc gtg ctc gac gcc gtg ggt ctt tct gca ttc gct 403

Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly Leu Ser Ala Phe Ala
 90 95 100

gtg atc ggc aca caa atc gca ctg gaa atg ggc tac gga ttc atc atc 451
 Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly Tyr Gly Phe Ile Ile
 105 110 115

gca gta gtg gca tca gtg ctc aca ggt gta ttc ggc ggc gtc atg cgt 499
 Ala Val Val Ala Ser Val Leu Thr Gly Val Phe Gly Gly Val Met Arg
 120 125 130

gac ctt ttg tgt gac cgc atc cca ctg gta ttt caa aaa gag ctc tac 547
 Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe Gln Lys Glu Leu Tyr
 135 140 145

gca tca atc 556
 Ala Ser Ile
 150

<210> 1534

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1534

Met Leu Leu Thr Ile Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met
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Thr Gly Ala Leu Ala Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val
 20 25 30

Ser Val Ile Ala Cys Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp
 35 40 45

Met Leu Leu Gly His Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr
 50 55 60

Leu Leu Leu Ile Ile Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe
 65 70 75 80

Leu Met Glu His Phe Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly
 85 90 95

Leu Ser Ala Phe Ala Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly
 100 105 110

Tyr Gly Phe Ile Ile Ala Val Val Ala Ser Val Leu Thr Gly Val Phe
 115 120 125

Gly Gly Val Met Arg Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe
 130 135 140

Gln Lys Glu Leu Tyr Ala Ser Ile
 145 150

<210> 1535

<211> 562

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> FRXA02884

<400> 1535

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                                         Met Leu Leu Thr Ile
                                         1 5

cta tgg gcc atc ggc atc acc gcc gaa ggc atg aca ggc gcg ctg gcc 163
Leu Trp Ala Ile Gly Ile Thr Ala Glu Gly Met Thr Gly Ala Leu Ala
                        10 15 20

gca ggc cga caa aaa atg gat ctc ttc gga gta tcc gtc atc gca tgc 211
Ala Gly Arg Gln Lys Met Asp Leu Phe Gly Val Ser Val Ile Ala Cys
                        25 30 35

gtt acc gcg atc ggc ggc gga tcc atc cgc gac atg ctg ctg gga cat 259
Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp Met Leu Leu Gly His
                        40 45 50

tac ccg ctg gtg tgg gtg gaa aag cca ctg tat cta ctg ctg atc att 307
Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr Leu Leu Ile Ile
                        55 60 65

ggc gca gcc att ttg aca gtg tcc att tcc ttc ctg atg gag cac ttc 355
Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe Leu Met Glu His Phe
                        70 75 80 85

cgt gtg ttg ttc ctc gtg ctc gac gcc gtg ggt ctt tct gca ttc gct 403
Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly Leu Ser Ala Phe Ala
                        90 95 100

gtg atc ggc aca caa atc gca ctg gaa atg ggc tac gga ttc atc atc 451
Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly Tyr Gly Phe Ile Ile
                        105 110 115

gca gta gtg gca tca gtg ctc aca ggt gta ttc ggc ggc gtc atg cgt 499
Ala Val Val Ala Ser Val Leu Thr Gly Val Phe Gly Gly Val Met Arg
                        120 125 130

gac ctt ttg tgt gac cgc atc cca ctg gta ttt caa aaa gag ctc tac 547
Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe Gln Lys Glu Leu Tyr
                        135 140 145

gca tca atc gca ttc 562
Ala Ser Ile Ala Phe
150

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<210> 1536

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 1536

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	20	25	30
Ser Val Ile	Ala Cys Val Thr Ala Ile Gly Gly Gly Ser Ile Arg Asp		
	35	40	45
Met Leu Leu	Gly His Tyr Pro Leu Val Trp Val Glu Lys Pro Leu Tyr		
	50	55	60
Leu Leu Leu	Ile Ile Gly Ala Ala Ile Leu Thr Val Ser Ile Ser Phe		
	65	70	75
Leu Met Glu	His Phe Arg Val Leu Phe Leu Val Leu Asp Ala Val Gly		
	85	90	95
Leu Ser Ala	Phe Ala Val Ile Gly Thr Gln Ile Ala Leu Glu Met Gly		
	100	105	110
Tyr Gly Phe	Ile Ile Ala Val Val Ala Ser Val Leu Thr Gly Val Phe		
	115	120	125
Gly Gly Val	Met Arg Asp Leu Leu Cys Asp Arg Ile Pro Leu Val Phe		
	130	135	140
Gln Lys Glu	Leu Tyr Ala Ser Ile Ala Phe		
	145	150	

<210> 1537

<211> 781

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (93)..(758)

<223> RXN03177

<400> 1537

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tatgggctga	acaattctaa	ggagaattat	cc	gtg	aaa	aag	aag	ctt	atg	ttg	113
				Val	Lys	Lys	Lys	Leu	Met	Leu	
				1				5			

cct	ttg	att	gtt	gca	gct	ttg	ggg	tta	agt	gcc	tgc	agc	tcc	gaa	cct	161
Pro	Leu	Ile	Val	Ala	Ala	Leu	Gly	Leu	Ser	Ala	Cys	Ser	Ser	Glu	Pro	
		10					15				20					

gca	gca	gcc	cca	ctc	gaa	gca	gag	cca	tta	cat	aac	ctg	ctc	att	gat	209
Ala	Ala	Ala	Pro	Leu	Glu	Ala	Glu	Pro	Leu	His	Asn	Leu	Leu	Ile	Asp	
		25				30					35					

ggc	tca	gag	tcc	ggc	ttg	gac	aat	gcc	act	gaa	gga	aac	gac	acc	tca	257
Gly	Ser	Glu	Ser	Gly	Leu	Asp	Asn	Ala	Thr	Glu	Gly	Asn	Asp	Thr	Ser	
		40			45				50					55		

tta	agt	ggc	caa	ccc	atc	aat	ctt	aca	gtg	gtc	aac	ggc	gaa	ttg	gat	305
Leu	Ser	Gly	Gln	Pro	Ile	Asn	Leu	Thr	Val	Val	Asn	Gly	Ala	Leu	Asp	

60	65	70	
atc gat ggc tcc tgc gga aaa gcc ctc caa gct gta gag gac gtc aat			353
Ile Asp Gly Ser Cys Gly Lys Ala Leu Gln Ala Val Glu Asp Val Asn			
75	80	85	
ctg gac agc gta gct agc gca tcc agg gca ctg gca tcc ggc gac aaa			401
Leu Asp Ser Val Ala Ser Ala Ser Arg Ala Leu Ala Ser Gly Asp Lys			
90	95	100	
caa gta ggc atc gcc atg tac tca acc gcc gaa gac aac gac atc tca			449
Gln Val Gly Ile Ala Met Tyr Ser Thr Ala Glu Asp Asn Asp Ile Ser			
105	110	115	
cca atg gac ctc tac gca gac atc gcg aat gct tgc gaa gac ccc gtc			497
Pro Met Asp Leu Tyr Ala Asp Ile Ala Asn Ala Cys Glu Asp Pro Val			
120	125	130	135
gtc gat tct tcc gac acc acc tac acc ttc ggc aaa ctc gat gat gct			545
Val Asp Ser Ser Asp Thr Thr Tyr Thr Phe Gly Lys Leu Asp Asp Ala			
140	145	150	
ccc gac ggc gcc gtt gga ttc acc ctc gac att gaa gtc acc cct gac			593
Pro Asp Gly Ala Val Gly Phe Thr Leu Asp Ile Glu Val Thr Pro Asp			
155	160	165	
aat caa ggc tcc acc gtg atg atg atc caa gaa tta gga aac cac cac			641
Asn Gln Gly Ser Thr Val Met Met Ile Gln Glu Leu Gly Asn His His			
170	175	180	
atc atc gtc gca gga ctt gaa acc acc cca gaa gaa acc gcc act gtc			689
Ile Ile Val Ala Gly Leu Glu Thr Thr Pro Glu Glu Thr Ala Thr Val			
185	190	195	
ttc gaa gca caa cgc acc aaa ctc gaa gaa ggc ttg cag ctt aaa cag			737
Phe Glu Ala Gln Arg Thr Lys Leu Glu Glu Gly Leu Gln Leu Lys Gln			
200	205	210	215
aat tgg cag ctt ggg tgg gtt taaatgcgcc caacctaaga aaa			781
Asn Trp Gln Leu Gly Trp Val			
220			

<210> 1538

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 1538

Val	Lys	Lys	Lys	Leu	Met	Leu	Pro	Leu	Ile	Val	Ala	Ala	Leu	Gly	Leu
1				5					10					15	

Ser	Ala	Cys	Ser	Ser	Glu	Pro	Ala	Ala	Ala	Pro	Leu	Glu	Ala	Glu	Pro
			20				25					30			

Leu	His	Asn	Leu	Leu	Ile	Asp	Gly	Ser	Glu	Ser	Gly	Leu	Asp	Asn	Ala
	35						40					45			

Thr	Glu	Gly	Asn	Asp	Thr	Ser	Leu	Ser	Gly	Gln	Pro	Ile	Asn	Leu	Thr
50						55					60				

Val Val Asn Gly Ala Leu Asp Ile Asp Gly Ser Cys Gly Lys Ala Leu
65 70 75 80

Gln Ala Val Glu Asp Val Asn Leu Asp Ser Val Ala Ser Ala Ser Arg
85 90 95

Ala Leu Ala Ser Gly Asp Lys Gln Val Gly Ile Ala Met Tyr Ser Thr
100 105 110

Ala Glu Asp Asn Asp Ile Ser Pro Met Asp Leu Tyr Ala Asp Ile Ala
115 120 125

Asn Ala Cys Glu Asp Pro Val Val Asp Ser Ser Asp Thr Thr Tyr Thr
130 135 140

Phe Gly Lys Leu Asp Asp Ala Pro Asp Gly Ala Val Gly Phe Thr Leu
145 150 155 160

Asp Ile Glu Val Thr Pro Asp Asn Gln Gly Ser Thr Val Met Met Ile
165 170 175

Gln Glu Leu Gly Asn His His Ile Ile Val Ala Gly Leu Glu Thr Thr
180 185 190

Pro Glu Glu Thr Ala Thr Val Phe Glu Ala Gln Arg Thr Lys Leu Glu
195 200 205

Glu Gly Leu Gln Leu Lys Gln Asn Trp Gln Leu Gly Trp Val
210 215 220

<210> 1539

<211> 782

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (94)..(759)

<223> FRXA02881

<400> 1539

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ttatgggctg aacaattcta aggagaatta tcc gtg aaa aag aag ctt atg ttg 114
Val Lys Lys Lys Leu Met Leu
1 5

cct ttg att gtt gca gct ttg ggg tta agt gcc tgc agc tcc gaa cct 162
Pro Leu Ile Val Ala Ala Leu Gly Leu Ser Ala Cys Ser Ser Glu Pro
10 15 20

gca gca gcc cca ctc gaa gca gag cca tta cat aac ctg ctc att gat 210
Ala Ala Ala Pro Leu Glu Ala Glu Pro Leu His Asn Leu Leu Ile Asp
25 30 35

ggg tca gag tcc ggc ttg gac aat gcc act gaa gga aac gac acc tca 258
Gly Ser Glu Ser Gly Leu Asp Asn Ala Thr Glu Gly Asn Asp Thr Ser
40 45 50 55

tta agt ggc caa ccc atc aat ctt aca gtg gtc aac ggt gcc tta gat 306

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<210> 1540
<211> 222
<212> PRT
<213> Corynebacterium glutamicum
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Val Lys Lys Lys Leu Met Leu Pro Leu Ile Val Ala Ala Leu Gly Leu
1 5 10 15

Ser Ala Cys Ser Ser Glu Pro Ala Ala Ala Pro Leu Glu Ala Glu Pro
20 25 30

Leu His Asn Leu Leu Ile Asp Gly Ser Glu Ser Gly Leu Asp Asn Ala
35 40 45

Thr Glu Gly Asn Asp Thr Ser Leu Ser Gly Gln Pro Ile Asn Leu Thr
50 55 60

Val Val Asn Gly Ala Leu Asp Ile Asp Gly Ser Cys Gly Lys Ala Leu
 65 70 75 80
 Gln Ala Val Glu Asp Val Asn Leu Asp Ser Val Ala Ser Ala Ser Arg
 85 90 95
 Ala Leu Ala Ser Gly Asp Lys Gln Val Gly Ile Ala Met Tyr Ser Thr
 100 105 110
 Ala Glu Asp Asn Asp Ile Ser Pro Met Asp Leu Tyr Ala Asp Ile Ala
 115 120 125
 Asn Ala Cys Glu Asp Pro Val Val Asp Ser Ser Asp Thr Thr Tyr Thr
 130 135 140
 Phe Gly Lys Leu Asp Asp Ala Pro Asp Gly Ala Val Gly Phe Thr Leu
 145 150 155 160
 Asp Ile Glu Val Thr Pro Asp Asn Gln Gly Ser Thr Val Met Met Ile
 165 170 175
 Gln Glu Leu Gly Asn His His Ile Ile Val Ala Gly Leu Glu Thr Thr
 180 185 190
 Pro Glu Glu Thr Ala Thr Val Phe Glu Ala Gln Arg Thr Lys Leu Glu
 195 200 205
 Glu Gly Leu Gln Leu Lys Gln Asn Trp Gln Leu Gly Trp Val
 210 215 220

<210> 1541

<211> 373

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(373)

<223> RXN03182

<400> 1541

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tgtatccgta gcccgcttcc gcaagaggga tgggtgcctaa atg acc ctg caa cta 115
 Met Thr Leu Gln Leu
 1 5

ttc acc gac atc gtg tct ctg gtg ttc att ctc agc ggc gca ttc ttg 163
 Phe Thr Asp Ile Val Ser Leu Val Phe Ile Leu Ser Gly Ala Phe Leu
 10 15 20

tca ttc tcc gca tcc atc ggc ctc ata cga ttc aaa gac acc atg tcc 211
 Ser Phe Ser Ala Ser Ile Gly Leu Ile Arg Phe Lys Asp Thr Met Ser
 25 30 35

aga gtc cac gcc atg acc aaa ccc caa aca acc ggc ctt atc ctc acc 259
 Arg Val His Ala Met Thr Lys Pro Gln Thr Thr Gly Leu Ile Leu Thr
 40 45 50

gtt gta ggc gca atc atc cgc atc tta ggc cac gaa cac ttc gat caa 307
 Val Val Gly Ala Ile Ile Arg Ile Leu Gly His Glu His Phe Asp Gln
 55 60 65

tca caa cgc agt gac ctc gga gtc ctt gtt ctc ctc gta ctg ttt gca 355
 Ser Gln Arg Ser Asp Leu Gly Val Leu Val Leu Leu Val Leu Phe Ala
 70 75 80 85

ctg ctc acc agc cca gtg 373
 Leu Leu Thr Ser Pro Val
 90

<210> 1542

<211> 91

<212> PRT

<213> Corynebacterium glutamicum

<400> 1542

Met Thr Leu Gln Leu Phe Thr Asp Ile Val Ser Leu Val Phe Ile Leu
 1 5 10 15

Ser Gly Ala Phe Leu Ser Phe Ser Ala Ser Ile Gly Leu Ile Arg Phe
 20 25 30

Lys Asp Thr Met Ser Arg Val His Ala Met Thr Lys Pro Gln Thr Thr
 35 40 45

Gly Leu Ile Leu Thr Val Val Gly Ala Ile Ile Arg Ile Leu Gly His
 50 55 60

Glu His Phe Asp Gln Ser Gln Arg Ser Asp Leu Gly Val Leu Val Leu
 65 70 75 80

Leu Val Leu Phe Ala Leu Leu Thr Ser Pro Val
 85 90

<210> 1543

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (87)..(584)

<223> RXN03184

<400> 1543

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ctggcctgct gtttggtgcc gcgggc atg gtt ggc gcg ttt ggc ggt ggc gtt 113
 Met Val Gly Ala Phe Gly Gly Gly Val
 1 5

ctc ggg ggc tac att cct ggc acg att ttg atg atc gcg ttt gcg ctc 161
 Leu Gly Gly Tyr Ile Pro Gly Thr Ile Leu Met Ile Ala Phe Ala Leu
 10 15 20 25

atg atg atc gcc acg tcg act gcg atg ttg cgg ggg cgt aag cag aag 209
 Met Met Ile Ala Thr Ser Thr Ala Met Leu Arg Gly Arg Lys Gln Lys

30	35	40	
aag ggg gcg tcg aaa agc tct ctt tgg cgc gtc ctt gtt gat ggc ctg			257
Lys Gly Ala Ser Lys Ser Ser Leu Trp Arg Val Leu Val Asp Gly Leu			
45	50	55	
gtg gtc ggc gcg gtg acc ggg ctt gtt ggt gcg ggc ggc ggc ttt ttg			305
Val Val Gly Ala Val Thr Gly Leu Val Gly Ala Gly Gly Phe Leu			
60	65	70	
gtg gtg ccg gcg ctg gcg ctg ctc ggc ggg ctg tcg atg ccg gtg gct			353
Val Val Pro Ala Leu Ala Leu Leu Gly Gly Leu Ser Met Pro Val Ala			
75	80	85	
gtg ggc acg tcg ttg gtg gtg atc acg atg aag tcg ttt gcg ggg ctt			401
Val Gly Thr Ser Leu Val Val Ile Thr Met Lys Ser Phe Ala Gly Leu			
90	95	100	105
gcc ggg tat ctg acc agc gtg cag ctg gat tgg ggg ctg gtg ctg atg			449
Ala Gly Tyr Leu Thr Ser Val Gln Leu Asp Trp Gly Leu Val Leu Met			
110	115	120	
gtg act gcg gcc gcc atc gtc ggt tcg ctt gcc ggt tcg cgc ctt gcg			497
Val Thr Ala Ala Ala Ile Val Gly Ser Leu Ala Gly Ser Arg Leu Ala			
125	130	135	
ggg cgc gtg cct gag act ttg ctc cgc aaa ggg ttc ggg gtg ttc gtg			545
Gly Arg Val Pro Glu Thr Leu Leu Arg Lys Gly Phe Gly Val Phe Val			
140	145	150	
ctg gtc atg ggc gtg ttc gtg ctc ggc ttg gag ctt tta taagcttttc			594
Leu Val Met Gly Val Phe Val Leu Gly Leu Glu Leu Leu			
155	160	165	
gacgtctcc			603
<210> 1544			
<211> 166			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1544			
Met Val Gly Ala Phe Gly Gly Gly Val Leu Gly Gly Tyr Ile Pro Gly			
1	5	10	15
Thr Ile Leu Met Ile Ala Phe Ala Leu Met Met Ile Ala Thr Ser Thr			
20	25	30	
Ala Met Leu Arg Gly Arg Lys Gln Lys Lys Gly Ala Ser Lys Ser Ser			
35	40	45	
Leu Trp Arg Val Leu Val Asp Gly Leu Val Val Gly Ala Val Thr Gly			
50	55	60	
Leu Val Gly Ala Gly Gly Gly Phe Leu Val Val Pro Ala Leu Ala Leu			
65	70	75	80
Leu Gly Gly Leu Ser Met Pro Val Ala Val Gly Thr Ser Leu Val Val			
85	90	95	

Ile Thr Met Lys Ser Phe Ala Gly Leu Ala Gly Tyr Leu Thr Ser Val
 100 105 110

Gln Leu Asp Trp Gly Leu Val Leu Met Val Thr Ala Ala Ala Ile Val
 115 120 125

Gly Ser Leu Ala Gly Ser Arg Leu Ala Gly Arg Val Pro Glu Thr Leu
 130 135 140

Leu Arg Lys Gly Phe Gly Val Phe Val Leu Val Met Gly Val Phe Val
 145 150 155 160

Leu Gly Leu Glu Leu Leu
 165

<210> 1545
 <211> 295
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (84)..(272)
 <223> RXN03185

<220>
 <221> misc_feature
 <222> (56)
 <223> n = a, c, t, or g

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tcaactgagct gtccgaaacc acc atg aat gat ctt gca gct gaa ggt gaa aac 113
 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
 1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
 Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
 15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
 Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
 30 35 40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
 Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
 45 50 55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295
 Ser Arg Glu Ser Leu
 60

<210> 1546
 <211> 63
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1546

Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
 1 5 10 15
 Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
 20 25 30
 Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
 35 40 45
 Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
 50 55 60

<210> 1547

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> RXA00003

<400> 1547

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aagcgccaag aaggccaccc ttgccttcgc ggtgcagcac gtg cag gtg aga atc 115
 Val Gln Val Arg Ile
 1 5

ctc agc agc gag ctt gtc tgc agc ctc tcc ggt gcc atc cgg ggc gtg 163
 Leu Ser Ser Glu Leu Val Cys Ser Leu Ser Gly Ala Ile Arg Gly Val
 10 15 20

aac cta gat att gca gca ccg aag ccc aag aag tca ggc cgc cgc aca 211
 Asn Leu Asp Ile Ala Ala Pro Lys Pro Lys Lys Ser Gly Arg Arg Thr
 25 30 35

ctc aca aaa ccc gaa tgg gat gcc gtc att aag cat ctg tta acg cgg 259
 Leu Thr Lys Pro Glu Trp Asp Ala Val Ile Lys His Leu Leu Thr Arg
 40 45 50

gat acc gag cca ctg tta acc ccc acc aag cac aag aac atc cga caa 307
 Asp Thr Glu Pro Leu Leu Thr Pro Thr Lys His Lys Asn Ile Arg Gln
 55 60 65

agc acc aag aac atc cat gcc cgc att gtg cgg ctc act ctc ctc caa 355
 Ser Thr Lys Asn Ile His Ala Arg Ile Val Arg Leu Thr Leu Leu Gln
 70 75 80 85

gcc gtt tca ggg ctg aga att gcc gaa gcc aat caa ttg cag tgg aag 403
 Ala Val Ser Gly Leu Arg Ile Ala Glu Ala Asn Gln Leu Gln Trp Lys
 90 95 100

cac atc atc gac ggt gac gat ggc atg ctc att aat gcc agc gcc gat 451
 His Ile Ile Asp Gly Asp Asp Gly Met Leu Ile Asn Ala Ser Ala Asp
 105 110 115

att gtc aag ggg cga aaa ggc aag gaa aga ggg cgg tat atc cct atc 499
 Ile Val Lys Gly Arg Lys Gly Lys Glu Arg Gly Arg Tyr Ile Pro Ile
 120 125 130

ctg agg gcc gac gta gcg gaa tac ctg cgt aca cac cgc gag gac gac 547
 Leu Arg Ala Asp Val Ala Glu Tyr Leu Arg Thr His Arg Glu Asp Asp
 135 140 145
 gag cat ttc atc gta ggc tca ccg acg acg acc gcg agg ccc tgg gac 595
 Glu His Phe Ile Val Gly Ser Pro Thr Thr Thr Ala Arg Pro Trp Asp
 150 155 160 165
 gcg acg aac gca gat gac aag gtg ccc gag cta tac cgg caa att gca 643
 Ala Thr Asn Ala Asp Asp Lys Val Pro Glu Leu Tyr Arg Gln Ile Ala
 170 175 180
 gaa gct aca ggc gtg aag act ctt caa gac ctc cga agc cac tcc tgg 691
 Glu Ala Thr Gly Val Lys Thr Leu Gln Asp Leu Arg Ser His Ser Trp
 185 190 195
 cgt gcg acg ctg cac ggt gtg tac gcg gac gtg atg gac cca gct aca 739
 Arg Ala Thr Leu His Gly Val Tyr Ala Asp Val Met Asp Pro Ala Thr
 200 205 210
 cgc gcc gcc att ttc ggc cac acc gag cag gta gct gag gag tac tac 787
 Arg Ala Ala Ile Phe Gly His Thr Glu Gln Val Ala Glu Glu Tyr Tyr
 215 220 225
 aac gac cgc caa aat att gaa tca ctc atg aga caa gtc aag cgc gcc 835
 Asn Asp Arg Gln Asn Ile Glu Ser Leu Met Arg Gln Val Lys Arg Ala
 230 235 240 245
 tac gcg taactacgct taagactacg cgt 864
 Tyr Ala

<210> 1548

<211> 247

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1548

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Ala Ile Arg Gly Val Asn Leu Asp Ile Ala Ala Pro Lys Pro Lys Lys
 20 25 30

Ser Gly Arg Arg Thr Leu Thr Lys Pro Glu Trp Asp Ala Val Ile Lys
 35 40 45

His Leu Leu Thr Arg Asp Thr Glu Pro Leu Leu Thr Pro Thr Lys His
 50 55 60

Lys Asn Ile Arg Gln Ser Thr Lys Asn Ile His Ala Arg Ile Val Arg
 65 70 75 80

Leu Thr Leu Leu Gln Ala Val Ser Gly Leu Arg Ile Ala Glu Ala Asn
 85 90 95

Gln Leu Gln Trp Lys His Ile Ile Asp Gly Asp Asp Gly Met Leu Ile
 100 105 110

Asn Ala Ser Ala Asp Ile Val Lys Gly Arg Lys Gly Lys Glu Arg Gly
 115 120 125
 Arg Tyr Ile Pro Ile Leu Arg Ala Asp Val Ala Glu Tyr Leu Arg Thr
 130 135 140
 His Arg Glu Asp Asp Glu His Phe Ile Val Gly Ser Pro Thr Thr Thr
 145 150 155 160
 Ala Arg Pro Trp Asp Ala Thr Asn Ala Asp Asp Lys Val Pro Glu Leu
 165 170 175
 Tyr Arg Gln Ile Ala Glu Ala Thr Gly Val Lys Thr Leu Gln Asp Leu
 180 185 190
 Arg Ser His Ser Trp Arg Ala Thr Leu His Gly Val Tyr Ala Asp Val
 195 200 205
 Met Asp Pro Ala Thr Arg Ala Ala Ile Phe Gly His Thr Glu Gln Val
 210 215 220
 Ala Glu Glu Tyr Tyr Asn Asp Arg Gln Asn Ile Glu Ser Leu Met Arg
 225 230 235 240
 Gln Val Lys Arg Ala Tyr Ala
 245

<210> 1549

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00008

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 Met Ala Lys Lys Lys
 1 5

aag aaa gtc gac gaa aac aac tca gtt ctc gcg acc aat cgc aag gcc 163
 Lys Lys Val Asp Glu Asn Asn Ser Val Leu Ala Thr Asn Arg Lys Ala
 10 15 20

cgc cat gac tac cac atc att gat acg tgg gag gcg ggc gtg gtg ctc 211
 Arg His Asp Tyr His Ile Ile Asp Thr Trp Glu Ala Gly Val Val Leu
 25 30 35

tta ggc acc gaa atc aaa tca ctg cgc gaa ggt aag gta tcc ctc gtg 259
 Leu Gly Thr Glu Ile Lys Ser Leu Arg Glu Gly Lys Val Ser Leu Val
 40 45 50

gat tcc ttt gcc acc att gat aac gga gaa atc tgg ctt cag cat ctc 307
 Asp Ser Phe Ala Thr Ile Asp Asn Gly Glu Ile Trp Leu Gln His Leu
 55 60 65

cac atc ccg cag tat tcc atg ggc tcc tgg aca aac cac acg ccc aag 355
 His Ile Pro Gln Tyr Ser Met Gly Ser Trp Thr Asn His Thr Pro Lys
 70 75 80 85
 cgc acc cgc aaa ctt ttg ctg cac cgc aac gag att gat tcc ctg atg 403
 Arg Thr Arg Lys Leu Leu Leu His Arg Asn Glu Ile Asp Ser Leu Met
 90 95 100
 ggt aaa gtc cgc gac ggc aac cgc acg ttg gtt ccg ctc aag ctt tac 451
 Gly Lys Val Arg Asp Gly Asn Arg Thr Leu Val Pro Leu Lys Leu Tyr
 105 110 115
 ctc aaa aac ggt cgc gtc aaa ctc gaa ctc gga ctc gca caa ggt aag 499
 Leu Lys Asn Gly Arg Val Lys Leu Glu Leu Gly Leu Ala Gln Gly Lys
 120 125 130
 cag gat tac gac aag cgc caa gat atc aag cgt cgc acc gaa gaa cgc 547
 Gln Asp Tyr Asp Lys Arg Gln Asp Ile Lys Arg Arg Thr Glu Glu Arg
 135 140 145
 gaa gtc acc cgt gag ctc ggc cgt cgc att aag gga atc aac gcg 592
 Glu Val Thr Arg Glu Leu Gly Arg Arg Ile Lys Gly Ile Asn Ala
 150 155 160
 taaatgagta ttcacatcgc aaa 615

<210> 1550

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1550

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 Thr Asn Arg Lys Ala Arg His Asp Tyr His Ile Ile Asp Thr Trp Glu
 20 25 30
 Ala Gly Val Val Leu Leu Gly Thr Glu Ile Lys Ser Leu Arg Glu Gly
 35 40 45
 Lys Val Ser Leu Val Asp Ser Phe Ala Thr Ile Asp Asn Gly Glu Ile
 50 55 60
 Trp Leu Gln His Leu His Ile Pro Gln Tyr Ser Met Gly Ser Trp Thr
 65 70 75 80
 Asn His Thr Pro Lys Arg Thr Arg Lys Leu Leu Leu His Arg Asn Glu
 85 90 95
 Ile Asp Ser Leu Met Gly Lys Val Arg Asp Gly Asn Arg Thr Leu Val
 100 105 110
 Pro Leu Lys Leu Tyr Leu Lys Asn Gly Arg Val Lys Leu Glu Leu Gly
 115 120 125
 Leu Ala Gln Gly Lys Gln Asp Tyr Asp Lys Arg Gln Asp Ile Lys Arg
 130 135 140
 Arg Thr Glu Glu Arg Glu Val Thr Arg Glu Leu Gly Arg Arg Ile Lys

145

150

155

160

Gly Ile Asn Ala

<210> 1551

<211> 432

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(409)

<223> RXA00015

<400> 1551

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acagcaaccg acgacactca acgagcgcga cctccaagac atg att gat atg tgc 115
 Met Ile Asp Met Cys
 1 5

acc act cct cga caa gag atc atg atc cgc gag caa ttt aag gag atc 163
 Thr Thr Pro Arg Gln Glu Ile Met Ile Arg Glu Gln Phe Lys Glu Ile
 10 15 20

aac aac ggt agg gtt gta cct cat tac gat cag ctt gaa cag ctc gca 211
 Asn Asn Gly Arg Val Val Pro His Tyr Asp Gln Leu Glu Gln Leu Ala
 25 30 35

gag att ttt tca act aaa gac tca atc gac atg gtc aac gag ata ctc 259
 Glu Ile Phe Ser Thr Lys Asp Ser Ile Asp Met Val Asn Glu Ile Leu
 40 45 50

aat cgc gat acg gat ttt ctc agt aat gaa ggc aca att ttt atg gaa 307
 Asn Arg Asp Thr Asp Phe Leu Ser Asn Glu Gly Thr Ile Phe Met Glu
 55 60 65

tac att ttc aac ggt gga ttc cat acg gac aac ggc tat caa ccg ttg 355
 Tyr Ile Phe Asn Gly Gly Phe His Thr Asp Asn Gly Tyr Gln Pro Leu
 70 75 80 85

tcc tat gca tat gtt gaa cga ggc tta gcg atc cgc cct cca cgc ata 403
 Ser Tyr Ala Tyr Val Glu Arg Gly Leu Ala Ile Arg Pro Pro Arg Ile
 90 95 100

gtg ctc tagatatgac acaaatcggt att 432
 Val Leu

<210> 1552

<211> 103

<212> PRT

<213> Corynebacterium glutamicum

<400> 1552

Met Ile Asp Met Cys Thr Thr Pro Arg Gln Glu Ile Met Ile Arg Glu
 1 5 10 15

Gln Phe Lys Glu Ile Asn Asn Gly Arg Val Val Pro His Tyr Asp Gln
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Leu Glu Gln Leu Ala Glu Ile Phe Ser Thr Lys Asp Ser Ile Asp Met
 35 40 45

Val Asn Glu Ile Leu Asn Arg Asp Thr Asp Phe Leu Ser Asn Glu Gly
 50 55 60

Thr Ile Phe Met Glu Tyr Ile Phe Asn Gly Gly Phe His Thr Asp Asn
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Arg Pro Pro Arg Ile Val Leu
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 Met Ser Ala Leu Ser
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aga ccg cac aag atc gcc acc ggc gtt gct gtc gca act ctt acc ctg 163
 Arg Pro His Lys Ile Ala Thr Gly Val Ala Val Ala Thr Leu Thr Leu
 10 15 20

acc ttg tgt acc tct gct gcc ggc gtt gtc cat gca gcg caa caa tcc 211
 Thr Leu Cys Thr Ser Ala Ala Gly Val Val His Ala Ala Gln Gln Ser
 25 30 35

atc agc ggt cca gaa tcc tcc tgt gct ttt aat caa cag cgt tgg gat 259
 Ile Ser Gly Pro Glu Ser Ser Cys Ala Phe Asn Gln Gln Arg Trp Asp
 40 45 50

gac agc aaa gtt aag ctt gac gac acc atc gct acg gcc aaa aac tca 307
 Asp Ser Lys Val Lys Leu Asp Asp Thr Ile Ala Thr Ala Lys Asn Ser
 55 60 65

ttg gta caa aca ggc gaa ctg cac cgc aac gaa cag gat cta ctt act 355
 Leu Val Gln Thr Gly Glu Leu His Arg Asn Glu Gln Asp Leu Leu Thr
 70 75 80 85

ggc tat ctt ttc cag caa ccg cac agc agc aat tac ctt gca ctg aac 403
 Gly Tyr Leu Phe Gln Gln Pro His Ser Ser Asn Tyr Leu Ala Leu Asn
 90 95 100

aac gct tat gcc gat gcc gta gca atc aaa gac agc ttt gtc cgc cca 451

Asn	Ala	Tyr	Ala	Asp	Ala	Val	Ala	Ile	Lys	Asp	Ser	Phe	Val	Arg	Pro		
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Thr	Cys	Asp	Gly	Ser	Lys	Glu	Ser	Lys	Ile	Ala	Ser	Glu	His	Ala	Val		
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tct	gag	gtt	gtg	ggg	gca	gtg	aat	gta	ctc	gcc	cga	gca	caa	aaa	gcg	547	
Ser	Glu	Val	Val	Gly	Ala	Val	Asn	Val	Leu	Ala	Arg	Ala	Gln	Lys	Ala		
			135			140					145						
ctg	cag	att	aac	tcc	gac	acc	tac	gaa	cag	caa	cgt	cgt	tgt	gat	gcc	595	
Leu	Gln	Ile	Asn	Ser	Asp	Thr	Tyr	Glu	Gln	Gln	Arg	Arg	Cys	Asp	Ala		
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ctt	cgt	cta	gca	agc	cga	gat	gaa	tca	gat	gtt	ctt	atg	cgc	att	gat	643	
Leu	Arg	Leu	Ala	Ser	Arg	Asp	Glu	Ser	Asp	Val	Leu	Met	Arg	Ile	Asp		
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cgc	acc	atg	ctg	cag	ctt	cgt	cgc	aca	cta	gct	gac	att	gac	cag	gcg	691	
Arg	Thr	Met	Leu	Gln	Leu	Arg	Arg	Thr	Leu	Ala	Asp	Ile	Asp	Gln	Ala		
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Ser	Thr	Asp	Ile	Arg	Asp	Ile	Arg	Ala	Gln	Thr	Thr	Ser	Phe	Glu	Arg		
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gat	ctt	gcc	cgc	gag	caa	aaa	gag	gcc	gac	gca	gca	gca	cgt	gct	caa	787	
Asp	Leu	Ala	Arg	Glu	Gln	Lys	Glu	Ala	Asp	Ala	Ala	Ala	Arg	Ala	Gln		
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gct	gta	gac	act	tcg	acc	aca	cca	aca	tca	agc	aca	gaa	gat	cgt	gtc	835	
Ala	Val	Asp	Thr	Ser	Thr	Thr	Pro	Thr	Ser	Ser	Thr	Glu	Asp	Arg	Val		
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aac	gac	att	ctt	aaa	gag	tcc	cgt	acc	gat	cac	agt	ggc	gac	agt	tac	883	
Asn	Asp	Ile	Leu	Lys	Glu	Ser	Arg	Thr	Asp	His	Ser	Gly	Asp	Ser	Tyr		
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acg	cgc	tca	acg	aca	acg	agc	gca	caa	agc	act	gag	ccg	gat	tct	gca	931	
Thr	Arg	Ser	Thr	Thr	Thr	Ser	Ala	Gln	Ser	Thr	Glu	Pro	Asp	Ser	Ala		
			265					270					275				
acc	aac	acc	tca	tat	ctg	tca	cgt	cgt	ctc	gac	agc	ctg	gaa	cgc	agt	979	
Thr	Asn	Thr	Ser	Tyr	Leu	Ser	Arg	Arg	Leu	Asp	Ser	Leu	Glu	Arg	Ser		
			280				285					290					
gcg	cag	cat	att	gat	ctc	aat	acc	cag	tgc	gac	aac	ctc	gat	gat	ctt	1027	
Ala	Gln	His	Ile	Asp	Leu	Asn	Thr	Gln	Cys	Asp	Asn	Leu	Asp	Asp	Leu		
			295			300					305						
cgt	gaa	ctc	acc	aac	aat	gac	acg	cgt	gat	cac	acc	ggc	tcc	gtc	att	1075	
Arg	Glu	Leu	Thr	Asn	Asn	Asp	Thr	Arg	Asp	His	Thr	Gly	Ser	Val	Ile		
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tcc	att	gcc	gat	caa	ctc	aca	gac	atc	acc	aat	gaa	atc	aat	gaa	tta	1123	
Ser	Ile	Ala	Asp	Gln	Leu	Thr	Asp	Ile	Thr	Asn	Glu	Ile	Asn	Glu	Leu		
				330				335						340			
cgc	gat	agc	act	ttt	gcc	acc	aga	gac	agt	gcc	caa	caa	gca	cag	gat	1171	
Arg	Asp	Ser	Thr	Phe	Ala	Thr	Arg	Asp	Ser	Ala	Gln	Gln	Ala	Gln	Asp		

345	350	355	
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Gln Val Ile Ala Gln Arg Glu Glu Leu Gln Arg Ala Lys Glu Ala Arg			
360	365	370	
cta gaa gaa cag cga ctc gcc aaa gaa gca gaa gag ggc gct cgc aac			1267
Leu Glu Glu Gln Arg Leu Ala Lys Glu Ala Glu Glu Gly Ala Arg Asn			
375	380	385	
gca gca att cag gaa cgt gac gcg gcc gaa gca gca ctg cgt gaa gca			1315
Ala Ala Ile Gln Glu Arg Asp Ala Ala Glu Ala Ala Leu Arg Glu Ala			
390	395	400	405
caa gac ctc ctc agt cgc ctc gat gac aca ggc aac gca acc agt gat			1363
Gln Asp Leu Leu Ser Arg Leu Asp Asp Thr Gly Asn Ala Thr Ser Asp			
410	415	420	
gac aca gca gcg cta gta gac ggt ctt ctc aat aac taacaatcag			1409
Asp Thr Ala Ala Leu Val Asp Gly Leu Leu Asn Asn			
425	430		
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Ala Thr Leu Thr Leu Thr Leu Cys Thr Ser Ala Ala Gly Val Val His			
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Ala Ala Gln Gln Ser Ile Ser Gly Pro Glu Ser Ser Cys Ala Phe Asn			
35	40	45	
Gln Gln Arg Trp Asp Asp Ser Lys Val Lys Leu Asp Asp Thr Ile Ala			
50	55	60	
Thr Ala Lys Asn Ser Leu Val Gln Thr Gly Glu Leu His Arg Asn Glu			
65	70	75	80
Gln Asp Leu Leu Thr Gly Tyr Leu Phe Gln Gln Pro His Ser Ser Asn			
85	90	95	
Tyr Leu Ala Leu Asn Asn Ala Tyr Ala Asp Ala Val Ala Ile Lys Asp			
100	105	110	
Ser Phe Val Arg Pro Thr Cys Asp Gly Ser Lys Glu Ser Lys Ile Ala			
115	120	125	
Ser Glu His Ala Val Ser Glu Val Val Gly Ala Val Asn Val Leu Ala			
130	135	140	
Arg Ala Gln Lys Ala Leu Gln Ile Asn Ser Asp Thr Tyr Glu Gln Gln			
145	150	155	160

Arg Arg Cys Asp Ala Leu Arg Leu Ala Ser Arg Asp Glu Ser Asp Val
 165 170 175
 Leu Met Arg Ile Asp Arg Thr Met Leu Gln Leu Arg Arg Thr Leu Ala
 180 185 190
 Asp Ile Asp Gln Ala Ser Thr Asp Ile Arg Asp Ile Arg Ala Gln Thr
 195 200 205
 Thr Ser Phe Glu Arg Asp Leu Ala Arg Glu Gln Lys Glu Ala Asp Ala
 210 215 220
 Ala Ala Arg Ala Gln Ala Val Asp Thr Ser Thr Thr Pro Thr Ser Ser
 225 230 235 240
 Thr Glu Asp Arg Val Asn Asp Ile Leu Lys Glu Ser Arg Thr Asp His
 245 250 255
 Ser Gly Asp Ser Tyr Thr Arg Ser Thr Thr Thr Ser Ala Gln Ser Thr
 260 265 270
 Glu Pro Asp Ser Ala Thr Asn Thr Ser Tyr Leu Ser Arg Arg Leu Asp
 275 280 285
 Ser Leu Glu Arg Ser Ala Gln His Ile Asp Leu Asn Thr Gln Cys Asp
 290 295 300
 Asn Leu Asp Asp Leu Arg Glu Leu Thr Asn Asn Asp Thr Arg Asp His
 305 310 315 320
 Thr Gly Ser Val Ile Ser Ile Ala Asp Gln Leu Thr Asp Ile Thr Asn
 325 330 335
 Glu Ile Asn Glu Leu Arg Asp Ser Thr Phe Ala Thr Arg Asp Ser Ala
 340 345 350
 Gln Gln Ala Gln Asp Gln Val Ile Ala Gln Arg Glu Glu Leu Gln Arg
 355 360 365
 Ala Lys Glu Ala Arg Leu Glu Glu Gln Arg Leu Ala Lys Glu Ala Glu
 370 375 380
 Glu Gly Ala Arg Asn Ala Ala Ile Gln Glu Arg Asp Ala Ala Glu Ala
 385 390 395 400
 Ala Leu Arg Glu Ala Gln Asp Leu Leu Ser Arg Leu Asp Asp Thr Gly
 405 410 415
 Asn Ala Thr Ser Asp Asp Thr Ala Ala Leu Val Asp Gly Leu Leu Asn
 420 425 430

Asn

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<211> 903

<212> DNA

<213> Corynebacterium glutamicum

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 <223> RXA00020

<400> 1555

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                                         Met Thr Val Thr Thr
                                         1           5

gca caa cga atc gct gac gaa ttt caa cgt ggc att agt atc ggc ccg 163
Ala Gln Arg Ile Ala Asp Glu Phe Gln Arg Gly Ile Ser Ile Gly Pro
                        10                15                20

tgg gat ctg tgc gaa gta cca gca ggc gat gac tat tta gag cac acc 211
Trp Asp Leu Cys Glu Val Pro Ala Gly Asp Asp Tyr Leu Glu His Thr
                        25                30                35

acc aag gtc agg cga cgc cac agc acg gct gta gag att cac act gac 259
Thr Lys Val Arg Arg Arg His Ser Thr Ala Val Glu Ile His Thr Asp
                        40                45                50

tct ttg atc att tgt gcg cct gaa ggc agt acg tac agc cac aac cgc 307
Ser Leu Ile Ile Cys Ala Pro Glu Gly Ser Thr Tyr Ser His Asn Arg
                        55                60                65

act aag gct ggt ctt gcg tcc acg ggc aca gtc act gtg cca gtg aag 355
Thr Lys Ala Gly Leu Ala Ser Thr Gly Thr Val Thr Val Pro Val Lys
                        70                75                80                85

ggg ctt tct gag cct gtg aag ctt agt ctc aat ctt ctt gct gat tat 403
Gly Leu Ser Glu Pro Val Lys Leu Ser Leu Asn Leu Leu Ala Asp Tyr
                        90                95                100

gga aac tcc ttt gac act gtg cac gac gat ctg tgg caa cga gag ctg 451
Gly Asn Ser Phe Asp Thr Val His Asp Asp Leu Trp Gln Arg Glu Leu
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cgt gag cag acg cgg ggg cag tta ctc aca ctt aat gca gtc tcc ggt 499
Arg Glu Gln Thr Arg Gly Gln Leu Leu Thr Leu Asn Ala Val Ser Gly
                        120                125                130

ctt ggg gat gac agc gtg gcg att atg ggc acg cca tgg ggc gat ggt 547
Leu Gly Asp Asp Ser Val Ala Ile Met Gly Thr Pro Trp Gly Asp Gly
                        135                140                145

ctc acc ggg gag gcc aac acc att aaa ggt cgt gag cat ttt gtc atg 595
Leu Thr Gly Glu Ala Asn Thr Ile Lys Gly Arg Glu His Phe Val Met
                        150                155                160                165

tgg gct gca ggg tgc cgc ttt gaa gac ggt tat ggt cgt cac gca ctt 643
Trp Ala Ala Gly Cys Arg Phe Glu Asp Gly Tyr Gly Arg His Ala Leu
                        170                175                180

cga gag gat cgc cat gtg cga cac cag gca cgt gcg ggt gag gat tcc 691
Arg Glu Asp Arg His Val Arg His Gln Ala Arg Ala Gly Glu Asp Ser
                        185                190                195

act gca cat cac ggt tgg ttg ctt aaa ggc aca gtg ttc ggg aaa gaa 739
Thr Ala His His Gly Trp Leu Leu Lys Gly Thr Val Phe Gly Lys Glu

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ctc acc ggt gat gct gtg acg gca gcc atg aca gtt ttt agt gat gtg			787
Leu Thr Gly Asp Ala Val Thr Ala Ala Met Thr Val Phe Ser Asp Val			
215	220	225	
gtg gtc act gtc gat gag ggg cgt atc cct ggc atg aaa tca gga caa			835
Val Val Thr Val Asp Glu Gly Arg Ile Pro Gly Met Lys Ser Gly Gln			
230	235	240	245
ccg ttt tct atg gca acc cgt tta cgc gca tca tct gcg cct gtg			880
Pro Phe Ser Met Ala Thr Arg Leu Arg Ala Ser Ser Ala Pro Val			
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Tyr Leu Glu His Thr Thr Lys Val Arg Arg Arg His Ser Thr Ala Val	
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Glu Ile His Thr Asp Ser Leu Ile Ile Cys Ala Pro Glu Gly Ser Thr	
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Tyr Ser His Asn Arg Thr Lys Ala Gly Leu Ala Ser Thr Gly Thr Val	
65 70 75 80	

Thr Val Pro Val Lys Gly Leu Ser Glu Pro Val Lys Leu Ser Leu Asn	
85 90 95	

Leu Leu Ala Asp Tyr Gly Asn Ser Phe Asp Thr Val His Asp Asp Leu	
100 105 110	

Trp Gln Arg Glu Leu Arg Glu Gln Thr Arg Gly Gln Leu Leu Thr Leu	
115 120 125	

Asn Ala Val Ser Gly Leu Gly Asp Asp Ser Val Ala Ile Met Gly Thr	
130 135 140	

Pro Trp Gly Asp Gly Leu Thr Gly Glu Ala Asn Thr Ile Lys Gly Arg	
145 150 155 160	

Glu His Phe Val Met Trp Ala Ala Gly Cys Arg Phe Glu Asp Gly Tyr	
165 170 175	

Gly Arg His Ala Leu Arg Glu Asp Arg His Val Arg His Gln Ala Arg	
180 185 190	

Ala Gly Glu Asp Ser Thr Ala His His Gly Trp Leu Leu Lys Gly Thr	
195 200 205	

Val Phe Gly Lys Glu Leu Thr Gly Asp Ala Val Thr Ala Ala Met Thr
 210 215 220

Val Phe Ser Asp Val Val Val Thr Val Asp Glu Gly Arg Ile Pro Gly
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Met Lys Ser Gly Gln Pro Phe Ser Met Ala Thr Arg Leu Arg Ala Ser
 245 250 255

Ser Ala Pro Val
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 <223> RXA00021

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 Met Ser Asp Thr Thr
 1 5

gac agc cac gac cca gca acc tcc cct aca gtc gat tca gcc gca tcc 163
 Asp Ser His Asp Pro Ala Thr Ser Pro Thr Val Asp Ser Ala Ala Ser
 10 15 20

ggt act tct gac ccc aac cag caa ccc aag aag aaa ttc acc atc att 211
 Gly Thr Ser Asp Pro Asn Gln Gln Pro Lys Lys Lys Phe Thr Ile Ile
 25 30 35

aag cag gtg aac atg att gcg cgt act gcc att gat gac tgc att aat 259
 Lys Gln Val Asn Met Ile Ala Arg Thr Ala Ile Asp Asp Cys Ile Asn
 40 45 50

cga cta ggc cca gat gtt gtc acc atg tcc agc gaa gac att gct gat 307
 Arg Leu Gly Pro Asp Val Val Thr Met Ser Ser Glu Asp Ile Ala Asp
 55 60 65

caa gtg gtc aac tcc att aac gtt gct att gcc aga gaa aac aca cgt 355
 Gln Val Val Asn Ser Ile Asn Val Ala Ile Ala Arg Glu Asn Thr Arg
 70 75 80 85

gcc caa gat gcc aat gct gcg gtg cgt tac aca cct atc ttt aag ctc 403
 Ala Gln Asp Ala Asn Ala Ala Val Arg Tyr Thr Pro Ile Phe Lys Leu
 90 95 100

gat ttc tcc cat gtc gct gtc ctt atg cgc aga ctg cat gtg att atc 451
 Asp Phe Ser His Val Ala Val Leu Met Arg Arg Leu His Val Ile Ile
 105 110 115

aac atc gcg cca tcg cat aac tct gat cct gac agc gat atg ttg gct 499
 Asn Ile Ala Pro Ser His Asn Ser Asp Pro Asp Ser Asp Met Leu Ala

120	125	130	
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tca gag gct gaa ata cgc cgc gta gcc cgt gaa tac tgc cct gac ctc Ser Glu Ala Glu Ile Arg Arg Val Ala Arg Glu Tyr Cys Pro Asp Leu 150 155 160 165			595
acc tca gcg cag ttt aga gaa ctg cag atg gca ctc tca gat gct gca Thr Ser Ala Gln Phe Arg Glu Leu Gln Met Ala Leu Ser Asp Ala Ala 170 175 180			643
cct cgt aaa gtc cgc cac aag cag cgt gac ttg att ccc gtg aaa aac Pro Arg Lys Val Arg His Lys Gln Arg Asp Leu Ile Pro Val Lys Asn 185 190 195			691
ggc atc ttt aat tac tcg act aaa caa cta gaa ccg ttt tct caa gag Gly Ile Phe Asn Tyr Ser Thr Lys Gln Leu Glu Pro Phe Ser Gln Glu 200 205 210			739
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aac cct gtc atc act cat ccc cag gat ggc tct gtc tgg gat gtt gaa Asn Pro Val Ile Thr His Pro Gln Asp Gly Ser Val Trp Asp Val Glu 230 235 240 245			835
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aag tca gca aac ctt aaa gcg att gtc acc aat gac gtc atc tcc att Lys Ser Ala Asn Leu Lys Ala Ile Val Thr Asn Asp Val Ile Ser Ile 345 350 355			1171
aac cgc aag cac aaa acc atg ctc agc tat cag ttt tat ggc ttt atg Asn Arg Lys His Lys Thr Met Leu Ser Tyr Gln Phe Tyr Gly Phe Met 360 365 370			1219

gtg cag tgt att aac ggc ttc ccc aag gtc aaa gac cag tcg gag tca	1267
Val Gln Cys Ile Asn Gly Phe Pro Lys Val Lys Asp Gln Ser Glu Ser	
375 380 385	
ttt ttc agg cgc caa ctc ttt gtg ccg ttt gag aaa agc ttc acc ggt	1315
Phe Phe Arg Arg Gln Leu Phe Val Pro Phe Glu Lys Ser Phe Thr Gly	
390 395 400 405	
gcc gag cgc aag tac atc aaa gac gac tac atg tcg cgc act gat gtc	1363
Ala Glu Arg Lys Tyr Ile Lys Asp Asp Tyr Met Ser Arg Thr Asp Val	
410 415 420	
ctc gaa tat gta ctg cac cgc gta ctg cat atg aac tac gac aat ctc	1411
Leu Glu Tyr Val Leu His Arg Val Leu His Met Asn Tyr Asp Asn Leu	
425 430 435	
tcc acc cct gct gca gct ctc gct gtg ctg gat gaa tac aaa gag ttt	1459
Ser Thr Pro Ala Ala Ala Leu Ala Val Leu Asp Glu Tyr Lys Glu Phe	
440 445 450	
gtc gat cct gtg cgc gca ttc tgg aat gaa ttc agc gat caa ttt gtc	1507
Val Asp Pro Val Arg Ala Phe Trp Asn Glu Phe Ser Asp Gln Phe Val	
455 460 465	
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Trp Asp Leu Leu Pro Leu Gln Phe Leu Tyr Glu Phe Tyr Arg Lys Trp	
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Phe Asp Arg Asp Ser Pro Ser Gly Ser Val Leu Gly Lys Arg Ser Phe	
490 495 500	
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Ile Gln Lys Ile Thr Thr Ile Ala Val Asp Ser Gly Gln Trp Glu Tyr	
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ccg ctg aca gca cag cgt ccc ggt ggc gat atg gcc gtt cct gag cca	1699
Pro Leu Thr Ala Gln Arg Pro Gly Gly Asp Met Ala Val Pro Glu Pro	
520 525 530	
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Leu Val Ile Asp Tyr Asp Leu Thr Glu Trp Gln Asn Ala Thr Val Pro	
535 540 545	
aaa ggt cac gtc aac aag ggg ctc cct cta cca ctc aag gct aat tat	1795
Lys Gly His Val Asn Lys Gly Leu Pro Leu Pro Leu Lys Ala Asn Tyr	
550 555 560 565	
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Arg Gly Leu Leu Arg Lys Pro Leu Thr Thr Pro Ala Thr Pro Ala	
570 575 580	
gcg ccg gtc aac ccc aca cca ccc acc cct taacaaccac aagaaagatt	1893
Ala Pro Val Asn Pro Thr Pro Pro Thr Pro	
585 590	
tat	1896

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1558

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Lys Phe Thr Ile Ile Lys Gln Val Asn Met Ile Ala Arg Thr Ala Ile
35 40 45

Asp Asp Cys Ile Asn Arg Leu Gly Pro Asp Val Val Thr Met Ser Ser
50 55 60

Glu Asp Ile Ala Asp Gln Val Val Asn Ser Ile Asn Val Ala Ile Ala
65 70 75 80

Arg Glu Asn Thr Arg Ala Gln Asp Ala Asn Ala Ala Val Arg Tyr Thr
85 90 95

Pro Ile Phe Lys Leu Asp Phe Ser His Val Ala Val Leu Met Arg Arg
100 105 110

Leu His Val Ile Ile Asn Ile Ala Pro Ser His Asn Ser Asp Pro Asp
115 120 125

Ser Asp Met Leu Ala Ile Tyr Asp Pro Asn Pro Arg Ser Glu His Tyr
130 135 140

Gly Ile Tyr Arg Thr Ser Glu Ala Glu Ile Arg Arg Val Ala Arg Glu
145 150 155 160

Tyr Cys Pro Asp Leu Thr Ser Ala Gln Phe Arg Glu Leu Gln Met Ala
165 170 175

Leu Ser Asp Ala Ala Pro Arg Lys Val Arg His Lys Gln Arg Asp Leu
180 185 190

Ile Pro Val Lys Asn Gly Ile Phe Asn Tyr Ser Thr Lys Gln Leu Glu
195 200 205

Pro Phe Ser Gln Glu Phe Val Phe Leu Ala Lys Ser Ala Val Asn Tyr
210 215 220

Asn Pro Asn Ala Gln Asn Pro Val Ile Thr His Pro Gln Asp Gly Ser
225 230 235 240

Val Trp Asp Val Glu Ser Trp Met Asn Asp Leu Ser Asp Asp Pro Glu
245 250 255

Val Val Asn Leu Leu Trp Glu Ile Ile Gly Ala Ile Val Arg Pro Tyr
260 265 270

Val Ser Trp Asn Lys Ser Ala Trp Phe Tyr Ser Glu Ala Gly Asn Asn
275 280 285

Gly Lys Gly Thr Leu Val Glu Leu Met Arg Asn Ile Leu Gly Ala Glu
290 295 300

Ala Tyr Thr Ser Ile Gln Leu Ser Asp Phe Ser Lys Glu Phe His Leu
 305 310 315 320
 Glu Ser Leu Thr Arg Ala Gln Ala Ile Leu Val Asp Glu Asn Asp Val
 325 330 335
 Gly Ala Phe Leu Glu Lys Ser Ala Asn Leu Lys Ala Ile Val Thr Asn
 340 345 350
 Asp Val Ile Ser Ile Asn Arg Lys His Lys Thr Met Leu Ser Tyr Gln
 355 360 365
 Phe Tyr Gly Phe Met Val Gln Cys Ile Asn Gly Phe Pro Lys Val Lys
 370 375 380
 Asp Gln Ser Glu Ser Phe Phe Arg Arg Gln Leu Phe Val Pro Phe Glu
 385 390 395 400
 Lys Ser Phe Thr Gly Ala Glu Arg Lys Tyr Ile Lys Asp Asp Tyr Met
 405 410 415
 Ser Arg Thr Asp Val Leu Glu Tyr Val Leu His Arg Val Leu His Met
 420 425 430
 Asn Tyr Asp Asn Leu Ser Thr Pro Ala Ala Ala Leu Ala Val Leu Asp
 435 440 445
 Glu Tyr Lys Glu Phe Val Asp Pro Val Arg Ala Phe Trp Asn Glu Phe
 450 455 460
 Ser Asp Gln Phe Val Trp Asp Leu Leu Pro Leu Gln Phe Leu Tyr Glu
 465 470 475 480
 Phe Tyr Arg Lys Trp Phe Asp Arg Asp Ser Pro Ser Gly Ser Val Leu
 485 490 495
 Gly Lys Arg Ser Phe Ile Gln Lys Ile Thr Thr Ile Ala Val Asp Ser
 500 505 510
 Gly Gln Trp Glu Tyr Pro Leu Thr Ala Gln Arg Pro Gly Gly Asp Met
 515 520 525
 Ala Val Pro Glu Pro Leu Val Ile Asp Tyr Asp Leu Thr Glu Trp Gln
 530 535 540
 Asn Ala Thr Val Pro Lys Gly His Val Asn Lys Gly Leu Pro Leu Pro
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<210> 1559

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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1537)

<223> RXA00025

<400> 1559

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Met Ala Trp Met Asn	
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gta tcc gtg att gtt cca ggc tct gat gag gaa cta ttt gta aaa ggc	163
Val Ser Val Ile Val Pro Gly Ser Asp Glu Glu Leu Phe Val Lys Gly	
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ctg ttc acc ggt gaa ggc cta acc tgg ttg act acg aat ctc ggg gca	211
Leu Phe Thr Gly Glu Gly Leu Thr Trp Leu Thr Thr Asn Leu Gly Ala	
25 30 35	
aac tac atc ggg ttc ccg ccg ttg ctc acc gtg ttg cca att ctg ttg	259
Asn Tyr Ile Gly Phe Pro Pro Leu Leu Thr Val Leu Pro Ile Leu Leu	
40 45 50	
gca gtg ggt gtt gct gaa cgt tcc ggc atg ttg gct gcg ctg att agg	307
Ala Val Gly Val Ala Glu Arg Ser Gly Met Leu Ala Ala Leu Ile Arg	
55 60 65	
aaa ctt ttt ggt tcg gcg aaa aag atc gtt ttg cca tat gca gtc ggt	355
Lys Leu Phe Gly Ser Ala Lys Lys Ile Val Leu Pro Tyr Ala Val Gly	
70 75 80 85	
gtg att ggc gtg acc gcg tcg atc atg gcg gac gct gcc ttc gtg gtg	403
Val Ile Gly Val Thr Ala Ser Ile Met Ala Asp Ala Ala Phe Val Val	
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gtg cca cct ttg gcc gcg atg gtg ttt aaa gct gct ggt cgg cac cct	451
Val Pro Pro Leu Ala Ala Met Val Phe Lys Ala Ala Gly Arg His Pro	
105 110 115	
gtg gct ggg cta ttg ggt tcg ttt gca gct gtg ggt gca gga tat tcc	499
Val Ala Gly Leu Leu Gly Ser Phe Ala Ala Val Gly Ala Gly Tyr Ser	
120 125 130	
aca gcg att gtg ccc acc agc ctt gat gca ctt ttt gcg gga att acc	547
Thr Ala Ile Val Pro Thr Ser Leu Asp Ala Leu Phe Ala Gly Ile Thr	
135 140 145	
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Asn Ala Val Met Glu Thr Leu Pro Gly Ile Ala Thr Thr Glu Val Asn	
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ccg gtt tct aac tat tac ttc aat att gca tcc tcg att gtg ttg ggt	643
Pro Val Ser Asn Tyr Tyr Phe Asn Ile Ala Ser Ser Ile Val Leu Gly	
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ctg tta tgt ggt ttc ctc att gat aag gtg ctg gaa cct cgg atg tgg	691
Leu Leu Cys Gly Phe Leu Ile Asp Lys Val Leu Glu Pro Arg Met Trp	
185 190 195	
cgt cag aaa atc gct acg gag tat gca gaa agc att gaa ccc acc agc	739

Arg	Gln	Lys	Ile	Ala	Thr	Glu	Tyr	Ala	Glu	Ser	Ile	Glu	Pro	Thr	Ser		
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Ala	Ala	Asp	Asp	Glu	Glu	Ile	Ser	Ala	Thr	Leu	Thr	Ala	Gln	Glu	Asn		
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cgc	gcg	ctg	aca	att	tcc	atg	tgg	acc	acc	ctg	gcg	acg	gcc	atc	atc	835	
Arg	Ala	Leu	Thr	Ile	Ser	Met	Trp	Thr	Thr	Leu	Ala	Thr	Ala	Ile	Ile		
230					235					240					245		
gtg	ctg	gtt	gtg	gtg	ctg	att	ccg	gga	tcc	cca	tgg	aga	aat	gag	gat	883	
Val	Leu	Val	Val	Val	Leu	Ile	Pro	Gly	Ser	Pro	Trp	Arg	Asn	Glu	Asp		
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ggg	gga	ttc	ttg	cct	acc	tcg	cca	ctg	ctg	agc	tct	gtg	gtg	ttt	att	931	
Gly	Gly	Phe	Leu	Pro	Thr	Ser	Pro	Leu	Leu	Ser	Ser	Val	Val	Phe	Ile		
			265					270						275			
gta	ttt	ttg	ttt	ttc	atg	gtg	atg	ggc	ctg	gcc	tac	ggc	atg	gtg	gtg	979	
Val	Phe	Leu	Phe	Phe	Met	Val	Met	Gly	Leu	Ala	Tyr	Gly	Met	Val	Val		
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ggc	acg	atc	aag	aac	atg	gat	gat	gtc	gtg	aac	atg	atg	ggc	gaa	gca	1027	
Gly	Thr	Ile	Lys	Asn	Met	Asp	Asp	Val	Val	Asn	Met	Met	Gly	Glu	Ala		
		295				300					305						
atc	aag	gac	atg	att	ggg	ttc	ttg	gtt	ttg	gcc	ttc	att	ttg	gga	cag	1075	
Ile	Lys	Asp	Met	Ile	Gly	Phe	Leu	Val	Leu	Ala	Phe	Ile	Leu	Gly	Gln		
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ttt	gtg	gcg	ctg	ttt	aac	tgg	acg	ggc	atc	ggg	acc	tgg	act	gct	gtt	1123	
Phe	Val	Ala	Leu	Phe	Asn	Trp	Thr	Gly	Ile	Gly	Thr	Trp	Thr	Ala	Val		
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cag	ggg	gct	gcg	gga	ttg	gaa	gcg	atc	ggg	ctt	acc	gga	ttc	cct	gcg	1171	
Gln	Gly	Ala	Ala	Gly	Leu	Glu	Ala	Ile	Gly	Leu	Thr	Gly	Phe	Pro	Ala		
			345					350					355				
atc	att	gca	ttt	att	att	ttg	gcg	tca	tgt	ttg	aac	ctg	ctg	att	att	1219	
Ile	Ile	Ala	Phe	Ile	Ile	Leu	Ala	Ser	Cys	Leu	Asn	Leu	Leu	Ile	Ile		
		360					365					370					
tcc	ggc	tct	gcg	atg	tgg	acg	ctg	atg	gct	gcg	gtg	ttc	gtc	ccg	atg	1267	
Ser	Gly	Ser	Ala	Met	Trp	Thr	Leu	Met	Ala	Ala	Val	Phe	Val	Pro	Met		
		375				380					385						
ttc	gct	ctg	ctt	ggc	tat	gaa	cca	tca	ttc	att	cag	gca	gca	ttc	cgc	1315	
Phe	Ala	Leu	Leu	Gly	Tyr	Glu	Pro	Ser	Phe	Ile	Gln	Ala	Ala	Phe	Arg		
390					395					400					405		
gtg	ggg	gac	tcg	gca	act	cag	gtg	atc	aca	ccg	ctg	aat	ccg	tac	atg	1363	
Val	Gly	Asp	Ser	Ala	Thr	Gln	Val	Ile	Thr	Pro	Leu	Asn	Pro	Tyr	Met		
				410					415					420			
att	gtg	atc	ctc	ggg	ttg	ctc	cgt	cga	tac	gaa	ccg	gat	gca	ggg	tta	1411	
Ile	Val	Ile	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Glu	Pro	Asp	Ala	Gly	Leu		
			425				430						435				
ggc	acc	ttg	atg	tca	agg	ctt	atc	cca	ttt	gtg	atc	cct	ttc	tgg	cta	1459	
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<212> PRT
<213> Corynebacterium glutamicum
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			20					25					30			
Thr	Asn	Leu	Gly	Ala	Asn	Tyr	Ile	Gly	Phe	Pro	Pro	Leu	Leu	Thr	Val	
		35					40					45				
Leu	Pro	Ile	Leu	Leu	Ala	Val	Gly	Val	Ala	Glu	Arg	Ser	Gly	Met	Leu	
	50					55					60					
Ala	Ala	Leu	Ile	Arg	Lys	Leu	Phe	Gly	Ser	Ala	Lys	Lys	Ile	Val	Leu	
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Pro	Tyr	Ala	Val	Gly	Val	Ile	Gly	Val	Thr	Ala	Ser	Ile	Met	Ala	Asp	
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Ala	Gly	Arg	His	Pro	Val	Ala	Gly	Leu	Leu	Gly	Ser	Phe	Ala	Ala	Val	
		115					120					125				
Gly	Ala	Gly	Tyr	Ser	Thr	Ala	Ile	Val	Pro	Thr	Ser	Leu	Asp	Ala	Leu	
	130					135					140					
Phe	Ala	Gly	Ile	Thr	Asn	Ala	Val	Met	Glu	Thr	Leu	Pro	Gly	Ile	Ala	
145					150					155					160	
Thr	Thr	Glu	Val	Asn	Pro	Val	Ser	Asn	Tyr	Tyr	Phe	Asn	Ile	Ala	Ser	
				165					170					175		
Ser	Ile	Val	Leu	Gly	Leu	Leu	Cys	Gly	Phe	Leu	Ile	Asp	Lys	Val	Leu	
			180					185					190			
Glu	Pro	Arg	Met	Trp	Arg	Gln	Lys	Ile	Ala	Thr	Glu	Tyr	Ala	Glu	Ser	
		195					200					205				
Ile	Glu	Pro	Thr	Ser	Ala	Ala	Asp	Asp	Glu	Glu	Ile	Ser	Ala	Thr	Leu	
	210					215					220					

Thr Ala Gln Glu Asn Arg Ala Leu Thr Ile Ser Met Trp Thr Thr Leu
 225 230 235 240
 Ala Thr Ala Ile Ile Val Leu Val Val Val Leu Ile Pro Gly Ser Pro
 245 250 255
 Trp Arg Asn Glu Asp Gly Gly Phe Leu Pro Thr Ser Pro Leu Leu Ser
 260 265 270
 Ser Val Val Phe Ile Val Phe Leu Phe Phe Met Val Met Gly Leu Ala
 275 280 285
 Tyr Gly Met Val Val Gly Thr Ile Lys Asn Met Asp Asp Val Val Asn
 290 295 300
 Met Met Gly Glu Ala Ile Lys Asp Met Ile Gly Phe Leu Val Leu Ala
 305 310 315 320
 Phe Ile Leu Gly Gln Phe Val Ala Leu Phe Asn Trp Thr Gly Ile Gly
 325 330 335
 Thr Trp Thr Ala Val Gln Gly Ala Ala Gly Leu Glu Ala Ile Gly Leu
 340 345 350
 Thr Gly Phe Pro Ala Ile Ile Ala Phe Ile Ile Leu Ala Ser Cys Leu
 355 360 365
 Asn Leu Leu Ile Ile Ser Gly Ser Ala Met Trp Thr Leu Met Ala Ala
 370 375 380
 Val Phe Val Pro Met Phe Ala Leu Leu Gly Tyr Glu Pro Ser Phe Ile
 385 390 395 400
 Gln Ala Ala Phe Arg Val Gly Asp Ser Ala Thr Gln Val Ile Thr Pro
 405 410 415
 Leu Asn Pro Tyr Met Ile Val Ile Leu Gly Leu Leu Arg Arg Tyr Glu
 420 425 430
 Pro Asp Ala Gly Leu Gly Thr Leu Met Ser Arg Leu Ile Pro Phe Val
 435 440 445
 Ile Pro Phe Trp Leu Ala Trp Ala Thr Leu Leu Ala Ile Trp Phe Tyr
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 Ala Asp Leu Pro Leu Gly Pro Gly Ser Ala Ile Phe Leu Glu Gly
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<210> 1561

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA00031

<400> 1561

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Val Ala Ala Gly Gln
1 5

tgg cta gct ggc aac atc ggc gaa att gat cat gtg ctg tgt tca gat 163
Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His Val Leu Cys Ser Asp
10 15 20

gcc acc cgc aca caa tta acg tgg gaa cgc gtc cag ctt ggt ggc gca 211
Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val Gln Leu Gly Gly Ala
25 30 35

acc gcc aaa ggc tct agc ttc cac aat gac atc tat gaa aac caa gtg 259
Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile Tyr Glu Asn Gln Val
40 45 50

tct gaa ttt aaa cat tta ata aca ggg ctc cca gat gta gtt ggt acc 307
Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro Asp Val Val Gly Thr
55 60 65

gcc cta ctc atc ggg cac tgg cca ggc gtg gaa gaa cta gcc cat tat 355
Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu Glu Leu Ala His Tyr
70 75 80 85

ttt ggc atc cgc gat gaa cat ccc ggt tgg gat cag atg gaa gaa aag 403
Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp Gln Met Glu Glu Lys
90 95 100

ttt ccc acc agc gcc att gcg gtg ttg gaa ttt aac acc cct tgg tca 451
Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe Asn Thr Pro Trp Ser
105 110 115

aaa ctt gag aga aac tct gct cgg ttg aca gat ttt gtc att cca cgg 499
Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp Phe Val Ile Pro Arg
120 125 130

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<210> 1562

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 1562

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20 25 30

Gln Leu Gly Gly Ala Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile
35 40 45

Tyr Glu Asn Gln Val Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro
50 55 60

Asp Val Val Gly Thr Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu

65		70		75		80									
Glu	Leu	Ala	His	Tyr	Phe	Gly	Ile	Arg	Asp	Glu	His	Pro	Gly	Trp	Asp
			85						90					95	
Gln	Met	Glu	Glu	Lys	Phe	Pro	Thr	Ser	Ala	Ile	Ala	Val	Leu	Glu	Phe
		100						105					110		
Asn	Thr	Pro	Trp	Ser	Lys	Leu	Glu	Arg	Asn	Ser	Ala	Arg	Leu	Thr	Asp
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	130														

<210> 1563
 <211> 810
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(787)
 <223> RXA00049

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 Met Pro Thr Pro Ser
 1 5
 cag cac aag gac gct tca aca gca caa acc gac aac cag gta cca act 163
 Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp Asn Gln Val Pro Thr
 10 15 20
 ggc cgc cgt gca caa aaa cgc gaa caa acc cgc gcg cgc ctg atc act 211
 Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg Ala Arg Leu Ile Thr
 25 30 35
 tcc gct cgc aca ctc atg gca gaa cgg ggt gtc gac aat gta gga ata 259
 Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val Asp Asn Val Gly Ile
 40 45 50
 gct gaa atc acc gaa ggc gca aac atc gga acg gga acc ttc tac aac 307
 Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr Gly Thr Phe Tyr Asn
 55 60 65
 tac ttc cca gac cgt gaa caa cta ctc caa gct gtc gca gaa gat gcc 355
 Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala Val Ala Glu Asp Ala
 70 75 80 85
 ttt gaa tcc gtg gga att gcc ctc gac cag gtg cta acc aaa tta gac 403
 Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val Leu Thr Lys Leu Asp
 90 95 100
 gat ccg gct gaa gta ttt gca ggg tcg ctt cga cat cta gta cgg cac 451
 Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg His Leu Val Arg His
 105 110 115
 tcg tta gaa gat cgg att tgg ggc gga ttt ttc ata caa atg ggt gct 499

Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe Ile Gln Met Gly Ala
 120 125 130

gct cat ccc gta ctc atg cgc atc cta gga ccc cgc gca cgc cga gat 547
 Ala His Pro Val Leu Met Arg Ile Leu Gly Pro Arg Ala Arg Arg Asp
 135 140 145

cta ctt cat ggt tta gaa act ggc cga ttc acc atc gaa gat ctg gac 595
 Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr Ile Glu Asp Leu Asp
 150 155 160 165

cta gca acc aca tgc act ttt ggt tca ctc atc gca gcg atc caa atg 643
 Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile Ala Ala Ile Gln Met
 170 175 180

gcg ctt tct gca gat caa gat tcc aac gat gac aaa gat cag att ttc 691
 Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp Lys Asp Gln Ile Phe
 185 190 195

gca gcc gcg atg ctc cgg atg gtg ggt gtt caa gca gca gaa gcc cgg 739
 Ala Ala Ala Met Leu Arg Met Val Gly Val Gln Ala Ala Glu Ala Arg
 200 205 210

gag atc gct tcg cgt cca ctc ccc gaa ata tcc cca gtc aaa ccg cag 787
 Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser Pro Val Lys Pro Gln
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<210> 1564

<211> 229

<212> PRT

<213> Corynebacterium glutamicum

<400> 1564

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Ala Arg Leu Ile Thr Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val
 35 40 45

Asp Asn Val Gly Ile Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr
 50 55 60

Gly Thr Phe Tyr Asn Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala
 65 70 75 80

Val Ala Glu Asp Ala Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val
 85 90 95

Leu Thr Lys Leu Asp Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg
 100 105 110

His Leu Val Arg His Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe
 115 120 125

Ile Gln Met Gly Ala Ala His Pro Val Leu Met Arg Ile Leu Gly Pro

gaa gat caa gta gaa aca ctc agt tgg gaa gac cag gaa ttg gta ttg 451
 Glu Asp Gln Val Glu Thr Leu Ser Trp Glu Asp Gln Glu Leu Val Leu
 105 110 115
 cca gta tct cac tac aag gag gat tca agc cgc cca gaa att aca agc 499
 Pro Val Ser His Tyr Lys Glu Asp Ser Ser Arg Pro Glu Ile Thr Ser
 120 125 130
 att gag gct ttt ctt tca gta acg gat tac ggt tca gga caa cca gat 547
 Ile Glu Ala Phe Leu Ser Val Thr Asp Tyr Gly Ser Gly Gln Pro Asp
 135 140 145
 gaa act gca ttg ccg gtg ttg gaa acc acc gat att tcc aac cca tac 595
 Glu Thr Ala Leu Pro Val Leu Glu Thr Thr Asp Ile Ser Asn Pro Tyr
 150 155 160 165
 gct ggt agt tac aat gcc tca ttt gcg ttg aaa aat gac tcc tca gat 643
 Ala Gly Ser Tyr Asn Ala Ser Phe Ala Leu Lys Asn Asp Ser Ser Asp
 170 175 180
 gat ttt aag aac ctg aga gtt ggt att gtt tgc tac aac gag caa act 691
 Asp Phe Lys Asn Leu Arg Val Gly Ile Val Cys Tyr Asn Glu Gln Thr
 185 190 195
 gac atc att ggt ggt ggt ttc aaa ttt ccg aac ctg gtt cca gcg ggt 739
 Asp Ile Ile Gly Gly Gly Phe Lys Phe Pro Asn Leu Val Pro Ala Gly
 200 205 210
 ggg agt att cga atg gac gct agt gtg acg gtc tcc gaa atg cca gct 787
 Gly Ser Ile Arg Met Asp Ala Ser Val Thr Val Ser Glu Met Pro Ala
 215 220 225
 tct tgt aag gca tat tta aat cac taatagattc ttaaaaggca gca 834
 Ser Cys Lys Ala Tyr Leu Asn His
 230 235

<210> 1566

<211> 237

<212> PRT

<213> Corynebacterium glutamicum

<400> 1566

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 20 25 30
 Gly Val Leu Ser Asp Gly Ala Glu Asn Ile Ala Ser Gln Ser Asp Glu
 35 40 45
 Ser Lys Ser Gly Val Glu Ile Ile Asp Ser Gly Phe Gly Gln Ser Ser
 50 55 60
 Asn Ser Ala Met Ala Ile Val Ile Ala Lys Thr Ser Gly Gly Ser Leu
 65 70 75 80
 Ala Gly Glu Phe Val Thr Ala Thr Val Asn Phe Leu Asp Glu Ser Gly
 85 90 95

Ala Val Val Ala Thr Glu Asp Gln Val Glu Thr Leu Ser Trp Glu Asp
 100 105 110

Gln Glu Leu Val Leu Pro Val Ser His Tyr Lys Glu Asp Ser Ser Arg
 115 120 125

Pro Glu Ile Thr Ser Ile Glu Ala Phe Leu Ser Val Thr Asp Tyr Gly
 130 135 140

Ser Gly Gln Pro Asp Glu Thr Ala Leu Pro Val Leu Glu Thr Thr Asp
 145 150 155 160

Ile Ser Asn Pro Tyr Ala Gly Ser Tyr Asn Ala Ser Phe Ala Leu Lys
 165 170 175

Asn Asp Ser Ser Asp Asp Phe Lys Asn Leu Arg Val Gly Ile Val Cys
 180 185 190

Tyr Asn Glu Gln Thr Asp Ile Ile Gly Gly Gly Phe Lys Phe Pro Asn
 195 200 205

Leu Val Pro Ala Gly Gly Ser Ile Arg Met Asp Ala Ser Val Thr Val
 210 215 220

Ser Glu Met Pro Ala Ser Cys Lys Ala Tyr Leu Asn His
 225 230 235

<210> 1567

<211> 3036

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(3013)

<223> RXA00054

<400> 1567

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 Met Ser Pro Phe Asp
 1 5

tca aag ctt ggt cgc gat acc cat ttt gga ttc ctc gat aag acc act 163
 Ser Lys Leu Gly Arg Asp Thr His Phe Gly Phe Leu Asp Lys Thr Thr
 10 15 20

gct tcg caa caa ctg ctg aat cct tca ttg att tct aat gag gat ccg 211
 Ala Ser Gln Gln Leu Leu Asn Pro Ser Leu Ile Ser Asn Glu Asp Pro
 25 30 35

cac acc atg ttg cag gcg atc aag tta gag ctt cgt acc gca cag tct 259
 His Thr Met Leu Gln Ala Ile Lys Leu Glu Leu Arg Thr Ala Gln Ser
 40 45 50

ttt aca ttt tca gtc gct ttt att tcc agt cgc ggt atc gcg ttg ttg 307
 Phe Thr Phe Ser Val Ala Phe Ile Ser Ser Arg Gly Ile Ala Leu Leu
 55 60 65

aaa cag gca ttg ttg gac ttc aag ggt aaa gga cga att atc acg tcc	355
Lys Gln Ala Leu Leu Asp Phe Lys Gly Lys Gly Arg Ile Ile Thr Ser	
70 75 80 85	
cgc tac ctg gat ttc aat gat cca acg atg ttt cgt gag ctt ctt act	403
Arg Tyr Leu Asp Phe Asn Asp Pro Thr Met Phe Arg Glu Leu Leu Thr	
90 95 100	
ttg gag aac gtg gaa gtc ctc ata cat caa ggc gat ggt ttc cac tcc	451
Leu Glu Asn Val Glu Val Leu Ile His Gln Gly Asp Gly Phe His Ser	
105 110 115	
aag ggc tac gtt ttc cat cac gac gtg gga atc acc gca gta gtg ggt	499
Lys Gly Tyr Val Phe His His Asp Val Gly Ile Thr Ala Val Val Gly	
120 125 130	
agt tcc aac ctc aca gat aat gct ctg ttg gta aac cgg gaa tgg aat	547
Ser Ser Asn Leu Thr Asp Asn Ala Leu Leu Val Asn Arg Glu Trp Asn	
135 140 145	
ctg aag ttc tct gcc agc aag aat ggc gac att gct ttt caa ctt gat	595
Leu Lys Phe Ser Ala Ser Lys Asn Gly Asp Ile Ala Phe Gln Leu Asp	
150 155 160 165	
gat gcg att aat cgc caa att gaa cga tcc acg cca ctg acg cct gaa	643
Asp Ala Ile Asn Arg Gln Ile Glu Arg Ser Thr Pro Leu Thr Pro Glu	
170 175 180	
tgg atc tca gag tat gag gca acc aga cgt gta cct gag cgt ttg gtg	691
Trp Ile Ser Glu Tyr Glu Ala Thr Arg Arg Val Pro Glu Arg Leu Val	
185 190 195	
tct cag aat att cct ctc gag gat caa agt aac gcc gga aca att gtt	739
Ser Gln Asn Ile Pro Leu Glu Asp Gln Ser Asn Ala Gly Thr Ile Val	
200 205 210	
cca aac gtc atg cag gaa gag gcc ctc gac gct cta ctt tct ttg acg	787
Pro Asn Val Met Gln Glu Glu Ala Leu Asp Ala Leu Leu Ser Leu Thr	
215 220 225	
gag aag gga gag aaa cgt ggt gtc att att tct gcg aca gga act ggc	835
Glu Lys Gly Glu Lys Arg Gly Val Ile Ile Ser Ala Thr Gly Thr Gly	
230 235 240 245	
aag act atc ctg gct gct cta gct aca aga atg ctc aag cct gaa cga	883
Lys Thr Ile Leu Ala Ala Leu Ala Thr Arg Met Leu Lys Pro Glu Arg	
250 255 260	
gtt ttg ttt gtc gtg cac cgc gaa caa att ctg gat aag gcg cga tcc	931
Val Leu Phe Val Val His Arg Glu Gln Ile Leu Asp Lys Ala Arg Ser	
265 270 275	
gag ttc atc aaa gtt ctt gaa cgt ccc gct gtt gat ttc gga aaa atg	979
Glu Phe Ile Lys Val Leu Glu Arg Pro Ala Val Asp Phe Gly Lys Met	
280 285 290	
tct ggc tcg acc aag gag cta gat aag ccg ttt gtg ttt ggc acc atc	1027
Ser Gly Ser Thr Lys Glu Leu Asp Lys Pro Phe Val Phe Gly Thr Ile	
295 300 305	

caa acg ctg aca aag gaa gct aca ctt tcc cag atc tcc cct act gac Gln Thr Leu Thr Lys Glu Ala Thr Leu Ser Gln Ile Ser Pro Thr Asp 310 315 320 325	1075
ttt gat tta gtc atc gtc gat gaa gtc cat cgc gcc ggt gcc gaa tcc Phe Asp Leu Val Ile Val Asp Glu Val His Arg Ala Gly Ala Glu Ser 330 335 340	1123
tat ttg gca ttg ctc aat cat ctg cag cca cag ttt tta ttg ggc ctg Tyr Leu Ala Leu Leu Asn His Leu Gln Pro Gln Phe Leu Leu Gly Leu 345 350 355	1171
act gct acc cca gag cga act gat gga ttc aat att tat gag ttg ttc Thr Ala Thr Pro Glu Arg Thr Asp Gly Phe Asn Ile Tyr Glu Leu Phe 360 365 370	1219
gat ttc aac gtg cca tat gag atc cga ctt caa gct gct tta gaa tcc Asp Phe Asn Val Pro Tyr Glu Ile Arg Leu Gln Ala Ala Leu Glu Ser 375 380 385	1267
aac atg ctc gta ccg ttt cac tat tac ggt gtc aca gac ttc acg ctt Asn Met Leu Val Pro Phe His Tyr Tyr Gly Val Thr Asp Phe Thr Leu 390 395 400 405	1315
gat tct gaa aca acg gtg act gat acc tcc aaa cta agt gcc ttg gtg Asp Ser Glu Thr Thr Val Thr Asp Thr Ser Lys Leu Ser Ala Leu Val 410 415 420	1363
agc gaa gag aga gtc cat cac att ctg gag gcc ctc aaa act tat ggt Ser Glu Glu Arg Val His His Ile Leu Glu Ala Leu Lys Thr Tyr Gly 425 430 435	1411
cat cca gaa aat gtt cgt gga ctg atc ttc tgt tcc aag act gaa gag His Pro Glu Asn Val Arg Gly Leu Ile Phe Cys Ser Lys Thr Glu Glu 440 445 450	1459
gct gag gag ctg tca aaa ctt ctc gac cag tcg ttg ttt aat ggc agc Ala Glu Glu Leu Ser Lys Leu Leu Asp Gln Ser Leu Phe Asn Gly Ser 455 460 465	1507
ttg ctt aaa acc aag gcg ctc tct gcg aag gac tca att ccc tac cgc Leu Leu Lys Thr Lys Ala Leu Ser Ala Lys Asp Ser Ile Pro Tyr Arg 470 475 480 485	1555
gaa gag gtt gta gct gag ctg gag tcc ggc gac ctg gac tac atc ttg Glu Glu Val Val Ala Glu Leu Glu Ser Gly Asp Leu Asp Tyr Ile Leu 490 495 500	1603
acg gtt gac atc ttc aat gaa ggc att gat att cct tcg gtg aat caa Thr Val Asp Ile Phe Asn Glu Gly Ile Asp Ile Pro Ser Val Asn Gln 505 510 515	1651
atc gta atg att cgt agt act caa tca agc att gtg ttt acg cag cag Ile Val Met Ile Arg Ser Thr Gln Ser Ser Ile Val Phe Thr Gln Gln 520 525 530	1699
ctc ggg cgt gga ctc cga aaa gct gct ggc aaa gac cat ctg cgc gtt Leu Gly Arg Gly Leu Arg Lys Ala Ala Gly Lys Asp His Leu Arg Val 535 540 545	1747
att gat ttc att ggc aac tac gcg aac aac tat ctc att ccc atc gca	1795

Ile Asp Phe Ile Gly Asn Tyr Ala Asn Asn Tyr Leu Ile Pro Ile Ala 550 555 560 565	
ttg ttt ggc gat aat tct cgc aat aag aac agc atc aga cgc cgc ctg Leu Phe Gly Asp Asn Ser Arg Asn Lys Asn Ser Ile Arg Arg Arg Leu 570 575 580	1843
att gag agc gat att gat gga aca atc tca ggt gtt tca agt gtt aac Ile Glu Ser Asp Ile Asp Gly Thr Ile Ser Gly Val Ser Ser Val Asn 585 590 595	1891
ttt gat ccc atc gcg cag gag aga att ttt gct gcg ttg aag gct gcg Phe Asp Pro Ile Ala Gln Glu Arg Ile Phe Ala Ala Leu Lys Ala Ala 600 605 610	1939
aag ttg gac tca aaa gca caa ttc aag cag gat att gtt cag ctt caa Lys Leu Asp Ser Lys Ala Gln Phe Lys Gln Asp Ile Val Gln Leu Gln 615 620 625	1987
gat cga ctc aat cat gtg cca gca ctg tta gac ttc gct cgc ttc aat Asp Arg Leu Asn His Val Pro Ala Leu Leu Asp Phe Ala Arg Phe Asn 630 635 640 645	2035
act gtt gat ccg ttt atc ctt gcc acg cat tct ggc aac tac tgg tcg Thr Val Asp Pro Phe Ile Leu Ala Thr His Ser Gly Asn Tyr Trp Ser 650 655 660	2083
ctg ctc agt tca gtg aag ttt gtc gat cac gct ccc agc gaa tcg gag Leu Leu Ser Ser Val Lys Phe Val Asp His Ala Pro Ser Glu Ser Glu 665 670 675	2131
aag tac ttt ctg gat ttc ctt acc gga gag ctt ctt aac ggc aag cga Lys Tyr Phe Leu Asp Phe Leu Thr Gly Glu Leu Leu Asn Gly Lys Arg 680 685 690	2179
cct cat gag ctg ttg ctg atc cag gaa cta atg aaa cag cct gaa act Pro His Glu Leu Leu Leu Ile Gln Glu Leu Met Lys Gln Pro Glu Thr 695 700 705	2227
tct act gaa gaa ttc cgt aag ctc ttg cag gcc caa tcg act agt tca Ser Thr Glu Glu Phe Arg Lys Leu Leu Gln Ala Gln Ser Thr Ser Ser 710 715 720 725	2275
gat gag caa aca atc aac tcg gtt gaa agg att ttg agc caa gaa ttc Asp Glu Gln Thr Ile Asn Ser Val Glu Arg Ile Leu Ser Gln Glu Phe 730 735 740	2323
tat acg gga cca aac cgc aag aag ttt ggc gaa cat ccg atc ctc tct Tyr Thr Gly Pro Asn Arg Lys Lys Phe Gly Glu His Pro Ile Leu Ser 745 750 755	2371
gtt caa aac cgc acc tac tct ttt act ccc gag ttc cga cgt gcc ctc Val Gln Asn Arg Thr Tyr Ser Phe Thr Pro Glu Phe Arg Arg Ala Leu 760 765 770	2419
gac gaa agc cta gaa gtg acg gac cga gat gag gct gct cag aat ttt Asp Glu Ser Leu Glu Val Thr Asp Arg Asp Glu Ala Ala Gln Asn Phe 775 780 785	2467
aag ttt cac gtc caa gac atc atc gac act ggt ttg ttt atc gcc aga Lys Phe His Val Gln Asp Ile Ile Asp Thr Gly Leu Phe Ile Ala Arg	2515

790	795	800	805	
aac aat gga ttt tgg caa gga aac ctc gtt gtt ggc gag aga tac tcc				2563
Asn Asn Gly Phe Trp Gln Gly Asn Leu Val Val Gly Glu Arg Tyr Ser				
	810	815	820	
cga cga gat gtc tgc cga att ctc aat tgg gaa cga aac aac gag agc				2611
Arg Arg Asp Val Cys Arg Ile Leu Asn Trp Glu Arg Asn Asn Glu Ser				
	825	830	835	
acg att tat gga tac aaa gtg gac agt tac aca tct act tgc cca atc				2659
Thr Ile Tyr Gly Tyr Lys Val Asp Ser Tyr Thr Ser Thr Cys Pro Ile				
	840	845	850	
ttt gtg acc tat cac aag gct gat gat gta tcc gaa agt act cgt tac				2707
Phe Val Thr Tyr His Lys Ala Asp Asp Val Ser Glu Ser Thr Arg Tyr				
	855	860	865	
cag gat gaa ctc gtc gat ccg aat acc ctt cat tgg tat tcc cgc ggc				2755
Gln Asp Glu Leu Val Asp Pro Asn Thr Leu His Trp Tyr Ser Arg Gly				
	870	875	880	885
aac cga aag atc acg tct aat gag atc aag ccc atc gct gcg aat gct				2803
Asn Arg Lys Ile Thr Ser Asn Glu Ile Lys Pro Ile Ala Ala Asn Ala				
	890	895	900	
gtg gat ctt cat gtt ttt gtg aag aag gac gat gcc gaa ggc ctt gat				2851
Val Asp Leu His Val Phe Val Lys Lys Asp Asp Ala Glu Gly Leu Asp				
	905	910	915	
ttc ttc tac ctt ggt caa gcg cat tca gaa aac agc aaa cag tca tcg				2899
Phe Phe Tyr Leu Gly Gln Ala His Ser Glu Asn Ser Lys Gln Ser Ser				
	920	925	930	
atg ccc gga aac aaa gga gtt gtg caa ccg gtg gtc aca atg gat cta				2947
Met Pro Gly Asn Lys Gly Val Val Gln Pro Val Val Thr Met Asp Leu				
	935	940	945	
cag ttc gac aca ccc gtc gaa caa agc ctg ttt gag tac ctg agc aca				2995
Gln Phe Asp Thr Pro Val Glu Gln Ser Leu Phe Glu Tyr Leu Ser Thr				
	950	955	960	965
aat ctc gcc gta acg gag taaccaccgc aaccaagcgt cga				3036
Asn Leu Ala Val Thr Glu				
	970			

<210> 1568

<211> 971

<212> PRT

<213> Corynebacterium glutamicum

<400> 1568

Met	Ser	Pro	Phe	Asp	Ser	Lys	Leu	Gly	Arg	Asp	Thr	His	Phe	Gly	Phe
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Leu	Asp	Lys	Thr	Thr	Ala	Ser	Gln	Gln	Leu	Leu	Asn	Pro	Ser	Leu	Ile
			20					25					30		

Ser	Asn	Glu	Asp	Pro	His	Thr	Met	Leu	Gln	Ala	Ile	Lys	Leu	Glu	Leu
		35					40					45			

Arg Thr Ala Gln Ser Phe Thr Phe Ser Val Ala Phe Ile Ser Ser Arg
50 55 60

Gly Ile Ala Leu Leu Lys Gln Ala Leu Leu Asp Phe Lys Gly Lys Gly
65 70 75 80

Arg Ile Ile Thr Ser Arg Tyr Leu Asp Phe Asn Asp Pro Thr Met Phe
85 90 95

Arg Glu Leu Leu Thr Leu Glu Asn Val Glu Val Leu Ile His Gln Gly
100 105 110

Asp Gly Phe His Ser Lys Gly Tyr Val Phe His His Asp Val Gly Ile
115 120 125

Thr Ala Val Val Gly Ser Ser Asn Leu Thr Asp Asn Ala Leu Leu Val
130 135 140

Asn Arg Glu Trp Asn Leu Lys Phe Ser Ala Ser Lys Asn Gly Asp Ile
145 150 155 160

Ala Phe Gln Leu Asp Asp Ala Ile Asn Arg Gln Ile Glu Arg Ser Thr
165 170 175

Pro Leu Thr Pro Glu Trp Ile Ser Glu Tyr Glu Ala Thr Arg Arg Val
180 185 190

Pro Glu Arg Leu Val Ser Gln Asn Ile Pro Leu Glu Asp Gln Ser Asn
195 200 205

Ala Gly Thr Ile Val Pro Asn Val Met Gln Glu Glu Ala Leu Asp Ala
210 215 220

Leu Leu Ser Leu Thr Glu Lys Gly Glu Lys Arg Gly Val Ile Ile Ser
225 230 235 240

Ala Thr Gly Thr Gly Lys Thr Ile Leu Ala Ala Leu Ala Thr Arg Met
245 250 255

Leu Lys Pro Glu Arg Val Leu Phe Val Val His Arg Glu Gln Ile Leu
260 265 270

Asp Lys Ala Arg Ser Glu Phe Ile Lys Val Leu Glu Arg Pro Ala Val
275 280 285

Asp Phe Gly Lys Met Ser Gly Ser Thr Lys Glu Leu Asp Lys Pro Phe
290 295 300

Val Phe Gly Thr Ile Gln Thr Leu Thr Lys Glu Ala Thr Leu Ser Gln
305 310 315 320

Ile Ser Pro Thr Asp Phe Asp Leu Val Ile Val Asp Glu Val His Arg
325 330 335

Ala Gly Ala Glu Ser Tyr Leu Ala Leu Leu Asn His Leu Gln Pro Gln
340 345 350

Phe Leu Leu Gly Leu Thr Ala Thr Pro Glu Arg Thr Asp Gly Phe Asn
355 360 365

Ile Tyr Glu Leu Phe Asp Phe Asn Val Pro Tyr Glu Ile Arg Leu Gln
 370 375 380
 Ala Ala Leu Glu Ser Asn Met Leu Val Pro Phe His Tyr Tyr Gly Val
 385 390 395 400
 Thr Asp Phe Thr Leu Asp Ser Glu Thr Thr Val Thr Asp Thr Ser Lys
 405 410 415
 Leu Ser Ala Leu Val Ser Glu Glu Arg Val His His Ile Leu Glu Ala
 420 425 430
 Leu Lys Thr Tyr Gly His Pro Glu Asn Val Arg Gly Leu Ile Phe Cys
 435 440 445
 Ser Lys Thr Glu Glu Ala Glu Glu Leu Ser Lys Leu Leu Asp Gln Ser
 450 455 460
 Leu Phe Asn Gly Ser Leu Leu Lys Thr Lys Ala Leu Ser Ala Lys Asp
 465 470 475 480
 Ser Ile Pro Tyr Arg Glu Glu Val Val Ala Glu Leu Glu Ser Gly Asp
 485 490 495
 Leu Asp Tyr Ile Leu Thr Val Asp Ile Phe Asn Glu Gly Ile Asp Ile
 500 505 510
 Pro Ser Val Asn Gln Ile Val Met Ile Arg Ser Thr Gln Ser Ser Ile
 515 520 525
 Val Phe Thr Gln Gln Leu Gly Arg Gly Leu Arg Lys Ala Ala Gly Lys
 530 535 540
 Asp His Leu Arg Val Ile Asp Phe Ile Gly Asn Tyr Ala Asn Asn Tyr
 545 550 555 560
 Leu Ile Pro Ile Ala Leu Phe Gly Asp Asn Ser Arg Asn Lys Asn Ser
 565 570 575
 Ile Arg Arg Arg Leu Ile Glu Ser Asp Ile Asp Gly Thr Ile Ser Gly
 580 585 590
 Val Ser Ser Val Asn Phe Asp Pro Ile Ala Gln Glu Arg Ile Phe Ala
 595 600 605
 Ala Leu Lys Ala Ala Lys Leu Asp Ser Lys Ala Gln Phe Lys Gln Asp
 610 615 620
 Ile Val Gln Leu Gln Asp Arg Leu Asn His Val Pro Ala Leu Leu Asp
 625 630 635 640
 Phe Ala Arg Phe Asn Thr Val Asp Pro Phe Ile Leu Ala Thr His Ser
 645 650 655
 Gly Asn Tyr Trp Ser Leu Leu Ser Ser Val Lys Phe Val Asp His Ala
 660 665 670
 Pro Ser Glu Ser Glu Lys Tyr Phe Leu Asp Phe Leu Thr Gly Glu Leu
 675 680 685
 Leu Asn Gly Lys Arg Pro His Glu Leu Leu Leu Ile Gln Glu Leu Met

690	695	700
Lys Gln Pro Glu Thr Ser Thr Glu Glu Phe Arg Lys Leu Leu Gln Ala		
705	710	715 720
Gln Ser Thr Ser Ser Asp Glu Gln Thr Ile Asn Ser Val Glu Arg Ile		
	725	730 735
Leu Ser Gln Glu Phe Tyr Thr Gly Pro Asn Arg Lys Lys Phe Gly Glu		
	740	745 750
His Pro Ile Leu Ser Val Gln Asn Arg Thr Tyr Ser Phe Thr Pro Glu		
	755	760 765
Phe Arg Arg Ala Leu Asp Glu Ser Leu Glu Val Thr Asp Arg Asp Glu		
	770	775 780
Ala Ala Gln Asn Phe Lys Phe His Val Gln Asp Ile Ile Asp Thr Gly		
	785	790 795 800
Leu Phe Ile Ala Arg Asn Asn Gly Phe Trp Gln Gly Asn Leu Val Val		
	805	810 815
Gly Glu Arg Tyr Ser Arg Arg Asp Val Cys Arg Ile Leu Asn Trp Glu		
	820	825 830
Arg Asn Asn Glu Ser Thr Ile Tyr Gly Tyr Lys Val Asp Ser Tyr Thr		
	835	840 845
Ser Thr Cys Pro Ile Phe Val Thr Tyr His Lys Ala Asp Asp Val Ser		
	850	855 860
Glu Ser Thr Arg Tyr Gln Asp Glu Leu Val Asp Pro Asn Thr Leu His		
	865	870 875 880
Trp Tyr Ser Arg Gly Asn Arg Lys Ile Thr Ser Asn Glu Ile Lys Pro		
	885	890 895
Ile Ala Ala Asn Ala Val Asp Leu His Val Phe Val Lys Lys Asp Asp		
	900	905 910
Ala Glu Gly Leu Asp Phe Phe Tyr Leu Gly Gln Ala His Ser Glu Asn		
	915	920 925
Ser Lys Gln Ser Ser Met Pro Gly Asn Lys Gly Val Val Gln Pro Val		
	930	935 940
Val Thr Met Asp Leu Gln Phe Asp Thr Pro Val Glu Gln Ser Leu Phe		
	945	950 955 960
Glu Tyr Leu Ser Thr Asn Leu Ala Val Thr Glu		
	965	970

<210> 1569

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXA00058

<400> 1569

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gctcgtgtaa tctccgctta tctagctcaa aggaatactt atg aag ttc ttc ggg 115
                                         Met Lys Phe Phe Gly
                                         1           5

ttt tat cgt cct att gct tta att gct ggc att acc gtt tca gca tct 163
Phe Tyr Arg Pro Ile Ala Leu Ile Ala Gly Ile Thr Val Ser Ala Ser
                10                15                20

att ctc aca tcc gta gct act gca gct gaa tct cca act agc ttt caa 211
Ile Leu Thr Ser Val Ala Thr Ala Ala Glu Ser Pro Thr Ser Phe Gln
                25                30                35

gcg att aca cct gca ttc tct tca tca tcg gct cca gaa gca gac gca 259
Ala Ile Thr Pro Ala Phe Ser Ser Ser Ser Ala Pro Glu Ala Asp Ala
                40                45                50

gaa gca aac acc agt gaa gct acc gca gac ctg ctt tac gtg gca gaa 307
Glu Ala Asn Thr Ser Glu Ala Thr Ala Asp Leu Leu Tyr Val Ala Glu
                55                60                65

aac caa cta ctt att aag ctt tct aac gcc gtc gtc gaa gat gtt aac 355
Asn Gln Leu Leu Ile Lys Leu Ser Asn Ala Val Val Glu Asp Val Asn
                70                75                80                85

ggc gaa atc tta atg aaa gat aat aag ggc act ctt ctg gag aat ttg 403
Gly Glu Ile Leu Met Lys Asp Asn Lys Gly Thr Leu Leu Glu Asn Leu
                90                95                100

aca gct gaa ctt caa gcc caa cca ggc ttc tca atc gag aaa gtc gat 451
Thr Ala Glu Leu Gln Ala Gln Pro Gly Phe Ser Ile Glu Lys Val Asp
                105                110                115

tcc cat act gct ttg ttg acc atg aat cca gat gag gtg cca gat tta 499
Ser His Thr Ala Leu Leu Thr Met Asn Pro Asp Glu Val Pro Asp Leu
                120                125                130

cag gac tgg cga tgc gga gtc ggc gct ttg tca ggc ggg gta gca ggt 547
Gln Asp Trp Arg Cys Gly Val Gly Ala Leu Ser Gly Gly Val Ala Gly
                135                140                145

gtg gtg gca act ggt cta gct ctc gcc gct ttg gga gtt gcc aca ggt 595
Val Val Ala Thr Gly Leu Ala Leu Ala Ala Leu Gly Val Ala Thr Gly
                150                155                160                165

ggc acg ggg ttt gct gtg ctt gca gca ggg gga ctt gct gga tat ggc 643
Gly Thr Gly Phe Ala Val Leu Ala Ala Gly Gly Leu Ala Gly Tyr Gly
                170                175                180

act ggc gct gtc gcc aac tgc taaggagaaa taatgggaat tgt 687
Thr Gly Ala Val Ala Asn Cys
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<210> 1570

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 1570

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Met Lys Phe Phe Gly Phe Tyr Arg Pro Ile Ala Leu Ile Ala Gly Ile
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Thr Val Ser Ala Ser Ile Leu Thr Ser Val Ala Thr Ala Ala Glu Ser
          20           25           30

Pro Thr Ser Phe Gln Ala Ile Thr Pro Ala Phe Ser Ser Ser Ser Ala
          35           40           45

Pro Glu Ala Asp Ala Glu Ala Asn Thr Ser Glu Ala Thr Ala Asp Leu
          50           55           60

Leu Tyr Val Ala Glu Asn Gln Leu Leu Ile Lys Leu Ser Asn Ala Val
 65           70           75           80

Val Glu Asp Val Asn Gly Glu Ile Leu Met Lys Asp Asn Lys Gly Thr
          85           90           95

Leu Leu Glu Asn Leu Thr Ala Glu Leu Gln Ala Gln Pro Gly Phe Ser
          100          105          110

Ile Glu Lys Val Asp Ser His Thr Ala Leu Leu Thr Met Asn Pro Asp
          115          120          125

Glu Val Pro Asp Leu Gln Asp Trp Arg Cys Gly Val Gly Ala Leu Ser
          130          135          140

Gly Gly Val Ala Gly Val Val Ala Thr Gly Leu Ala Leu Ala Ala Leu
          145          150          155          160

Gly Val Ala Thr Gly Gly Thr Gly Phe Ala Val Leu Ala Ala Gly Gly
          165          170          175

Leu Ala Gly Tyr Gly Thr Gly Ala Val Ala Asn Cys
          180          185

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<210> 1571

<211> 405

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(382)

<223> RXA00059

<400> 1571

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cggtggtgat gtcactcaaa ctgcccgact ggtgttgtgg gtg ttg acc gga atc    115
                               Val Leu Thr Gly Ile
                               1           5

tta ctg gct atg gtc tct acc gcc cta cga atc cgc ttc gga tca ggg    163
Leu Leu Ala Met Val Ser Thr Ala Leu Arg Ile Arg Phe Gly Ser Gly
          10           15           20

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gta gct atc gct gca acc gtg ctg tgg aca gtt atc tca ata acc ttg 211
 Val Ala Ile Ala Ala Thr Val Leu Trp Thr Val Ile Ser Ile Thr Leu
 25 30 35

 ggc gga gat gtg cta gcc gag acc atg ctc tgg ctt gta gca gta cca 259
 Gly Gly Asp Val Leu Ala Glu Thr Met Leu Trp Leu Val Ala Val Pro
 40 45 50

 tcc tgg cca gaa aca gcg gat act act acc cgc ttc ctt att gcg atg 307
 Ser Trp Pro Glu Thr Ala Asp Thr Thr Thr Arg Phe Leu Ile Ala Met
 55 60 65

 cta ctg cag gca gtt ctt atc acc ggc agc act atc tgg gct atc cga 355
 Leu Leu Gln Ala Val Leu Ile Thr Gly Ser Thr Ile Trp Ala Ile Arg
 70 75 80 85

 gag atc cgg gat tca gag cgc cgt ggc taagtccagc acctccgaca 402
 Glu Ile Arg Asp Ser Glu Arg Arg Gly
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 acg 405

<210> 1572
 <211> 94
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1572
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 Arg Phe Gly Ser Gly Val Ala Ile Ala Ala Thr Val Leu Trp Thr Val
 20 25 30

 Ile Ser Ile Thr Leu Gly Gly Asp Val Leu Ala Glu Thr Met Leu Trp
 35 40 45

 Leu Val Ala Val Pro Ser Trp Pro Glu Thr Ala Asp Thr Thr Thr Arg
 50 55 60

 Phe Leu Ile Ala Met Leu Leu Gln Ala Val Leu Ile Thr Gly Ser Thr
 65 70 75 80

 Ile Trp Ala Ile Arg Glu Ile Arg Asp Ser Glu Arg Arg Gly
 85 90

<210> 1573
 <211> 396
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(373)
 <223> RXA00065

<400> 1573
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                               Met Ala Asn Leu Pro
                               1                               5

caa gag ggt ttt tct gtg gtg cac gga att ttg gcg gat ccc cgc att 163
Gln Glu Gly Phe Ser Val Val His Gly Ile Leu Ala Asp Pro Arg Ile
                10                15                20

tgg ggc ccg gag att ccg tat gtt cgt gaa gaa gca ggt caa gta aat 211
Trp Gly Pro Glu Ile Pro Tyr Val Arg Glu Glu Ala Gly Gln Val Asn
                25                30                35

gtg gaa gca ccc gac gag gct ggc gat cta gcc cga ttg acg ttg cct 259
Val Glu Ala Pro Asp Glu Ala Gly Asp Leu Ala Arg Leu Thr Leu Pro
                40                45                50

ctg cag ttg atc ctg ctc acg gag gaa gag ttt gcc atc gct ctc aac 307
Leu Gln Leu Ile Leu Leu Thr Glu Glu Glu Phe Ala Ile Ala Leu Asn
                55                60                65

gag ggc agc gac gtc atg ttc gaa cga atg gcg gag caa gaa gtc gat 355
Glu Gly Ser Asp Val Met Phe Glu Arg Met Ala Glu Gln Glu Val Asp
                70                75                80                85

ctt ctg gat ctg aaa cgt taagacggtg ggctcaattc cgt 396
Leu Leu Asp Leu Lys Arg
                90

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<210> 1574

<211> 91

<212> PRT

<213> Corynebacterium glutamicum

<400> 1574

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  1                               5                10                15

Ala Asp Pro Arg Ile Trp Gly Pro Glu Ile Pro Tyr Val Arg Glu Glu
                20                25                30

Ala Gly Gln Val Asn Val Glu Ala Pro Asp Glu Ala Gly Asp Leu Ala
                35                40                45

Arg Leu Thr Leu Pro Leu Gln Leu Ile Leu Leu Thr Glu Glu Glu Phe
                50                55                60

Ala Ile Ala Leu Asn Glu Gly Ser Asp Val Met Phe Glu Arg Met Ala
                65                70                75                80

Glu Gln Glu Val Asp Leu Leu Asp Leu Lys Arg
                85                90

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<210> 1575

<211> 705

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(682)
 <223> RXA00068

<400> 1575

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atatagcacc ggcttaacag gccgggtgcta ttctgttcgc atg act tcg aag gat 115
 Met Thr Ser Lys Asp
 1 5

ctg att gtg acc tcc tat acg tct tgg ggc aag cgt ttc aag aat gac 163
 Leu Ile Val Thr Ser Tyr Thr Ser Trp Gly Lys Arg Phe Lys Asn Asp
 10 15 20

ggg aag ctt ttt att aac cta ctt cgc agc acc act gat agt gct gat 211
 Gly Lys Leu Phe Ile Asn Leu Leu Arg Ser Thr Thr Asp Ser Ala Asp
 25 30 35

gaa aag gtt tta gcc act ttc ggt gaa gtt ccc agc aaa tca ttt gaa 259
 Glu Lys Val Leu Ala Thr Phe Gly Glu Val Pro Ser Lys Ser Phe Glu
 40 45 50

acc acc gca acg gtt gat gag cag cag tgg gaa ctg tcc ttc agt att 307
 Thr Thr Ala Thr Val Asp Glu Gln Gln Trp Glu Leu Ser Phe Ser Ile
 55 60 65

gat gga acg gca act gcc aag ctt cct gat ggt cgt gtg ttc agc gcg 355
 Asp Gly Thr Ala Thr Ala Lys Leu Pro Asp Gly Arg Val Phe Ser Ala
 70 75 80 85

aat gca ggt gag aag acc ttt acc aag tcc aag cgg att gaa atc gac 403
 Asn Ala Gly Glu Lys Thr Phe Thr Lys Ser Lys Arg Ile Glu Ile Asp
 90 95 100

atg gac ggc acc gcg atg gct gct gtt aat gaa gat aaa aac aat tgg 451
 Met Asp Gly Thr Ala Met Ala Ala Val Asn Glu Asp Lys Asn Asn Trp
 105 110 115

att atc gac gat tct gaa gag aat aaa gtc gct cag ttt acc ggt atg 499
 Ile Ile Asp Asp Ser Glu Glu Asn Lys Val Ala Gln Phe Thr Gly Met
 120 125 130

aac aac ggt gtg cgt cgc gcg att gtg gag ttt gag cct gac gta gaa 547
 Asn Asn Gly Val Arg Arg Ala Ile Val Glu Phe Glu Pro Asp Val Glu
 135 140 145

gtc acc cag gag cag gaa att ttc ttg tcg tgg gtt gct cgg aaa act 595
 Val Thr Gln Glu Gln Glu Ile Phe Leu Ser Trp Val Ala Arg Lys Thr
 150 155 160 165

ctg gaa tcc cgc atg ttg ggc tcc agt tgg gga ctg act ctg ttt ttg 643
 Leu Glu Ser Arg Met Leu Gly Ser Ser Trp Gly Leu Thr Leu Phe Leu
 170 175 180

atc att ttg acg cca atc att att ttc ctc act ttc agc taaaaggacc 692
 Ile Ile Leu Thr Pro Ile Ile Ile Phe Leu Thr Phe Ser
 185 190

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<210> 1576
 <211> 194
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1576
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 Arg Phe Lys Asn Asp Gly Lys Leu Phe Ile Asn Leu Leu Arg Ser Thr
 20 25 30
 Thr Asp Ser Ala Asp Glu Lys Val Leu Ala Thr Phe Gly Glu Val Pro
 35 40 45
 Ser Lys Ser Phe Glu Thr Thr Ala Thr Val Asp Glu Gln Gln Trp Glu
 50 55 60
 Leu Ser Phe Ser Ile Asp Gly Thr Ala Thr Ala Lys Leu Pro Asp Gly
 65 70 75 80
 Arg Val Phe Ser Ala Asn Ala Gly Glu Lys Thr Phe Thr Lys Ser Lys
 85 90 95
 Arg Ile Glu Ile Asp Met Asp Gly Thr Ala Met Ala Ala Val Asn Glu
 100 105 110
 Asp Lys Asn Asn Trp Ile Ile Asp Asp Ser Glu Glu Asn Lys Val Ala
 115 120 125
 Gln Phe Thr Gly Met Asn Asn Gly Val Arg Arg Ala Ile Val Glu Phe
 130 135 140
 Glu Pro Asp Val Glu Val Thr Gln Glu Gln Glu Ile Phe Leu Ser Trp
 145 150 155 160
 Val Ala Arg Lys Thr Leu Glu Ser Arg Met Leu Gly Ser Ser Trp Gly
 165 170 175
 Leu Thr Leu Phe Leu Ile Ile Leu Thr Pro Ile Ile Ile Phe Leu Thr
 180 185 190
 Phe Ser

<210> 1577
 <211> 345
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(322)
 <223> RXA00079

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 ttcgcttatc gacgccaact ccctccattt ggaatccccc atg ggc cta gtt cac 115

	Met	Gly	Leu	Val	His	
	1				5	
acc gaa ttc acc cca ata aac acc tac gga atc ctc gac cac gta gtc						163
Thr Glu Phe Thr Pro Ile Asn Thr Tyr Gly Ile Leu Asp His Val Val						
	10				20	
acc ctc ccc gac gga act aaa gtg ctc aac cct ttc cga gtc atc ccc						211
Thr Leu Pro Asp Gly Thr Lys Val Leu Asn Pro Phe Arg Val Ile Pro						
	25				35	
cac gac acc ggc tcc gaa ctc att ttc acc gtc cgc ccc aac gaa aac						259
His Asp Thr Gly Ser Glu Leu Ile Phe Thr Val Arg Pro Asn Glu Asn						
	40				50	
ttc gaa gaa gat tgc caa gca gtc gca gca gac ctc gaa agg ctg gtc						307
Phe Glu Glu Asp Cys Gln Ala Val Ala Ala Asp Leu Glu Arg Leu Val						
	55				65	
gca ctg gcc gaa aaa tgacccacaca gaatggtctc taa						345
Ala Leu Ala Glu Lys						
	70					

<210> 1578

<211> 74

<212> PRT

<213> Corynebacterium glutamicum

<400> 1578

Met	Gly	Leu	Val	His	Thr	Glu	Phe	Thr	Pro	Ile	Asn	Thr	Tyr	Gly	Ile
1				5					10					15	

Leu	Asp	His	Val	Val	Thr	Leu	Pro	Asp	Gly	Thr	Lys	Val	Leu	Asn	Pro
			20					25					30		

Phe	Arg	Val	Ile	Pro	His	Asp	Thr	Gly	Ser	Glu	Leu	Ile	Phe	Thr	Val
		35					40					45			

Arg	Pro	Asn	Glu	Asn	Phe	Glu	Glu	Asp	Cys	Gln	Ala	Val	Ala	Ala	Asp
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Leu	Glu	Arg	Leu	Val	Ala	Leu	Ala	Glu	Lys
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<210> 1579

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (80)..(643)

<223> RXA00082

<400> 1579

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tattcaagaa	gatgggcta	gtg	aac	gtc	act	gaa	caa	tcc	ggc	gag	tcc	cat	112
Val	Asn	Val	Thr	Glu	Gln	Ser	Gly	Glu	Ser	His			

	1	5	10	
atc gac atc ccg gaa tca cac cag ctg ccc gga cct cgt cca gtt ggc				160
Ile Asp Ile Pro Glu Ser His Gln Leu Pro Gly Pro Arg Pro Val Gly				
	15	20	25	
gag ggc act ttc tgg gaa ggc cgc tcc ggg ctc atc atg ccc gca att				208
Glu Gly Thr Phe Trp Glu Gly Arg Ser Gly Leu Ile Met Pro Ala Ile				
	30	35	40	
ctt acg gca ttt agt ttg tat ttg ctc atc ggt gtt tta aac atg gat				256
Leu Thr Ala Phe Ser Leu Tyr Leu Leu Ile Gly Val Leu Asn Met Asp				
	45	50	55	
gtg ggc aat gca gca ttc cca gga cct cga ttc ttc cca aca atc ctc				304
Val Gly Asn Ala Ala Phe Pro Gly Pro Arg Phe Phe Pro Thr Ile Leu				
	60	65	70	75
ggc atc gcg ggt ttg ttg gtg gca gtg gca ttg acc att caa acc atc				352
Gly Ile Ala Gly Leu Leu Val Ala Val Ala Leu Thr Ile Gln Thr Ile				
	80	85	90	
aag tac ccc atg cat cca gaa aat gaa tct ggc cga agc tgg aaa ttc				400
Lys Tyr Pro Met His Pro Glu Asn Glu Ser Gly Arg Ser Trp Lys Phe				
	95	100	105	
cac tct gat tac gtc tca ctc gcg tgg gcg atc ggt ggc ttc ttc gcc				448
His Ser Asp Tyr Val Ser Leu Ala Trp Ala Ile Gly Gly Phe Phe Ala				
	110	115	120	
ttt gca gtc ttg ctt cca tat ctt ggc tgg gtc ctt gct ggc tcc ttg				496
Phe Ala Val Leu Leu Pro Tyr Leu Gly Trp Val Leu Ala Gly Ser Leu				
	125	130	135	
ttg ttc tgg aca atg acc agg gct ttc ggt tcc aaa cgc cca ggt ttc				544
Leu Phe Trp Thr Met Thr Arg Ala Phe Gly Ser Lys Arg Pro Gly Phe				
	140	145	150	155
gat gtt ctt gtt tcc ctc atg atg agc tcc gtg gtc tac ctc gca ttc				592
Asp Val Leu Val Ser Leu Met Met Ser Ser Val Val Tyr Leu Ala Phe				
	160	165	170	
gat gtg ggc ttg gga ctt aat ctt cct tcc gga ctt ttg ggt ggt ggc				640
Asp Val Gly Leu Gly Leu Asn Leu Pro Ser Gly Leu Leu Gly Gly Gly				
	175	180	185	
ttt taatggatat tttgtccctc ttg				666
Phe				

<210> 1580

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 1580

Val	Asn	Val	Thr	Glu	Gln	Ser	Gly	Glu	Ser	His	Ile	Asp	Ile	Pro	Glu
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Ser His Gln Leu Pro Gly Pro Arg Pro Val Gly Glu Gly Thr Phe Trp

20										25										30																																		
Glu	Gly	Arg	Ser	Gly	Leu	Ile	Met	Pro	Ala	Ile	Leu	Thr	Ala	Phe	Ser																																							
			35					40					45																																									
Leu	Tyr	Leu	Leu	Ile	Gly	Val	Leu	Asn	Met	Asp	Val	Gly	Asn	Ala	Ala																																							
			50				55				60																																											
Phe	Pro	Gly	Pro	Arg	Phe	Phe	Pro	Thr	Ile	Leu	Gly	Ile	Ala	Gly	Leu																																							
			65				70				75																																											
Leu	Val	Ala	Val	Ala	Leu	Thr	Ile	Gln	Thr	Ile	Lys	Tyr	Pro	Met	His																																							
				85				90																																														
Pro	Glu	Asn	Glu	Ser	Gly	Arg	Ser	Trp	Lys	Phe	His	Ser	Asp	Tyr	Val																																							
			100					105					110																																									
Ser	Leu	Ala	Trp	Ala	Ile	Gly	Gly	Phe	Phe	Ala	Phe	Ala	Val	Leu	Leu																																							
			115				120					125																																										
Pro	Tyr	Leu	Gly	Trp	Val	Leu	Ala	Gly	Ser	Leu	Leu	Phe	Trp	Thr	Met																																							
			130				135				140																																											
Thr	Arg	Ala	Phe	Gly	Ser	Lys	Arg	Pro	Gly	Phe	Asp	Val	Leu	Val	Ser																																							
				145			150				155																																											
Leu	Met	Met	Ser	Ser	Val	Val	Tyr	Leu	Ala	Phe	Asp	Val	Gly	Leu	Gly																																							
				165				170																																														
Leu	Asn	Leu	Pro	Ser	Gly	Leu	Leu	Gly	Gly	Gly	Phe																																											
			180					185																																														

<210> 1581

<211> 423

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(400)

<223> RXA00083

<400> 1581

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cggattcgac	caagaaaacg	tacaccactc	aggagcactc	gtg	ctt	gcc	ctt	cca	115
				Val	Leu	Ala	Leu	Pro	
				1				5	

tcc	tct	atc	atc	gac	ccc	ctc	tgg	tgc	cag	ttc	gcc	gcg	ctg	atc	cca	163
Ser	Ser	Ile	Ile	Asp	Pro	Leu	Trp	Cys	Gln	Phe	Ala	Ala	Leu	Ile	Pro	
				10				15						20		

ccc	gtg	acc	gac	acc	cac	cca	ctt	cgg	tgc	cac	cgc	cca	cgc	atc	ccg	211
Pro	Val	Thr	Asp	Thr	His	Pro	Leu	Arg	Cys	His	Arg	Pro	Arg	Ile	Pro	
				25				30						35		

gac	cgg	atc	atc	ttc	gac	aag	ctc	atc	cag	gtc	ctc	gtc	ctc	ggc	gcc	259
Asp	Arg	Ile	Ile	Phe	Asp	Lys	Leu	Ile	Gln	Val	Leu	Val	Leu	Gly	Ala	
				40				45						50		

taagttcgga ttggctcgaa ttg 423

<213> Corynebacterium glutamicum

Gly Leu Asp Leu
100

<213> Corynebacterium glutamicum

<223> RXA00093

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Val Thr Thr Leu Leu
1 5

gca gca acc cgc ccc acc ctg cgc gat gcc ttt aaa cac cca tgg cga	163
Ala Ala Thr Arg Pro Thr Leu Arg Asp Ala Phe Lys His Pro Trp Arg	
10 15 20	
tcg ctg gca gcc atc ttg ttg gtg gcc gta ccg atg ttc ctg gtg agt	211
Ser Leu Ala Ala Ile Leu Leu Val Ala Val Pro Met Phe Leu Val Ser	
25 30 35	
ttc ttt ctt acc tat gat caa tca atc aac aat gca gct agc tat cct	259
Phe Phe Leu Thr Tyr Asp Gln Ser Ile Asn Asn Ala Ala Ser Tyr Pro	
40 45 50	
ggg tcc cag gta caa gct cac tat gac gga gaa gga gcc tac caa ctc	307
Gly Ser Gln Val Gln Ala His Tyr Asp Gly Glu Gly Ala Tyr Gln Leu	
55 60 65	
ctc caa gaa aac ctt cca gaa gac ttc cac ctg gaa ctc ttt gcc aat	355
Leu Gln Glu Asn Leu Pro Glu Asp Phe His Leu Glu Leu Phe Ala Asn	
70 75 80 85	
ggg tat cca gaa gtc tcc ttc ggt gat gaa gaa gtc aat ttc ttt gtt	403
Gly Tyr Pro Glu Val Ser Phe Gly Asp Glu Glu Val Asn Phe Phe Val	
90 95 100	
gtg caa tca aca aac gta caa caa gcc tca ttt ccc gcc gat gca ctc	451
Val Gln Ser Thr Asn Val Gln Gln Ala Ser Phe Pro Ala Asp Ala Leu	
105 110 115	
gat gtt tta ggt gcc aca atc ggt gat acc gtg acc att cac ggc acc	499
Asp Val Leu Gly Ala Thr Ile Gly Asp Thr Val Thr Ile His Gly Thr	
120 125 130	
ccg gtg gaa gtt cag tcg att tct ccc aca aat atc tta ttg ccc gaa	547
Pro Val Glu Val Gln Ser Ile Ser Pro Thr Asn Ile Leu Leu Pro Glu	
135 140 145	
ggg act ctg ttt tct ctt gag aat ttc tcc gaa tca gaa act ttt tcc	595
Gly Thr Leu Phe Ser Leu Glu Asn Phe Ser Glu Ser Glu Thr Phe Ser	
150 155 160 165	
ggc acc tgg tac ttc ccc gga tcg aat ttc acc gaa gaa aac cga caa	643
Gly Thr Trp Tyr Phe Pro Gly Ser Asn Phe Thr Glu Glu Asn Arg Gln	
170 175 180	
gca cta gaa gca gtt ggc ttt gaa gtt aat gaa tat cgg cgc ggc ccc	691
Ala Leu Glu Ala Val Gly Phe Glu Val Asn Glu Tyr Arg Arg Gly Pro	
185 190 195	
ata tcc gtc gac cca aat ttg atc cca agc tac atc atg gga ttt tta	739
Ile Ser Val Asp Pro Asn Leu Ile Pro Ser Tyr Ile Met Gly Phe Leu	
200 205 210	
tcg acg aca att ctc gcc gtc gtt gca ctc atg ctg atc tca cca gta	787
Ser Thr Thr Ile Leu Ala Val Val Ala Leu Met Leu Ile Ser Pro Val	
215 220 225	
ttt aca att tcc gcc tca agg caa acc aga act ttc gca ctg ctc gcc	835
Phe Thr Ile Ser Ala Ser Arg Gln Thr Arg Thr Phe Ala Leu Leu Ala	
230 235 240 245	
tca cag ggt gcc aca cct aga cac att cgg tgg gca gtg ctt aca tat	883

Ser	Gln	Gly	Ala	Thr	Pro	Arg	His	Ile	Arg	Trp	Ala	Val	Leu	Thr	Tyr		
				250					255					260			
ggg	ctc	ttc	gca	ggg	ctt	gtt	ggg	gca	tcc	att	ggg	tta	gtt	ctg	ggg	931	
Gly	Leu	Phe	Ala	Gly	Leu	Val	Gly	Ala	Ser	Ile	Gly	Leu	Val	Leu	Gly		
			265					270					275				
caa	ata	ggc	atc	tac	ggc	tgg	tgg	aaa	tac	acc	tat	cct	gaa	ttc	tcc	979	
Gln	Ile	Gly	Ile	Tyr	Gly	Trp	Trp	Lys	Tyr	Thr	Tyr	Pro	Glu	Phe	Ser		
		280					285					290					
ctc	acc	acc	ccc	tgg	cta	gtt	ctt	gta	ggg	ttt	tgg	gcg	ctg	gca	atc	1027	
Leu	Thr	Thr	Pro	Trp	Leu	Val	Leu	Val	Gly	Phe	Trp	Ala	Leu	Ala	Ile		
	295					300					305						
atc	gct	tca	acg	att	gct	gca	ttc	tta	ccg	gca	gtt	ttt	gtc	agt	aga	1075	
Ile	Ala	Ser	Thr	Ile	Ala	Ala	Phe	Leu	Pro	Ala	Val	Phe	Val	Ser	Arg		
310					315				320						325		
tca	agc	atc	atc	aac	gga	atc	tac	gga	gga	atc	tcc	gac	aaa	atc	atc	1123	
Ser	Ser	Ile	Ile	Asn	Gly	Ile	Tyr	Gly	Gly	Ile	Ser	Asp	Lys	Ile	Ile		
				330				335						340			
cgg	tgg	agc	cct	cga	atg	ctc	atc	ggg	cca	atc	gtc	tta	att	gca	gct	1171	
Arg	Trp	Ser	Pro	Arg	Met	Leu	Ile	Gly	Pro	Ile	Val	Leu	Ile	Ala	Ala		
			345					350					355				
gcg	gta	atc	gcc	ttg	ttt	atc	ggg	gac	gga	gag	tgg	gga	ggc	gtc	gtc	1219	
Ala	Val	Ile	Ala	Leu	Phe	Ile	Gly	Asp	Gly	Glu	Trp	Gly	Gly	Val	Val		
		360					365					370					
aag	caa	tta	tgc	ttc	ctg	gca	gcc	gtc	atc	gcc	ctg	ccg	gcc	tca	gtg	1267	
Lys	Gln	Leu	Cys	Phe	Leu	Ala	Ala	Val	Ile	Ala	Leu	Pro	Ala	Ser	Val		
	375					380					385						
cct	gcg	gtg	ttg	tgg	gcg	ctt	ggg	cgc	ctg	cct	ggg	ttg	aca	ttc	aaa	1315	
Pro	Ala	Val	Leu	Trp	Ala	Leu	Gly	Arg	Leu	Pro	Gly	Leu	Thr	Phe	Lys		
390					395					400					405		
cta	gct	acg	cgc	gat	atg	ctg	cgc	cga	tca	atg	cac	tcc	att	cct	gcg	1363	
Leu	Ala	Thr	Arg	Asp	Met	Leu	Arg	Arg	Ser	Met	His	Ser	Ile	Pro	Ala		
				410				415						420			
att	ggg	gcg	ctg	gcg	gca	gtg	att	atg	ctt	ggg	aca	ttt	atg	caa	aca	1411	
Ile	Gly	Ala	Leu	Ala	Ala	Val	Ile	Met	Leu	Gly	Thr	Phe	Met	Gln	Thr		
			425					430					435				
act	gga	ctt	gca	acc	caa	gcc	agc	gat	aga	gaa	gct	acc	gcc	tcg	gtg	1459	
Thr	Gly	Leu	Ala	Thr	Gln	Ala	Ser	Asp	Arg	Glu	Ala	Thr	Ala	Ser	Val		
		440					445					450					
tat	cct	gag	gcc	gta	ttc	tta	cgc	ggg	gac	aca	caa	atc	cct	gga	ctc	1507	
Tyr	Pro	Glu	Ala	Val	Phe	Leu	Arg	Gly	Asp	Thr	Gln	Ile	Pro	Gly	Leu		
	455					460					465						
atg	ggg	caa	aaa	atc	gat	gta	tac	ggg	gat	aac	cat	ggc	ttt	ggg	atc	1555	
Met	Gly	Gln	Lys	Ile	Asp	Val	Tyr	Gly	Asp	Asn	His	Gly	Phe	Gly	Ile		
470					475				480						485		
tat	gaa	cta	gat	gta	gat	ttt	tac	tcg	gcc	aac	tat	gtg	ccc	gca	ctg	1603	
Tyr	Glu	Leu	Asp	Val	Asp	Phe	Tyr	Ser	Ala	Asn	Tyr	Val	Pro	Ala	Leu		

490										495					500					
acc	tca	ttt	ttt	ggc	gga	cca	gtt	att	gcc	acg	ccc	aag	att	tta	gac	1651				
Thr	Ser	Phe	Phe	Gly	Gly	Pro	Val	Ile	Ala	Thr	Pro	Lys	Ile	Leu	Asp					
505				510				515												
atg	ttc	ggg	gtc	cac	gaa	caa	gcc	gac	atc	tac	gcg	cca	tca	acc	tat	1699				
Met	Phe	Gly	Val	His	Glu	Gln	Ala	Asp	Ile	Tyr	Ala	Pro	Ser	Thr	Tyr					
520				525				530												
aat	tcc	ggg	ctg	caa	gaa	tac	gca	ata	tac	ccc	ggc	gat	gaa	acc	tac	1747				
Asn	Ser	Gly	Leu	Gln	Glu	Tyr	Ala	Ile	Tyr	Pro	Gly	Asp	Glu	Thr	Tyr					
535				540				545												
atg	cta	gac	acc	gct	gct	gtt	tta	ccg	ccg	ctg	tac	tca	cat	gtt	tta	1795				
Met	Leu	Asp	Thr	Ala	Ala	Val	Leu	Pro	Pro	Leu	Tyr	Ser	His	Val	Leu					
550				555				560				565								
tta	agc	cca	gaa	act	ttt	gaa	gaa	atc	gga	gga	caa	aca	gaa	ttc	ttg	1843				
Leu	Ser	Pro	Glu	Thr	Phe	Glu	Glu	Ile	Gly	Gly	Gln	Thr	Glu	Phe	Leu					
570				575				580												
gga	aca	atc	gtg	ctt	ccc	caa	gaa	cta	gat	gac	caa	act	gta	caa	gca	1891				
Gly	Thr	Ile	Val	Leu	Pro	Gln	Glu	Leu	Asp	Asp	Gln	Thr	Val	Gln	Ala					
585				590				595												
atc	aat	cgg	tca	aga	gat	gcg	cat	ttc	agc	cac	gac	ggc	cat	aat	tct	1939				
Ile	Asn	Arg	Ser	Arg	Asp	Ala	His	Phe	Ser	His	Asp	Gly	His	Asn	Ser					
600				605				610												
tca	ctt	gct	tcc	agt	gct	gca	cta	act	gcg	gtg	gca	att	gtg	gtc	gtt	1987				
Ser	Leu	Ala	Ser	Ser	Ala	Ala	Leu	Thr	Ala	Val	Ala	Ile	Val	Val	Val					
615				620				625												
tcc	ctt	gtg	atc	gtg	ctg	gct	aat	cgc	aaa	ctc	caa	cag	cac	gca	ttg	2035				
Ser	Leu	Val	Ile	Val	Leu	Ala	Asn	Arg	Lys	Leu	Gln	Gln	His	Ala	Leu					
630				635				640				645								
att	gcc	atc	gga	gca	aca	cct	gga	aca	atc	tac	aaa	gtc	aat	gcc	tta	2083				
Ile	Ala	Ile	Gly	Ala	Thr	Pro	Gly	Thr	Ile	Tyr	Lys	Val	Asn	Ala	Leu					
650				655				660												
aat	gca	gcg	ttg	ctt	gcc	ctt	gtc	gga	ggc	atc	atg	ggc	ctt	gtc	tcc	2131				
Asn	Ala	Ala	Leu	Leu	Ala	Leu	Val	Gly	Gly	Ile	Met	Gly	Leu	Val	Ser					
665				670				675												
gga	tgg	att	gca	gcg	ctg	ctg	aca	ggc	acc	act	gat	gaa	att	gtt	gat	2179				
Gly	Trp	Ile	Ala	Ala	Leu	Leu	Thr	Gly	Thr	Thr	Asp	Glu	Ile	Val	Asp					
680				685				690												
gga	gca	att	ttg	aac	tac	ggc	acg	ctt	gaa	cac	atg	atg	ctg	ccg	tgg	2227				
Gly	Ala	Ile	Leu	Asn	Tyr	Gly	Thr	Leu	Glu	His	Met	Met	Leu	Pro	Trp					
695				700				705												
cct	ctg	ttg	gta	agc	ctc	ctc	gtt	gtg	gcg	ccg	ctg	gtg	tgc	gcc	gtg	2275				
Pro	Leu	Leu	Val	Ser	Leu	Leu	Val	Val	Ala	Pro	Leu	Val	Cys	Ala	Val					
710				715				720				725								
att	ggg	gct	ata	gct	tct	cca	tcg	gga	cgc	cac	caa	gaa	gca	tca	atc	2323				
Ile	Gly	Ala	Ile	Ala	Ser	Pro	Ser	Gly	Arg	His	Gln	Glu	Ala	Ser	Ile					
730				735				740												

taaccttgcc ggaggaaccg aaa

2346

<210> 1584

<211> 741

<212> PRT

<213> Corynebacterium glutamicum

<400> 1584

Val Thr Thr Leu Leu Ala Ala Thr Arg Pro Thr Leu Arg Asp Ala Phe
1 5 10 15

Lys His Pro Trp Arg Ser Leu Ala Ala Ile Leu Leu Val Ala Val Pro
20 25 30

Met Phe Leu Val Ser Phe Phe Leu Thr Tyr Asp Gln Ser Ile Asn Asn
35 40 45

Ala Ala Ser Tyr Pro Gly Ser Gln Val Gln Ala His Tyr Asp Gly Glu
50 55 60

Gly Ala Tyr Gln Leu Leu Gln Glu Asn Leu Pro Glu Asp Phe His Leu
65 70 75 80

Glu Leu Phe Ala Asn Gly Tyr Pro Glu Val Ser Phe Gly Asp Glu Glu
85 90 95

Val Asn Phe Phe Val Val Gln Ser Thr Asn Val Gln Gln Ala Ser Phe
100 105 110

Pro Ala Asp Ala Leu Asp Val Leu Gly Ala Thr Ile Gly Asp Thr Val
115 120 125

Thr Ile His Gly Thr Pro Val Glu Val Gln Ser Ile Ser Pro Thr Asn
130 135 140

Ile Leu Leu Pro Glu Gly Thr Leu Phe Ser Leu Glu Asn Phe Ser Glu
145 150 155 160

Ser Glu Thr Phe Ser Gly Thr Trp Tyr Phe Pro Gly Ser Asn Phe Thr
165 170 175

Glu Glu Asn Arg Gln Ala Leu Glu Ala Val Gly Phe Glu Val Asn Glu
180 185 190

Tyr Arg Arg Gly Pro Ile Ser Val Asp Pro Asn Leu Ile Pro Ser Tyr
195 200 205

Ile Met Gly Phe Leu Ser Thr Thr Ile Leu Ala Val Val Ala Leu Met
210 215 220

Leu Ile Ser Pro Val Phe Thr Ile Ser Ala Ser Arg Gln Thr Arg Thr
225 230 235 240

Phe Ala Leu Leu Ala Ser Gln Gly Ala Thr Pro Arg His Ile Arg Trp
245 250 255

Ala Val Leu Thr Tyr Gly Leu Phe Ala Gly Leu Val Gly Ala Ser Ile
260 265 270

Gly Leu Val Leu Gly Gln Ile Gly Ile Tyr Gly Trp Trp Lys Tyr Thr
275 280 285

Tyr Pro Glu Phe Ser Leu Thr Thr Pro Trp Leu Val Leu Val Gly Phe
290 295 300

Trp Ala Leu Ala Ile Ile Ala Ser Thr Ile Ala Ala Phe Leu Pro Ala
305 310 315 320

Val Phe Val Ser Arg Ser Ser Ile Ile Asn Gly Ile Tyr Gly Gly Ile
325 330 335

Ser Asp Lys Ile Ile Arg Trp Ser Pro Arg Met Leu Ile Gly Pro Ile
340 345 350

Val Leu Ile Ala Ala Ala Val Ile Ala Leu Phe Ile Gly Asp Gly Glu
355 360 365

Trp Gly Gly Val Val Lys Gln Leu Cys Phe Leu Ala Ala Val Ile Ala
370 375 380

Leu Pro Ala Ser Val Pro Ala Val Leu Trp Ala Leu Gly Arg Leu Pro
385 390 395 400

Gly Leu Thr Phe Lys Leu Ala Thr Arg Asp Met Leu Arg Arg Ser Met
405 410 415

His Ser Ile Pro Ala Ile Gly Ala Leu Ala Ala Val Ile Met Leu Gly
420 425 430

Thr Phe Met Gln Thr Thr Gly Leu Ala Thr Gln Ala Ser Asp Arg Glu
435 440 445

Ala Thr Ala Ser Val Tyr Pro Glu Ala Val Phe Leu Arg Gly Asp Thr
450 455 460

Gln Ile Pro Gly Leu Met Gly Gln Lys Ile Asp Val Tyr Gly Asp Asn
465 470 475 480

His Gly Phe Gly Ile Tyr Glu Leu Asp Val Asp Phe Tyr Ser Ala Asn
485 490 495

Tyr Val Pro Ala Leu Thr Ser Phe Phe Gly Gly Pro Val Ile Ala Thr
500 505 510

Pro Lys Ile Leu Asp Met Phe Gly Val His Glu Gln Ala Asp Ile Tyr
515 520 525

Ala Pro Ser Thr Tyr Asn Ser Gly Leu Gln Glu Tyr Ala Ile Tyr Pro
530 535 540

Gly Asp Glu Thr Tyr Met Leu Asp Thr Ala Ala Val Leu Pro Pro Leu
545 550 555 560

Tyr Ser His Val Leu Leu Ser Pro Glu Thr Phe Glu Glu Ile Gly Gly
565 570 575

Gln Thr Glu Phe Leu Gly Thr Ile Val Leu Pro Gln Glu Leu Asp Asp
580 585 590

Gln Thr Val Gln Ala Ile Asn Arg Ser Arg Asp Ala His Phe Ser His

595	600	605
Asp Gly His Asn Ser Ser Leu Ala Ser Ser Ala Ala Leu Thr Ala Val 610 615 620		
Ala Ile Val Val Val Ser Leu Val Ile Val Leu Ala Asn Arg Lys Leu 625 630 635 640		
Gln Gln His Ala Leu Ile Ala Ile Gly Ala Thr Pro Gly Thr Ile Tyr 645 650 655		
Lys Val Asn Ala Leu Asn Ala Ala Leu Leu Ala Leu Val Gly Gly Ile 660 665 670		
Met Gly Leu Val Ser Gly Trp Ile Ala Ala Leu Leu Thr Gly Thr Thr 675 680 685		
Asp Glu Ile Val Asp Gly Ala Ile Leu Asn Tyr Gly Thr Leu Glu His 690 695 700		
Met Met Leu Pro Trp Pro Leu Leu Val Ser Leu Leu Val Val Ala Pro 705 710 715 720		
Leu Val Cys Ala Val Ile Gly Ala Ile Ala Ser Pro Ser Gly Arg His 725 730 735		
Gln Glu Ala Ser Ile 740		

<210> 1585

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA00101

<400> 1585

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ctggtggtgt cgcgcgtgcc aaccgctaaa ctcgtgaagc	atg aga cta ata ctc	115
	Met Arg Leu Ile Leu	
	1 5	

aac ctg att tgg tta ttc ttc ggt ggc att tgg ctc gcg ttg gga tac	163
Asn Leu Ile Trp Leu Phe Phe Gly Gly Ile Trp Leu Ala Leu Gly Tyr	
10 15 20	

gta ttc ttc gga atc atc gca tgt atc ttc atc gtg acg att ccc gcc	211
Val Phe Phe Gly Ile Ile Ala Cys Ile Phe Ile Val Thr Ile Pro Ala	
25 30 35	

ggt atc gca agc ttc cgc atg gct aac tac gcg ctg tgg ccg ttt ggt	259
Gly Ile Ala Ser Phe Arg Met Ala Asn Tyr Ala Leu Trp Pro Phe Gly	
40 45 50	

agg acg gtt gtt cgt aat cct aaa gcc gga ggg ttt tct gcc ctg agc	307
Arg Thr Val Val Arg Asn Pro Lys Ala Gly Gly Phe Ser Ala Leu Ser	

55	60	65	
aac gga ctg tgg ttt atc att gct gga ctg tgg ctg gcg atc ggg cac			355
Asn Gly Leu Trp Phe Ile Ile Ala Gly Leu Trp Leu Ala Ile Gly His			
70	75	80	85
ctc acc acc gcg gct gcc cag gcg atc acc atc atc gga att cca ctg			403
Leu Thr Thr Ala Ala Ala Gln Ala Ile Thr Ile Ile Gly Ile Pro Leu			
	90	95	100
gcg atc gca aac atc cga atg atc ccc gtg acg tgt ttc ccg ttc ggc			451
Ala Ile Ala Asn Ile Arg Met Ile Pro Val Thr Cys Phe Pro Phe Gly			
	105	110	115
aaa gaa atc tat gac agc aac cgc att ccc ttc ggc tac gaa ccg atg			499
Lys Glu Ile Tyr Asp Ser Asn Arg Ile Pro Phe Gly Tyr Glu Pro Met			
	120	125	130
gtt aag ttt taattcggcg acggactaaa cca			531
Val Lys Phe			
135			

<210> 1586

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 1586

Met Arg Leu Ile Leu Asn Leu Ile Trp Leu Phe Phe Gly Gly Ile Trp			
1	5	10	15
Leu Ala Leu Gly Tyr Val Phe Phe Gly Ile Ile Ala Cys Ile Phe Ile			
	20	25	30
Val Thr Ile Pro Ala Gly Ile Ala Ser Phe Arg Met Ala Asn Tyr Ala			
	35	40	45
Leu Trp Pro Phe Gly Arg Thr Val Val Arg Asn Pro Lys Ala Gly Gly			
	50	55	60
Phe Ser Ala Leu Ser Asn Gly Leu Trp Phe Ile Ile Ala Gly Leu Trp			
65	70	75	80
Leu Ala Ile Gly His Leu Thr Thr Ala Ala Ala Gln Ala Ile Thr Ile			
	85	90	95
Ile Gly Ile Pro Leu Ala Ile Ala Asn Ile Arg Met Ile Pro Val Thr			
	100	105	110
Cys Phe Pro Phe Gly Lys Glu Ile Tyr Asp Ser Asn Arg Ile Pro Phe			
	115	120	125
Gly Tyr Glu Pro Met Val Lys Phe			
130	135		

<210> 1587

<211> 643

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(643)

<223> RXA00108

<400> 1587

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gaattggggtt ttgagcatcg tggcgggtgct tgttggttgca agtgccatcg tcatgatgat 60

tgcaaagaat cgtaaccaga aataagaggg tttattcacc atg aag aag ttt ttt 115
Met Lys Lys Phe Phe
1 5

gtc gca ggt gct gta ctg agc agt gcg ttg gtt atg gcg gcg tgt tcg 163
Val Ala Gly Ala Val Leu Ser Ser Ala Leu Val Met Ala Ala Cys Ser
10 15 20

cct gct aat caa agt gat tcc acc tcc acg agc gtg gag act act tcc 211
Pro Ala Asn Gln Ser Asp Ser Thr Ser Thr Ser Val Glu Thr Thr Ser
25 30 35

tcc agc agc acg cag gta agc gat gct gtg atc acc acg gaa aac gct 259
Ser Ser Ser Thr Gln Val Ser Asp Ala Val Ile Thr Thr Glu Asn Ala
40 45 50

gtt gtt cgt gcg tct gtg gag gac agc gac atg acg gca gtg ttc gct 307
Val Val Arg Ala Ser Val Glu Asp Ser Asp Met Thr Ala Val Phe Ala
55 60 65

acg ttg gtg aac aat tct gat gat gag atc aac gtt tct ggc ttt act 355
Thr Leu Val Asn Asn Ser Asp Asp Glu Ile Asn Val Ser Gly Phe Thr
70 75 80 85

gct gat gtt gat gct gcc agc ttt gag gtc cat gag gtt gtt gat ggc 403
Ala Asp Val Asp Ala Ala Ser Phe Glu Val His Glu Val Val Asp Gly
90 95 100

gtc atg cag gaa aag cca ggt ggt ttt gtg atc cct gca ggg gag agc 451
Val Met Gln Glu Lys Pro Gly Gly Phe Val Ile Pro Ala Gly Glu Ser
105 110 115

atc gag ctg gca cca ggt ggc gat cat ttg atg atc atg ggg ctt gcg 499
Ile Glu Leu Ala Pro Gly Gly Asp His Leu Met Ile Met Gly Leu Ala
120 125 130

aac cca atc gag gct ggc gat gaa gtg acg gtc act ctt gaa ttg gct 547
Asn Pro Ile Glu Ala Gly Asp Glu Val Thr Val Thr Leu Glu Leu Ala
135 140 145

gat ggt tct gaa gtt aag ctt gat ccg atc ccg gcg cgc acc att gct 595
Asp Gly Ser Glu Val Lys Leu Asp Pro Ile Pro Ala Arg Thr Ile Ala
150 155 160 165

gct ggt gat gag gat tat ggc gat ctg gga act gaa ggc cac gag ggc 643
Ala Gly Asp Glu Asp Tyr Gly Asp Leu Gly Thr Glu Gly His Glu Gly
170 175 180

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<210> 1588

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 1588

Met Lys Lys Phe Phe Val Ala Gly Ala Val Leu Ser Ser Ala Leu Val
 1 5 10 15

Met Ala Ala Cys Ser Pro Ala Asn Gln Ser Asp Ser Thr Ser Thr Ser
 20 25 30

Val Glu Thr Thr Ser Ser Ser Ser Thr Gln Val Ser Asp Ala Val Ile
 35 40 45

Thr Thr Glu Asn Ala Val Val Arg Ala Ser Val Glu Asp Ser Asp Met
 50 55 60

Thr Ala Val Phe Ala Thr Leu Val Asn Asn Ser Asp Asp Glu Ile Asn
 65 70 75 80

Val Ser Gly Phe Thr Ala Asp Val Asp Ala Ala Ser Phe Glu Val His
 85 90 95

Glu Val Val Asp Gly Val Met Gln Glu Lys Pro Gly Gly Phe Val Ile
 100 105 110

Pro Ala Gly Glu Ser Ile Glu Leu Ala Pro Gly Gly Asp His Leu Met
 115 120 125

Ile Met Gly Leu Ala Asn Pro Ile Glu Ala Gly Asp Glu Val Thr Val
 130 135 140

Thr Leu Glu Leu Ala Asp Gly Ser Glu Val Lys Leu Asp Pro Ile Pro
 145 150 155 160

Ala Arg Thr Ile Ala Ala Gly Asp Glu Asp Tyr Gly Asp Leu Gly Thr
 165 170 175

Glu Gly His Glu Gly
 180

<210> 1589

<211> 672

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(649)

<223> RXA00110

<400> 1589

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aataacgaac gctaatttta aacactggag gagcttccac gtg agc aac aaa gac 115
 Val Ser Asn Lys Asp
 1 5

ggc ctt ttt act gac ggt aac agc acg ttt gca cct aag gtg gat tca 163
 Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala Pro Lys Val Asp Ser
 10 15 20

att ccc ctc agc gat gtg gat acc agc gtt agc ggt gaa gcc tcc atc 211
 Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser Gly Glu Ala Ser Ile
 25 30 35

ggc acg ctg atc tcc aac gca acc tcc caa atg tcc agc ctt ttc cgc 259
 Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met Ser Ser Leu Phe Arg
 40 45 50

gca gaa gtt gag ctg gcg aag act gaa ctc gca ggc gaa gcc aag aaa 307
 Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala Gly Glu Ala Lys Lys
 55 60 65

gct gcc atc ggc ggc ggc gca ttc agc gtt gct ggc gta atc gca ctg 355
 Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala Gly Val Ile Ala Leu
 70 75 80 85

tac agc tcc ttc ttc ttt ttc ttc ttc gtc gca gca ctg ctg agc gag 403
 Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala Ala Leu Leu Ser Glu
 90 95 100

tgg att aag cct tgg gca gca ttc ctc atc gtg ttc ctc ttc atg ctg 451
 Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val Phe Leu Phe Met Leu
 105 110 115

gtc atc gcc gca gct ctc gca ctg ttc ggc tgg cgc aag gtg aag aag 499
 Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp Arg Lys Val Lys Lys
 120 125 130

atg ggc gct ccg aag aac acc atc caa tcg gtc aac caa ctg aag aac 547
 Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val Asn Gln Leu Lys Asn
 135 140 145

ctg gtc cca ggt cag gca tcc gag aag ctg gag aag gcc aac aag cgt 595
 Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu Lys Ala Asn Lys Arg
 150 155 160 165

ggc ctc tac acc tcc gcg tcc ttc cac agc ccc ggc gcc atc act ggc 643
 Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro Gly Ala Ile Thr Gly
 170 175 180

gac cac taaaaaagga gacttcgatg gcc 672
 Asp His

<210> 1590

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 1590

Val Ser Asn Lys Asp Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala
 1 5 10 15

Pro Lys Val Asp Ser Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser
 20 25 30

Gly Glu Ala Ser Ile Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met
 35 40 45

Ser Ser Leu Phe Arg Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala

50	55	60
Gly Glu Ala Lys Lys Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala		
65	70	75
Gly Val Ile Ala Leu Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala		
	85	90
Ala Leu Leu Ser Glu Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val		
	100	105
Phe Leu Phe Met Leu Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp		
	115	120
Arg Lys Val Lys Lys Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val		
	130	135
Asn Gln Leu Lys Asn Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu		
	145	150
Lys Ala Asn Lys Arg Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro		
	165	170
Gly Ala Ile Thr Gly Asp His		
	180	

<210> 1591

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXA00117

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ttggaatcgc ccatcacttt gagattgaaa aggacaaggt	atg act tcc gct caa	115
	Met Thr Ser Ala Gln	
	1 5	

ccg att act tcc gta gat gca cag act cta aaa tcg tgg atc gat aag	163
Pro Ile Thr Ser Val Asp Ala Gln Thr Leu Lys Ser Trp Ile Asp Lys	
	10 15 20

cat gaa gga ctc acc gtc att gac gtc cgc act gca cat gag ttt tca	211
His Glu Gly Leu Thr Val Ile Asp Val Arg Thr Ala His Glu Phe Ser	
	25 30 35

aat ttg cac att aaa ggc tct tac aac gtg cct cta act aca ctt gct	259
Asn Leu His Ile Lys Gly Ser Tyr Asn Val Pro Leu Thr Thr Leu Ala	
	40 45 50

gag cat tcc gaa gag att tcc tct cgt gtt gga gaa cat gtt gtt ttg	307
Glu His Ser Glu Glu Ile Ser Ser Arg Val Gly Glu His Val Val Leu	
	55 60 65

gtg tgt caa tcc ggc att cga gca ggt cag gca caa caa aag ctg gca	355
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Val Cys Gln Ser Gly Ile Arg Ala Gly Gln Ala Gln Gln Lys Leu Ala
 70 75 80 85
 cct ttg gga att tcc acc gtg gct gtt ttg gag ggt ggc atc aat agt 403
 Pro Leu Gly Ile Ser Thr Val Ala Val Leu Glu Gly Gly Ile Asn Ser
 90 95 100
 ttt gct aag gct gac ggt gat gtg gtc cgc gga acc cag gtg tgg gat 451
 Phe Ala Lys Ala Asp Gly Asp Val Val Arg Gly Thr Gln Val Trp Asp
 105 110 115
 atc gaa cgt cag gtg cgt ttt gcc gct gga tca ttg gtg ctc gca ggg 499
 Ile Glu Arg Gln Val Arg Phe Ala Ala Gly Ser Leu Val Leu Ala Gly
 120 125 130
 ctt gcg gga ggt aaa ttc ctt tca cca aaa gtt cgc acc ctg tcg gga 547
 Leu Ala Gly Gly Lys Phe Leu Ser Pro Lys Val Arg Thr Leu Ser Gly
 135 140 145
 att att ggt gcg ggt ctg aca ttt tct ggc gtt tcc aac acc tgt gcc 595
 Ile Ile Gly Ala Gly Leu Thr Phe Ser Gly Val Ser Asn Thr Cys Ala
 150 155 160 165
 atg ggc aaa gct ctg tcc gcc ttg ccg tgg aat aaa act aag cca gtt 643
 Met Gly Lys Ala Leu Ser Ala Leu Pro Trp Asn Lys Thr Lys Pro Val
 170 175 180
 cct acc gaa acc gag aca ttg agc aag ctt cca agc cct aag gag aac 691
 Pro Thr Glu Thr Glu Thr Leu Ser Lys Leu Pro Ser Pro Lys Glu Asn
 185 190 195
 taaatgtcta tcaccattac tga 714

<210> 1592

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 1592

Met Thr Ser Ala Gln Pro Ile Thr Ser Val Asp Ala Gln Thr Leu Lys
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 Ser Trp Ile Asp Lys His Glu Gly Leu Thr Val Ile Asp Val Arg Thr
 20 25 30
 Ala His Glu Phe Ser Asn Leu His Ile Lys Gly Ser Tyr Asn Val Pro
 35 40 45
 Leu Thr Thr Leu Ala Glu His Ser Glu Glu Ile Ser Ser Arg Val Gly
 50 55 60
 Glu His Val Val Leu Val Cys Gln Ser Gly Ile Arg Ala Gly Gln Ala
 65 70 75 80
 Gln Gln Lys Leu Ala Pro Leu Gly Ile Ser Thr Val Ala Val Leu Glu
 85 90 95
 Gly Gly Ile Asn Ser Phe Ala Lys Ala Asp Gly Asp Val Val Arg Gly
 100 105 110

Thr Gln Val Trp Asp Ile Glu Arg Gln Val Arg Phe Ala Ala Gly Ser
 115 120 125

Leu Val Leu Ala Gly Leu Ala Gly Gly Lys Phe Leu Ser Pro Lys Val
 130 135 140

Arg Thr Leu Ser Gly Ile Ile Gly Ala Gly Leu Thr Phe Ser Gly Val
 145 150 155 160

Ser Asn Thr Cys Ala Met Gly Lys Ala Leu Ser Ala Leu Pro Trp Asn
 165 170 175

Lys Thr Lys Pro Val Pro Thr Glu Thr Glu Thr Leu Ser Lys Leu Pro
 180 185 190

Ser Pro Lys Glu Asn
 195

<210> 1593
 <211> 378
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(355)
 <223> RXA00118

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actgtgggat caacgttcca gggcaacaaa aggagaaaaa atg caa ctc aat cct 115
 Met Gln Leu Asn Pro
 1 5

gat gag atc acc cca gtg ctc aac cga ctc aag cgc gcc caa ggt caa 163
 Asp Glu Ile Thr Pro Val Leu Asn Arg Leu Lys Arg Ala Gln Gly Gln
 10 15 20

ctc acc gga gta atc cga atg ctt gat gaa ggc gaa gac tgt aaa gcc 211
 Leu Thr Gly Val Ile Arg Met Leu Asp Glu Gly Glu Asp Cys Lys Ala
 25 30 35

gta gtc acc caa ctt gcc gca gtc aca aaa gcg ctg gac agg gca ggc 259
 Val Val Thr Gln Leu Ala Ala Val Thr Lys Ala Leu Asp Arg Ala Gly
 40 45 50

ttc gcc atc att gcc aca ggt ttg gaa cag tgc ctc acc aac cct gat 307
 Phe Ala Ile Ile Ala Thr Gly Leu Glu Gln Cys Leu Thr Asn Pro Asp
 55 60 65

ggc gac atg gac aaa aag gaa cta gaa aaa ctg ttc ctg tcg ctg gct 355
 Gly Asp Met Asp Lys Lys Glu Leu Glu Lys Leu Phe Leu Ser Leu Ala
 70 75 80 85

taactatggc ctagttcagg gcg 378

<210> 1594
 <211> 85

<212> PRT

<213> Corynebacterium glutamicum

<400> 1594

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Met Gln Leu Asn Pro Asp Glu Ile Thr Pro Val Leu Asn Arg Leu Lys
 1              5              10              15

Arg Ala Gln Gly Gln Leu Thr Gly Val Ile Arg Met Leu Asp Glu Gly
          20              25              30

Glu Asp Cys Lys Ala Val Val Thr Gln Leu Ala Ala Val Thr Lys Ala
          35              40              45

Leu Asp Arg Ala Gly Phe Ala Ile Ile Ala Thr Gly Leu Glu Gln Cys
          50              55              60

Leu Thr Asn Pro Asp Gly Asp Met Asp Lys Lys Glu Leu Glu Lys Leu
          65              70              75              80

Phe Leu Ser Leu Ala
          85

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<210> 1595

<211> 882

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA00119

<400> .1595

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gcttccaatc aagtgggggtc catcgcggtgg agaatttggc atg ctg gag ttt cct 115
                               Met Leu Glu Phe Pro
                               1              5

gca gat gtc att ccc gag aac atc aaa cac att gcg cag aca aag ttc 163
Ala Asp Val Ile Pro Glu Asn Ile Lys His Ile Ala Gln Thr Lys Phe
          10              15              20

cag act gaa gca act tcg gtg gag gat att cgt cgt gcg att aac ctg 211
Gln Thr Glu Ala Thr Ser Val Glu Asp Ile Arg Arg Ala Ile Asn Leu
          25              30              35

ctg agt gat cag gcg gag cgt gcg ggt gcg tcc ttt aat cct ggt ttc 259
Leu Ser Asp Gln Ala Glu Arg Ala Gly Ala Ser Phe Asn Pro Gly Phe
          40              45              50

att ctt gcg cag gtg ggc tcc acc atc gtg gag gtt tat ggc ggt gct 307
Ile Leu Ala Gln Val Gly Ser Thr Ile Val Glu Val Tyr Gly Gly Ala
          55              60              65

ccg gtt gct tgg ctg gat gcg gtt gag ctg ttg att agt cct gat gtg 355
Pro Val Ala Trp Leu Asp Ala Val Glu Leu Leu Ile Ser Pro Asp Val
          70              75              80              85

gag tgg gtt ggg gtt cat ggc tca agg aag ctc gat att aat gtc agc 403

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<210> 1596
<211> 253
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1596
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Ala Gln Thr Lys Phe Gln Thr Glu Ala Thr Ser Val Glu Asp Ile Arg
20 25 30
Arg Ala Ile Asn Leu Leu Ser Asp Gln Ala Glu Arg Ala Gly Ala Ser
35 40 45
Phe Asn Pro Gly Phe Ile Leu Ala Gln Val Gly Ser Thr Ile Val Glu
50 55 60

Val Tyr Gly Gly Ala Pro Val Ala Trp Leu Asp Ala Val Glu Leu Leu
 65 70 75 80
 Ile Ser Pro Asp Val Glu Trp Val Gly Val His Gly Ser Arg Lys Leu
 85 90 95
 Asp Ile Asn Val Ser Gly Glu Leu Ser Gly Val Ile Ser Ala Gly Asp
 100 105 110
 Lys Leu Gly Glu Leu Leu Gly Asp Asp Trp Thr Ile Asn Ile Val His
 115 120 125
 Gly Glu Tyr Lys Ile Gln Ile Glu Asp Ala Arg Pro Ser Thr Ala Phe
 130 135 140
 Leu Ala Asp Ala Thr Glu Leu Ile Asn Gln Ala Asn Ser Glu Ile Val
 145 150 155 160
 Pro Phe His Val Arg Met Leu Ser Asn Ser Lys Ile Val Met Ser Gly
 165 170 175
 Phe Ser Asp Tyr Ser Leu Ala Gly Asp Ala Ile Thr Ser Ala Gly Lys
 180 185 190
 Leu Ala Glu Leu Ala Arg Pro Phe Ala His Trp Lys Glu Asn Val Ile
 195 200 205
 Pro Thr Ile Glu Ile Ala Met Asp Tyr Glu Pro Ser Pro Val Ala Asp
 210 215 220
 Leu Trp Gln Gly Asp Ser Ser Glu Thr Pro Glu Pro Phe Asp Asp Phe
 225 230 235 240
 Glu Arg Leu Leu Arg Glu Glu Met Leu Ile Pro Glu Ile
 245 250

<210> 1597

<211> 834

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(811)

<223> RXA00121

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 cgctgtcgcac cccatcttct aaacaagaaa ggcccctcca atg ttg agc gat ctg 115
 Met Leu Ser Asp Leu
 1 5

 agc tcc att ttt gac ttc caa gac ctc tcc ggc acc ttc tct gtc gtc 163
 Ser Ser Ile Phe Asp Phe Gln Asp Leu Ser Gly Thr Phe Ser Val Val
 10 15 20

 gac gtt ctc atc act ttg gtc ttg tcc ttc gtc ctg acc tcc atc gtg 211
 Asp Val Leu Ile Thr Leu Val Leu Ser Phe Val Leu Thr Ser Ile Val

25	30	35	
ggt gtg gtg tac caa aag acc cac cgc cac atc tcc tac agc cag tca			259
Gly Val Val Tyr Gln Lys Thr His Arg His Ile Ser Tyr Ser Gln Ser			
40	45	50	
ttc gta caa acg ttg gtg ctg gtg gga atg gtc att gca atc atc atg			307
Phe Val Gln Thr Leu Val Leu Val Gly Met Val Ile Ala Ile Ile Met			
55	60	65	
ctg gtg gtc ggc tcc aac att gca cgt gca ttc gcc ctg gtt ggc gcg			355
Leu Val Val Gly Ser Asn Ile Ala Arg Ala Phe Ala Leu Val Gly Ala			
70	75	80	85
ctt tcg gtg att cga ttc cgc aac gca gtg aaa gaa acc cga gat gtg			403
Leu Ser Val Ile Arg Phe Arg Asn Ala Val Lys Glu Thr Arg Asp Val			
90	95	100	
ggc ttc ctt ttc ctt gcc atg gca atc ggc atg act tgc ggt acc cgc			451
Gly Phe Leu Phe Leu Ala Met Ala Ile Gly Met Thr Cys Gly Thr Arg			
105	110	115	
ttc tac gtt ctg gcg atc gct gca acc atc gtt gtc tgt ggc gtt ctg			499
Phe Tyr Val Leu Ala Ile Ala Ala Thr Ile Val Val Cys Gly Val Leu			
120	125	130	
ttc atc atg tac cgc ttc gac tgg ttc aag gct gat atc cag cgc cag			547
Phe Ile Met Tyr Arg Phe Asp Trp Phe Lys Ala Asp Ile Gln Arg Gln			
135	140	145	
gtc atc aag gtg cag gtc cca gcc gat gga caa gct gat tcc ggc agg			595
Val Ile Lys Val Gln Val Pro Ala Asp Gly Gln Ala Asp Ser Gly Arg			
150	155	160	165
tcc tac gca gaa gaa gtt gaa ctg atc ctc gca cag tac tgc act tcc			643
Ser Tyr Ala Glu Glu Val Glu Leu Ile Leu Ala Gln Tyr Cys Thr Ser			
170	175	180	
ttt gag atg atg tcc gct gaa tct gtc cgc ggc gga gcc ctg acc gag			691
Phe Glu Met Met Ser Ala Glu Ser Val Arg Gly Gly Ala Leu Thr Glu			
185	190	195	
ttc tcc tac acc gct caa atg cgc aag aac gtg aag cca cat gag ctg			739
Phe Ser Tyr Thr Ala Gln Met Arg Lys Asn Val Lys Pro His Glu Leu			
200	205	210	
gtc gcc aag atg cgc gat gtg aac tac ggc caa aaa gcg act gtc ctg			787
Val Ala Lys Met Arg Asp Val Asn Tyr Gly Gln Lys Ala Thr Val Leu			
215	220	225	
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Thr Gly His Asp Gln Thr Asp Val			
230	235		

<210> 1598

<211> 237

<212> PRT

<213> Corynebacterium glutamicum

<400> 1598

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 Leu Thr Ser Ile Val Gly Val Val Tyr Gln Lys Thr His Arg His Ile
 35 40 45
 Ser Tyr Ser Gln Ser Phe Val Gln Thr Leu Val Leu Val Gly Met Val
 50 55 60
 Ile Ala Ile Ile Met Leu Val Val Gly Ser Asn Ile Ala Arg Ala Phe
 65 70 75 80
 Ala Leu Val Gly Ala Leu Ser Val Ile Arg Phe Arg Asn Ala Val Lys
 85 90 95
 Glu Thr Arg Asp Val Gly Phe Leu Phe Leu Ala Met Ala Ile Gly Met
 100 105 110
 Thr Cys Gly Thr Arg Phe Tyr Val Leu Ala Ile Ala Ala Thr Ile Val
 115 120 125
 Val Cys Gly Val Leu Phe Ile Met Tyr Arg Phe Asp Trp Phe Lys Ala
 130 135 140
 Asp Ile Gln Arg Gln Val Ile Lys Val Gln Val Pro Ala Asp Gly Gln
 145 150 155 160
 Ala Asp Ser Gly Arg Ser Tyr Ala Glu Glu Val Glu Leu Ile Leu Ala
 165 170 175
 Gln Tyr Cys Thr Ser Phe Glu Met Met Ser Ala Glu Ser Val Arg Gly
 180 185 190
 Gly Ala Leu Thr Glu Phe Ser Tyr Thr Ala Gln Met Arg Lys Asn Val
 195 200 205
 Lys Pro His Glu Leu Val Ala Lys Met Arg Asp Val Asn Tyr Gly Gln
 210 215 220
 Lys Ala Thr Val Leu Thr Gly His Asp Gln Thr Asp Val
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<210> 1599

<211> 1746

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1723)

<223> RXA00122

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 Met Asn Arg Arg Leu

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ttc cta gga act tcc gca gct atc atc gct gtc ggt ggc gtg ctc ggt			163
Phe Leu Gly Thr Ser Ala Ala Ile Ile Ala Val Gly Gly Val Leu Gly			
	10	15	20
gga gtg cag gtt gta cct tat att tcc tct ggt gaa atc caa acg tca			211
Gly Val Gln Val Val Pro Tyr Ile Ser Ser Gly Glu Ile Gln Thr Ser			
	25	30	35
gca tca tcg act gcc acg atc gat gtc ggt gca ggc aat gtc gat att			259
Ala Ser Ser Thr Ala Thr Ile Asp Val Gly Ala Gly Asn Val Asp Ile			
	40	45	50
ttt gat acc tcc gtt tcc cat gaa atc agc ctg cag gtt tcg cag gaa			307
Phe Asp Thr Ser Val Ser His Glu Ile Ser Leu Gln Val Ser Gln Glu			
	55	60	65
agc ctc gat gag atg ctc gcg gac tat caa gaa gac ggt tcc aaa acc			355
Ser Leu Asp Glu Met Leu Ala Asp Tyr Gln Glu Asp Gly Ser Lys Thr			
	70	75	80
tggtgtg aaa gca acc atc acg att gat ggc gtg acc att gaa aac gtc			403
Trp Val Lys Ala Thr Ile Thr Ile Asp Gly Val Thr Ile Glu Asn Val			
	90	95	100
ggc atc cgc ctc aag ggc aac tcc acg ctg tcc ggg ttg ggt cga aca			451
Gly Ile Arg Leu Lys Gly Asn Ser Thr Leu Ser Gly Leu Gly Arg Thr			
	105	110	115
tct gaa gaa ggc gga cct cag gca cca gaa ggc gtc gaa gag ttt aca			499
Ser Glu Glu Gly Gly Pro Gln Ala Pro Glu Gly Val Glu Glu Phe Thr			
	120	125	130
gat ctc agt gaa gag gaa atc gcc cag ttt gag gaa cag ttc gcg gcg			547
Asp Leu Ser Glu Glu Glu Ile Ala Gln Phe Glu Glu Gln Phe Ala Ala			
	135	140	145
cag caa gag act act gac gct tca gag acc ggt gaa act gcg gaa aat			595
Gln Gln Glu Thr Thr Asp Ala Ser Glu Thr Gly Glu Thr Ala Glu Asn			
	150	155	160
gaa gag act cgc ggc ccc ggc ggt ggc atg ggt ggt ggc ggc atg ggt			643
Glu Glu Thr Arg Gly Pro Gly Gly Gly Met Gly Gly Gly Gly Met Gly			
	170	175	180
ggc atg act tcg gtc gat gcc gac gat gtc agc acc tgg cca ctt ctg			691
Gly Met Thr Ser Val Asp Ala Asp Asp Val Ser Thr Trp Pro Leu Leu			
	185	190	195
atc agc ttc gac aaa tac gaa gac ggc cgc gtc tac caa ggc atg acc			739
Ile Ser Phe Asp Lys Tyr Glu Asp Gly Arg Val Tyr Gln Gly Met Thr			
	200	205	210
caa ctg gca cta cgc ccc ggc acc acc gtg gtc aac gaa gca atg gcg			787
Gln Leu Ala Leu Arg Pro Gly Thr Thr Val Val Asn Glu Ala Met Ala			
	215	220	225
ctg gcc ctg acc gca gaa acc ggc cag gtc tcg cag caa tcc agc ttc			835
Leu Ala Leu Thr Ala Glu Thr Gly Gln Val Ser Gln Gln Ser Ser Phe			
	230	235	240
			245

aca acg ttt tcg ctt aac gac gag ccc tcc acc act cga ctc ctt ttg	883
Thr Thr Phe Ser Leu Asn Asp Glu Pro Ser Thr Thr Arg Leu Leu Leu	
250 255 260	
aag cac ccc gat gaa aat tat gcc gac gcg ctc ggc aac gga gtc ctc	931
Lys His Pro Asp Glu Asn Tyr Ala Asp Ala Leu Gly Asn Gly Val Leu	
265 270 275	
ttc aaa gca gat tcc aac agt tcc ttc acc tac caa ggc gaa gac caa	979
Phe Lys Ala Asp Ser Asn Ser Ser Phe Thr Tyr Gln Gly Glu Asp Gln	
280 285 290	
act gaa tac gac gga cag ttc aag cag atc aac ggt gac ggc aac gga	1027
Thr Glu Tyr Asp Gly Gln Phe Lys Gln Ile Asn Gly Asp Gly Asn Gly	
295 300 305	
gac atc caa ccg atc atc aac ctg ctg aaa tgg ctc gac acc gca agc	1075
Asp Ile Gln Pro Ile Ile Asn Leu Leu Lys Trp Leu Asp Thr Ala Ser	
310 315 320 325	
gat gaa gag ttt gct gaa cac ctc tct gac tac gtc gat gtg gaa agc	1123
Asp Glu Glu Phe Ala Glu His Leu Ser Asp Tyr Val Asp Val Glu Ser	
330 335 340	
ttt gct cgc tac gtt gcc act caa aac ctg ttg gta aat tcc gac gac	1171
Phe Ala Arg Tyr Val Ala Thr Gln Asn Leu Leu Val Asn Ser Asp Asp	
345 350 355	
atg gct ggt ccc ggt agt aat tac tac ctg tgg tac gac tac gac acc	1219
Met Ala Gly Pro Gly Ser Asn Tyr Tyr Leu Trp Tyr Asp Tyr Asp Thr	
360 365 370	
ggc ctg atc agc gtg atc tct tgg gat ttg aac ctc gca atg tcc ggc	1267
Gly Leu Ile Ser Val Ile Ser Trp Asp Leu Asn Leu Ala Met Ser Gly	
375 380 385	
tca act gat gct ggc cca gat gat gaa atc tcc atg ggc gga ggt ggc	1315
Ser Thr Asp Ala Gly Pro Asp Asp Glu Ile Ser Met Gly Gly Gly Gly	
390 395 400 405	
ggt ggc gga atg cgt cct ggt gga acg acc gac act gaa att gaa ggt	1363
Gly Gly Gly Met Arg Pro Gly Gly Thr Thr Asp Thr Glu Ile Glu Gly	
410 415 420	
act gcg acc gag gat atg cct gac atg ggc aat atg cag caa cgt gaa	1411
Thr Ala Thr Glu Asp Met Pro Asp Met Gly Asn Met Gln Gln Arg Glu	
425 430 435	
cgc cct gaa gga atg cca gac atg ggt gag atg cct gat atg ggt gac	1459
Arg Pro Glu Gly Met Pro Asp Met Gly Glu Met Pro Asp Met Gly Asp	
440 445 450	
cgg gaa ggc ggt gga tcg atg gga gga aac cag ctc aag gaa cgt ttc	1507
Arg Glu Gly Gly Gly Ser Met Gly Gly Asn Gln Leu Lys Glu Arg Phe	
455 460 465	
ctc gct tcc gat gca ttc acg gaa atc tat gag cag gtg tac tgg gag	1555
Leu Ala Ser Asp Ala Phe Thr Glu Ile Tyr Glu Gln Val Tyr Trp Glu	
470 475 480 485	

ctg tat gaa gaa atg tat ggt tcc gga act gcc atc gag ttg ttg gat 1603
 Leu Tyr Glu Glu Met Tyr Gly Ser Gly Thr Ala Ile Glu Leu Leu Asp
 490 495 500

gag att gca gcg tca att cca gaa act gat gcg gtg act gca gat gag 1651
 Glu Ile Ala Ala Ser Ile Pro Glu Thr Asp Ala Val Thr Ala Asp Glu
 505 510 515

atc gct acg gaa gtg gcg tca atg cgg gaa tgg atc act gcc cgc aca 1699
 Ile Ala Thr Glu Val Ala Ser Met Arg Glu Trp Ile Thr Ala Arg Thr
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gaa gcg ttg gct gct ttg caa gag tgatcaaact agaaaaccaa caa 1746
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<210> 1600

<211> 541

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1600

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 35 40 45

Gly Asn Val Asp Ile Phe Asp Thr Ser Val Ser His Glu Ile Ser Leu
 50 55 60

Gln Val Ser Gln Glu Ser Leu Asp Glu Met Leu Ala Asp Tyr Gln Glu
 65 70 75 80

Asp Gly Ser Lys Thr Trp Val Lys Ala Thr Ile Thr Ile Asp Gly Val
 85 90 95

Thr Ile Glu Asn Val Gly Ile Arg Leu Lys Gly Asn Ser Thr Leu Ser
 100 105 110

Gly Leu Gly Arg Thr Ser Glu Glu Gly Gly Pro Gln Ala Pro Glu Gly
 115 120 125

Val Glu Glu Phe Thr Asp Leu Ser Glu Glu Glu Ile Ala Gln Phe Glu
 130 135 140

Glu Gln Phe Ala Ala Gln Gln Glu Thr Thr Asp Ala Ser Glu Thr Gly
 145 150 155 160

Glu Thr Ala Glu Asn Glu Glu Thr Arg Gly Pro Gly Gly Gly Met Gly
 165 170 175

Gly Gly Gly Met Gly Gly Met Thr Ser Val Asp Ala Asp Asp Val Ser
 180 185 190

Thr Trp Pro Leu Leu Ile Ser Phe Asp Lys Tyr Glu Asp Gly Arg Val
 195 200 205

Tyr Gln Gly Met Thr Gln Leu Ala Leu Arg Pro Gly Thr Thr Val Val
 210 215 220
 Asn Glu Ala Met Ala Leu Ala Leu Thr Ala Glu Thr Gly Gln Val Ser
 225 230 235 240
 Gln Gln Ser Ser Phe Thr Thr Phe Ser Leu Asn Asp Glu Pro Ser Thr
 245 250 255
 Thr Arg Leu Leu Leu Lys His Pro Asp Glu Asn Tyr Ala Asp Ala Leu
 260 265 270
 Gly Asn Gly Val Leu Phe Lys Ala Asp Ser Asn Ser Ser Phe Thr Tyr
 275 280 285
 Gln Gly Glu Asp Gln Thr Glu Tyr Asp Gly Gln Phe Lys Gln Ile Asn
 290 295 300
 Gly Asp Gly Asn Gly Asp Ile Gln Pro Ile Ile Asn Leu Leu Lys Trp
 305 310 315 320
 Leu Asp Thr Ala Ser Asp Glu Glu Phe Ala Glu His Leu Ser Asp Tyr
 325 330 335
 Val Asp Val Glu Ser Phe Ala Arg Tyr Val Ala Thr Gln Asn Leu Leu
 340 345 350
 Val Asn Ser Asp Asp Met Ala Gly Pro Gly Ser Asn Tyr Tyr Leu Trp
 355 360 365
 Tyr Asp Tyr Asp Thr Gly Leu Ile Ser Val Ile Ser Trp Asp Leu Asn
 370 375 380
 Leu Ala Met Ser Gly Ser Thr Asp Ala Gly Pro Asp Asp Glu Ile Ser
 385 390 395 400
 Met Gly Gly Gly Gly Gly Gly Gly Met Arg Pro Gly Gly Thr Thr Asp
 405 410 415
 Thr Glu Ile Glu Gly Thr Ala Thr Glu Asp Met Pro Asp Met Gly Asn
 420 425 430
 Met Gln Gln Arg Glu Arg Pro Glu Gly Met Pro Asp Met Gly Glu Met
 435 440 445
 Pro Asp Met Gly Asp Arg Glu Gly Gly Gly Ser Met Gly Gly Asn Gln
 450 455 460
 Leu Lys Glu Arg Phe Leu Ala Ser Asp Ala Phe Thr Glu Ile Tyr Glu
 465 470 475 480
 Gln Val Tyr Trp Glu Leu Tyr Glu Glu Met Tyr Gly Ser Gly Thr Ala
 485 490 495
 Ile Glu Leu Leu Asp Glu Ile Ala Ala Ser Ile Pro Glu Thr Asp Ala
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 <211> 579
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(556)
 <223> RXA00127

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 Leu Ser Pro Tyr Asp
 1 5
 ggc ccg cat cgc aac gtg ctc att gcg ctg aag gag cac ggc cgt gca 163
 Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys Glu His Gly Arg Ala
 10 15 20
 gac ctt gtg gcg ttt gtg ggc gcg gtg gtg ggg gcg tgc ata agc tat 211
 Asp Leu Val Ala Phe Val Gly Ala Val Val Gly Ala Ser Ile Ser Tyr
 25 30 35
 ctg gcg gct cag ggg gaa att gag cac gac atc acg ctg gtt ccg gcg 259
 Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile Thr Leu Val Pro Ala
 40 45 50
 ccc acc cgc gcc acc tgc cga cgc cgg cgg ggc ggc gat ccg gtt gag 307
 Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly Gly Asp Pro Val Glu
 55 60 65
 cgg gtg tgc aat gca tca cgc tta tgc acg ttt ccc tgc ctt caa atc 355
 Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe Pro Cys Leu Gln Ile
 70 75 80 85
 tca tcc cgc aca cca gac tcc gtc ggt caa act gcg caa cag cga aga 403
 Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr Ala Gln Gln Arg Arg
 90 95 100
 ctc aat atg cga gtg gag tta gtc cga caa cct cgg ggt tct gtc ttg 451
 Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro Arg Gly Ser Val Leu
 105 110 115
 atc atc gac gat gtg gta aca acg ggg gca act att tcc gca tct gca 499
 Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr Ile Ser Ala Ser Ala
 120 125 130
 aac gtt ctt cgc gca gcg ggt gtg cag gtc aga gga gct tta act tat 547
 Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg Gly Ala Leu Thr Tyr
 135 140 145
 tgc caa gcg tgatcttgga tataaaaggg gcc 579
 Cys Gln Ala
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<210> 1602

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1602

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Ala Ser Ile Ser Tyr Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile
          35           40           45
Thr Leu Val Pro Ala Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly
          50           55           60
Gly Asp Pro Val Glu Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe
          65           70           75           80
Pro Cys Leu Gln Ile Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr
          85           90           95
Ala Gln Gln Arg Arg Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro
          100          105          110
Arg Gly Ser Val Leu Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr
          115          120          125
Ile Ser Ala Ser Ala Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg
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Gly Ala Leu Thr Tyr Cys Gln Ala
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<211> 693

<212> DNA

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<222> (101)..(670)

<223> RXA00134

<400> 1603

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acc aag atc tat acg cga acc ggg gac gat gga acc acg ggg ctc tca 163
Thr Lys Ile Tyr Thr Arg Thr Gly Asp Asp Gly Thr Thr Gly Leu Ser
          10           15           20
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Asn Phe Glu Arg Val Pro Lys Asp Asp Pro Arg Leu Ile Ala Tyr Ala

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Asp Ser Asp Glu Ala Asn Cys Ala Ile Gly Gln Val Leu Ala Leu Ser			
40	45	50	
agc cct acg gaa gat atg gca acc tta ttg cgg act att caa aat gaa			307
Ser Pro Thr Glu Asp Met Ala Thr Leu Leu Arg Thr Ile Gln Asn Glu			
55	60	65	
ctt ttt gat gtg ggc gca gac tta gca acc ccg att gag gag aat ccg			355
Leu Phe Asp Val Gly Ala Asp Leu Ala Thr Pro Ile Glu Glu Asn Pro			
70	75	80	85
aag tat ccc cca ctt cga gtt ctt ccg gaa tat atc gaa cga ctt gag			403
Lys Tyr Pro Pro Leu Arg Val Leu Pro Glu Tyr Ile Glu Arg Leu Glu			
90	95	100	
aag gag tgc gat aaa tgg aac gag gat gtg ccg gcg ttg gat tcc ttc			451
Lys Glu Cys Asp Lys Trp Asn Glu Asp Val Pro Ala Leu Asp Ser Phe			
105	110	115	
att ttg ccg ggt ggc acg cca gca gcg gca ctc ttg cac acc gca agg			499
Ile Leu Pro Gly Gly Thr Pro Ala Ala Ala Leu Leu His Thr Ala Arg			
120	125	130	
gta att acg agg cgc gcg gag aga gca gct tgg ata gcg gtg cgg gaa			547
Val Ile Thr Arg Arg Ala Glu Arg Ala Ala Trp Ile Ala Val Arg Glu			
135	140	145	
ttt ccg agc acc acc tct acc ttg cca gcc caa tac ctg aat cgt ctt			595
Phe Pro Ser Thr Thr Ser Thr Leu Pro Ala Gln Tyr Leu Asn Arg Leu			
150	155	160	165
agc gat ctg ctg ttt att ctt tcc cgt gtt gcc aac aat ggc aat gat			643
Ser Asp Leu Leu Phe Ile Leu Ser Arg Val Ala Asn Asn Gly Asn Asp			
170	175	180	
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<210> 1604

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 1604

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			20					25					30		

Leu	Ile	Ala	Tyr	Ala	Asp	Ser	Asp	Glu	Ala	Asn	Cys	Ala	Ile	Gly	Gln
		35					40					45			

Val	Leu	Ala	Leu	Ser	Ser	Pro	Thr	Glu	Asp	Met	Ala	Thr	Leu	Leu	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50				55				60							
Thr 65	Ile	Gln	Asn	Glu	Leu 70	Phe	Asp	Val	Gly	Ala 75	Asp	Leu	Ala	Thr	Pro 80
Ile	Glu	Glu	Asn 85	Pro	Lys	Tyr	Pro	Pro	Leu 90	Arg	Val	Leu	Pro	Glu 95	Tyr
Ile	Glu	Arg	Leu 100	Glu	Lys	Glu	Cys	Asp 105	Lys	Trp	Asn	Glu	Asp 110	Val	Pro
Ala	Leu	Asp 115	Ser	Phe	Ile	Leu	Pro 120	Gly	Gly	Thr	Pro	Ala 125	Ala	Ala	Leu
Leu 130	His	Thr	Ala	Arg	Val 135	Ile	Thr	Arg	Arg	Ala	Glu 140	Arg	Ala	Ala	Trp
Ile 145	Ala	Val	Arg	Glu	Phe 150	Pro	Ser	Thr	Thr	Ser 155	Thr	Leu	Pro	Ala	Gln 160
Tyr	Leu	Asn	Arg	Leu 165	Ser	Asp	Leu	Leu	Phe 170	Ile	Leu	Ser	Arg	Val 175	Ala
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<213> Corynebacterium glutamicum
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<223> RXA00140
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Met Ser Asp Glu Ser
1 5

atc gaa gag cag gaa aaa gaa ctc gcg gcg ctg aag gct caa atc gat 163
Ile Glu Glu Gln Glu Lys Glu Leu Ala Ala Leu Lys Ala Gln Ile Asp
10 15 20

gaa ctg gaa aag aaa gac aag cag aac aag cta atc atc gag att ttg 211
Glu Leu Glu Lys Lys Asp Lys Gln Asn Lys Leu Ile Ile Glu Ile Leu
25 30 35

tcc aag gcc gtc gaa aag aat gtg gca gag gca gaa gcg aaa aga gcc 259
Ser Lys Ala Val Glu Lys Asn Val Ala Glu Ala Glu Ala Lys Arg Ala
40 45 50

cgc aaa tat ccg ccc aat ccc ctg tgg tgaattctaa ggcgtcgaac 306
Arg Lys Tyr Pro Pro Asn Pro Leu Trp
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ttt 309

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<210> 1606

<211> 62

<212> PRT

<213> Corynebacterium glutamicum

<400> 1606

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Ile Ile Glu Ile Leu Ser Lys Ala Val Glu Lys Asn Val Ala Glu Ala
 35 40 45

Glu Ala Lys Arg Ala Arg Lys Tyr Pro Pro Asn Pro Leu Trp
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<210> 1607

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> RXA00141

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cagcaattcc cagatctagt cacctggaag gacgaacacc atg acc act gat tcc 115
 Met Thr Thr Asp Ser
 1 5

aat tct gcg aca atc cca acc cca aag ccg att cca gtg acc atc gac 163
 Asn Ser Ala Thr Ile Pro Thr Pro Lys Pro Ile Pro Val Thr Ile Asp
 10 15 20

cga atc tcc ctc atc atg aaa gaa ttc ggc att gac cta tcc atc gcc 211
 Arg Ile Ser Leu Ile Met Lys Glu Phe Gly Ile Asp Leu Ser Ile Ala
 25 30 35

gat gaa caa ggc acc gga tcc caa gta gcc agc gcc aac ctc aac ggc 259
 Asp Glu Gln Gly Thr Gly Ser Gln Val Ala Ser Ala Asn Leu Asn Gly
 40 45 50

cat cac gtc atg ttc gct gtc atc ggt tca gtc ctg atc gtt cgt gcc 307
 His His Val Met Phe Ala Val Ile Gly Ser Val Leu Ile Val Arg Ala
 55 60 65

gat cgc gcc acc gaa atg cca gtc tcc gac ggc aac ccc gca tgg cat 355
 Asp Arg Ala Thr Glu Met Pro Val Ser Asp Gly Asn Pro Ala Trp His
 70 75 80 85

ctc gcc tgc aac caa gtc aac tgt ttc aac ttc gct gcc aag gct gtc 403
 Leu Ala Cys Asn Gln Val Asn Cys Phe Asn Phe Ala Ala Lys Ala Val
 90 95 100

gta gtt gat cgc acc gac aac atc gtg atc cgc gcc gag aag gat gtc 451
Val Val Asp Arg Thr Asp Asn Ile Val Ile Arg Ala Glu Lys Asp Val
105 110 115

ccc atc gcc gct ggg ctc aac gat att cag ctt tcc gca atg ctg aaa 499
Pro Ile Ala Ala Gly Leu Asn Asp Ile Gln Leu Ser Ala Met Leu Lys
120 125 130

aac gcc atc gat cac gtc ctc gcg att caa gat gcc gta gcc aat gca 547
Asn Ala Ile Asp His Val Leu Ala Ile Gln Asp Ala Val Ala Asn Ala
135 140 145

ggc aag gaa atc ggc taacatgtcg gacgagtcca tcg 585
Gly Lys Glu Ile Gly
150

<210> 1608

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 1608

Met Thr Thr Asp Ser Asn Ser Ala Thr Ile Pro Thr Pro Lys Pro Ile
1 5 10 15

Pro Val Thr Ile Asp Arg Ile Ser Leu Ile Met Lys Glu Phe Gly Ile
20 25 30

Asp Leu Ser Ile Ala Asp Glu Gln Gly Thr Gly Ser Gln Val Ala Ser
35 40 45

Ala Asn Leu Asn Gly His His Val Met Phe Ala Val Ile Gly Ser Val
50 55 60

Leu Ile Val Arg Ala Asp Arg Ala Thr Glu Met Pro Val Ser Asp Gly
65 70 75 80

Asn Pro Ala Trp His Leu Ala Cys Asn Gln Val Asn Cys Phe Asn Phe
85 90 95

Ala Ala Lys Ala Val Val Val Asp Arg Thr Asp Asn Ile Val Ile Arg
100 105 110

Ala Glu Lys Asp Val Pro Ile Ala Ala Gly Leu Asn Asp Ile Gln Leu
115 120 125

Ser Ala Met Leu Lys Asn Ala Ile Asp His Val Leu Ala Ile Gln Asp
130 135 140

Ala Val Ala Asn Ala Gly Lys Glu Ile Gly
145 150

<210> 1609

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(577)
 <223> RXA00142

<400> 1609

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gttacttttta aaaggattttt ggaaggactg aaactcccca gtg cct caa tca ccc 115
                               Val Pro Gln Ser Pro
                               1 5

aca gca cac gac ccc aac gac atc cag gaa ttt aac ctc gat gcc gtt 163
Thr Ala His Asp Pro Asn Asp Ile Gln Glu Phe Asn Leu Asp Ala Val
                               10 15 20

gca ggg att ctc cag gac gaa aaa ctg gac tac cgc atc gat gaa cac 211
Ala Gly Ile Leu Gln Asp Glu Lys Leu Asp Tyr Arg Ile Asp Glu His
                               25 30 35

gac ggc gaa aaa gta atc cgc acc gga ttc atc aac gcc gcc atc agc 259
Asp Gly Glu Lys Val Ile Arg Thr Gly Phe Ile Asn Ala Ala Ile Ser
                               40 45 50

ttc atc ctc tta gac ggc agc tta acc atg gaa gcc atg tgg cga gga 307
Phe Ile Leu Leu Asp Gly Ser Leu Thr Met Glu Ala Met Trp Arg Gly
                               55 60 65

gcc ccc tcc acc gat gct gcc gca caa gtt ctc gcg gcc acc aac gaa 355
Ala Pro Ser Thr Asp Ala Ala Ala Gln Val Leu Ala Ala Thr Asn Glu
                               70 75 80 85

tgg aac ctc acc cag ttc gca ccc acc att cga ttc ttc gaa ctc aac 403
Trp Asn Leu Thr Gln Phe Ala Pro Thr Ile Arg Phe Phe Glu Leu Asn
                               90 95 100

gaa ggc acc ctc gcc atc aat gca ctg cga cac gtc gtt gtt tcc gca 451
Glu Gly Thr Leu Ala Ile Asn Ala Leu Arg His Val Val Val Ser Ala
                               105 110 115

ggc atg agc cac aac caa gtc ggc tcc tac gtt atg agc tcc atc gaa 499
Gly Met Ser His Asn Gln Val Gly Ser Tyr Val Met Ser Ser Ile Glu
                               120 125 130

tcc gct gtt cag tgc ttc gaa tgg ctt gag cag caa ttc cca gat cta 547
Ser Ala Val Gln Cys Phe Glu Trp Leu Glu Gln Gln Phe Pro Asp Leu
                               135 140 145

gtc acc tgg aag gac gaa cac cat gac cac tgattccaat tctgcgacaa 597
Val Thr Trp Lys Asp Glu His His Asp His
150 155

tcc 600

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<210> 1610
 <211> 159
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1610

Val Pro Gln Ser Pro Thr Ala His Asp Pro Asn Asp Ile Gln Glu Phe

1	5	10	15
Asn Leu Asp	Ala Val Ala Gly Ile	Leu Gln Asp Glu Lys	Leu Asp Tyr
	20	25	30
Arg Ile Asp	Glu His Asp Gly Glu Lys	Val Ile Arg Thr	Gly Phe Ile
	35	40	45
Asn Ala Ala	Ile Ser Phe Ile Leu Leu	Asp Gly Ser Leu Thr	Met Glu
	50	55	60
Ala Met Trp	Arg Gly Ala Pro Ser Thr	Asp Ala Ala Ala	Gln Val Leu
	65	70	75
Ala Ala Thr	Asn Glu Trp Asn Leu Thr	Gln Phe Ala Pro	Thr Ile Arg
	85	90	95
Phe Phe Glu	Leu Asn Glu Gly Thr Leu	Ala Ile Asn Ala	Leu Arg His
	100	105	110
Val Val Val	Ser Ala Gly Met Ser His	Asn Gln Val Gly	Ser Tyr Val
	115	120	125
Met Ser Ser	Ile Glu Ser Ala Val Gln	Cys Phe Glu Trp	Leu Glu Gln
	130	135	140
Gln Phe Pro	Asp Leu Val Thr Trp Lys	Asp Glu His His	Asp His
	145	150	155

<210> 1611

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA00150

<400> 1611

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tcaaaatggc ggaatatattt gatcacgggg gtgcaactgt	atg gtg ttt tct atg	115
	Met Val Phe Ser Met	
	1 5	

cat gac aaa ggt gag acc cag gag aat cct gcg gac atg tca gga cgc	163
His Asp Lys Gly Glu Thr Gln Glu Asn Pro Ala Asp Met Ser Gly Arg	
	10 15 20

cta aac aca cca att tcc acg gtc ttt cac ttc ttt agc tca ctt ttc	211
Leu Asn Thr Pro Ile Ser Thr Val Phe His Phe Phe Ser Ser Leu Phe	
	25 30 35

cat gac gct ctg cgc agt gtt gcc cag tgg agt gcg tgg aag aaa atc	259
His Asp Ala Leu Arg Ser Val Ala Gln Trp Ser Ala Trp Lys Lys Ile	
	40 45 50

gct gta tcg gtt gtc atc gtc gca att att tcc gta act ttt ctt gtc	307
Ala Val Ser Val Val Ile Val Ala Ile Ile Ser Val Thr Phe Leu Val	

55	60	65	
gat gtc ccc ccg att tcg gtt tat cgt gac tgg gca aac aac gcc ggc			355
Asp Val Pro Pro Ile Ser Val Tyr Arg Asp Trp Ala Asn Asn Ala Gly			
70	75	80	85
gac gct ttt gtc tta gtt ttt tgc gcc ttt tat atc ctc att act cag			403
Asp Ala Phe Val Leu Val Phe Cys Ala Phe Tyr Ile Leu Ile Thr Gln			
	90	95	100
ttc cct atc ccc cgc aca gtt ctc aca ctg gcc tcc ggc gtg ctg ttc			451
Phe Pro Ile Pro Arg Thr Val Leu Thr Leu Ala Ser Gly Val Leu Phe			
	105	110	115
ggg ccg gtt ctt gga tca gtc gtg gcg ctg ggt tcc acc aca gtg tca			499
Gly Pro Val Leu Gly Ser Val Val Ala Leu Gly Ser Thr Thr Val Ser			
	120	125	130
gcg gta atc tcg ctc ctc att gtt cgg ggt ctg ctt ggc gat tgg atg			547
Ala Val Ile Ser Leu Leu Ile Val Arg Gly Leu Leu Gly Asp Trp Met			
	135	140	145
gcg cca cgt tta acg cac ccc gca gtc tca cgc atc aat acc cga ctt			595
Ala Pro Arg Leu Thr His Pro Ala Val Ser Arg Ile Asn Thr Arg Leu			
	150	155	165
gag caa cgt gga tgg ctg gcg att acc tct tta aga atg atc gcc gct			643
Glu Gln Arg Gly Trp Leu Ala Ile Thr Ser Leu Arg Met Ile Ala Ala			
	170	175	180
atc ccc ttt tcc atc ctc aac tat gtt gca gcc ttg act agc gtt cct			691
Ile Pro Phe Ser Ile Leu Asn Tyr Val Ala Ala Leu Thr Ser Val Pro			
	185	190	195
gtt ttt tct ttt gcc atc gct acc ttg atc gga tct gca cca gga acc			739
Val Phe Ser Phe Ala Ile Ala Thr Leu Ile Gly Ser Ala Pro Gly Thr			
	200	205	210
atc gtc acc gtc gtt ttg gga gat gca gtc aca ggt tct gga aac tgg			787
Ile Val Thr Val Val Leu Gly Asp Ala Val Thr Gly Ser Gly Asn Trp			
	215	220	225
act gcc gtt gca ttc acg gta ttt tta gcg att ttg ggt gtt tta ggt			835
Thr Ala Val Ala Phe Thr Val Phe Leu Ala Ile Leu Gly Val Leu Gly			
	230	235	240
atc ttt tta gat caa aag atg cca gtc aag cct gga aag tagacaatat			884
Ile Phe Leu Asp Gln Lys Met Pro Val Lys Pro Gly Lys			
	250	255	
aaggtagggt tgg			897

<210> 1612

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 1612

Met	Val	Phe	Ser	Met	His	Asp	Lys	Gly	Glu	Thr	Gln	Glu	Asn	Pro	Ala
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Asp Met Ser Gly Arg Leu Asn Thr Pro Ile Ser Thr Val Phe His Phe
 20 25 30
 Phe Ser Ser Leu Phe His Asp Ala Leu Arg Ser Val Ala Gln Trp Ser
 35 40 45
 Ala Trp Lys Lys Ile Ala Val Ser Val Val Ile Val Ala Ile Ile Ser
 50 55 60
 Val Thr Phe Leu Val Asp Val Pro Pro Ile Ser Val Tyr Arg Asp Trp
 65 70 75 80
 Ala Asn Asn Ala Gly Asp Ala Phe Val Leu Val Phe Cys Ala Phe Tyr
 85 90 95
 Ile Leu Ile Thr Gln Phe Pro Ile Pro Arg Thr Val Leu Thr Leu Ala
 100 105 110
 Ser Gly Val Leu Phe Gly Pro Val Leu Gly Ser Val Val Ala Leu Gly
 115 120 125
 Ser Thr Thr Val Ser Ala Val Ile Ser Leu Leu Ile Val Arg Gly Leu
 130 135 140
 Leu Gly Asp Trp Met Ala Pro Arg Leu Thr His Pro Ala Val Ser Arg
 145 150 155 160
 Ile Asn Thr Arg Leu Glu Gln Arg Gly Trp Leu Ala Ile Thr Ser Leu
 165 170 175
 Arg Met Ile Ala Ala Ile Pro Phe Ser Ile Leu Asn Tyr Val Ala Ala
 180 185 190
 Leu Thr Ser Val Pro Val Phe Ser Phe Ala Ile Ala Thr Leu Ile Gly
 195 200 205
 Ser Ala Pro Gly Thr Ile Val Thr Val Val Leu Gly Asp Ala Val Thr
 210 215 220
 Gly Ser Gly Asn Trp Thr Ala Val Ala Phe Thr Val Phe Leu Ala Ile
 225 230 235 240
 Leu Gly Val Leu Gly Ile Phe Leu Asp Gln Lys Met Pro Val Lys Pro
 245 250 255

Gly Lys

<210> 1613

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(697)

<223> RXA00151

<400> 1613

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acagcgaatc cactacaata aacaaagggg gcagccaccc atg tgg gca ctg cat 115
Met Trp Ala Leu His
1 5
gcc aga tac cgc ggc cga gac aca cga cga gcc gaa ttg gtt aaa aga 163
Ala Arg Tyr Arg Gly Arg Asp Thr Arg Arg Ala Glu Leu Val Lys Arg
10 15 20
ttt gca gaa gct ttg tcc acc ctc gaa ggt gct ggc cag ttt gaa gtc 211
Phe Ala Glu Ala Leu Ser Thr Leu Glu Gly Ala Gly Gln Phe Glu Val
25 30 35
att ggt gtc gaa gac atc cga gca cac atc acc tca ccg tta acc aca 259
Ile Gly Val Glu Asp Ile Arg Ala His Ile Thr Ser Pro Leu Thr Thr
40 45 50
tgt gat gtt gtc atg gcg cta ctc gca gct ggc gat tgg gca atc gga 307
Cys Asp Val Val Met Ala Leu Leu Ala Ala Gly Asp Trp Ala Ile Gly
55 60 65
att ggt gtt atc ccc acc gtt gac gga aca gtc gat gaa tcg gat gag 355
Ile Gly Val Ile Pro Thr Val Asp Gly Thr Val Asp Glu Ser Asp Glu
70 75 80 85
gcc atc atc gaa cag gta aag aaa att tcc tct gat gct ctg cgc ccc 403
Ala Ile Ile Glu Gln Val Lys Lys Ile Ser Ser Asp Ala Leu Arg Pro
90 95 100
acc gcc aag gcg gga acg gtc aaa gtt agg atc gcc gga acc aaa cgg 451
Thr Ala Lys Ala Gly Thr Val Lys Val Arg Ile Ala Gly Thr Lys Arg
105 110 115
gac aat act caa gcc ttc aac atc tcc gct gca ttc acg ttg att ggg 499
Asp Asn Thr Gln Ala Phe Asn Ile Ser Ala Ala Phe Thr Leu Ile Gly
120 125 130
caa gtt ctg tca aag cgc acc atc gaa gga cgc gaa gcc acc gca ctc 547
Gln Val Leu Ser Lys Arg Thr Ile Glu Gly Arg Glu Ala Thr Ala Leu
135 140 145
gtc cgt tct gga ctg aat caa aat gag gca gcc caa gag ctc ggt att 595
Val Arg Ser Gly Leu Asn Gln Asn Glu Ala Ala Gln Glu Leu Gly Ile
150 155 160 165
tcc aag cag gca atg tcg cag cga ttg cag gcg gca ggt tgg cag gcg 643
Ser Lys Gln Ala Met Ser Gln Arg Leu Gln Ala Ala Gly Trp Gln Ala
170 175 180
gaa tct gct ggt tgg caa ttg gcc gta aac ctc atc gag cag gct ggc 691
Glu Ser Ala Gly Trp Gln Leu Ala Val Asn Leu Ile Glu Gln Ala Gly
185 190 195
aag cgc tagcaggcga ttttaagagcc tga 720
Lys Arg

<210> 1614

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 1614

Met Trp Ala Leu His Ala Arg Tyr Arg Gly Arg Asp Thr Arg Arg Ala
 1 5 10 15

Glu Leu Val Lys Arg Phe Ala Glu Ala Leu Ser Thr Leu Glu Gly Ala
 20 25 30

Gly Gln Phe Glu Val Ile Gly Val Glu Asp Ile Arg Ala His Ile Thr
 35 40 45

Ser Pro Leu Thr Thr Cys Asp Val Val Met Ala Leu Leu Ala Ala Gly
 50 55 60

Asp Trp Ala Ile Gly Ile Gly Val Ile Pro Thr Val Asp Gly Thr Val
 65 70 75 80

Asp Glu Ser Asp Glu Ala Ile Ile Glu Gln Val Lys Lys Ile Ser Ser
 85 90 95

Asp Ala Leu Arg Pro Thr Ala Lys Ala Gly Thr Val Lys Val Arg Ile
 100 105 110

Ala Gly Thr Lys Arg Asp Asn Thr Gln Ala Phe Asn Ile Ser Ala Ala
 115 120 125

Phe Thr Leu Ile Gly Gln Val Leu Ser Lys Arg Thr Ile Glu Gly Arg
 130 135 140

Glu Ala Thr Ala Leu Val Arg Ser Gly Leu Asn Gln Asn Glu Ala Ala
 145 150 155 160

Gln Glu Leu Gly Ile Ser Lys Gln Ala Met Ser Gln Arg Leu Gln Ala
 165 170 175

Ala Gly Trp Gln Ala Glu Ser Ala Gly Trp Gln Leu Ala Val Asn Leu
 180 185 190

Ile Glu Gln Ala Gly Lys Arg
 195

<210> 1615

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA00153

<400> 1615

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agccctgcct ggcccttcca aattatgtag ggtggcctgc gtg gga gca ata att 115
 Val Gly Ala Ile Ile
 1 5

tgg ttt atc gga gca ttg gtt ctt gct ggc ttg gaa ttg gca gta ggt 163
 Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu Glu Leu Ala Val Gly
 10 15 20

gag ttc acc tta ttg atg ctc ggc ggt gca gct ttg gca acc gcc ggc 211
 Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala Leu Ala Thr Ala Gly
 25 30 35

gtg gca ctc atc ggt gtc cca gta tgg gct gaa ttt gtc acc ttc gcg 259
 Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu Phe Val Thr Phe Ala
 40 45 50

gtg gcc tca gct gct cta ctg atg ttc att agg ccg gcc att aga aag 307
 Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg Pro Ala Ile Arg Lys
 55 60 65

cgt ctg ctg aaa cca aag gtt ctg gac tct tca cca cga gca ctt gtt 355
 Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser Pro Arg Ala Leu Val
 70 75 80 85

ggc cac cgt gct gaa gtg ctc gaa gat gtc gga gcg acc agc ggg cag 403
 Gly His Arg Ala Glu Val Leu Glu Asp Val Gly Ala Thr Ser Gly Gln
 90 95 100

gtc cgc ctg gat ggt tca att tgg tcc gcc cgc agc atg gat ccc aca 451
 Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg Ser Met Asp Pro Thr
 105 110 115

cac acc ttc gcg gaa ggt gaa att gtc agt gtc att gat atc caa ggc 499
 His Thr Phe Ala Glu Gly Glu Ile Val Ser Val Ile Asp Ile Gln Gly
 120 125 130

acg acc gcg att gta tgg aaa gaa gcc taaattttta acaatcaaatt 546
 Thr Thr Ala Ile Val Trp Lys Glu Ala
 135 140

agt 549

<210> 1616

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 1616

Val Gly Ala Ile Ile Trp Phe Ile Gly Ala Leu Val Leu Ala Gly Leu
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Glu Leu Ala Val Gly Glu Phe Thr Leu Leu Met Leu Gly Gly Ala Ala
 20 25 30

Leu Ala Thr Ala Gly Val Ala Leu Ile Gly Val Pro Val Trp Ala Glu
 35 40 45

Phe Val Thr Phe Ala Val Ala Ser Ala Ala Leu Leu Met Phe Ile Arg
 50 55 60

Pro Ala Ile Arg Lys Arg Leu Leu Lys Pro Lys Val Leu Asp Ser Ser
 65 70 75 80

Pro Arg Ala Leu Val Gly His Arg Ala Glu Val Leu Glu Asp Val Gly

	85		90		95
Ala Thr Ser Gly Gln Val Arg Leu Asp Gly Ser Ile Trp Ser Ala Arg					
	100		105		110
Ser Met Asp Pro Thr His Thr Phe Ala Glu Gly Glu Ile Val Ser Val					
	115		120		125
Ile Asp Ile Gln Gly Thr Thr Ala Ile Val Trp Lys Glu Ala					
	130		135		140

<210> 1617

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXA00155

<400> 1617

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ccaccctagt caaagcactg cactacactt ccctaacact atg gaa att cga gca 115
                                         Met Glu Ile Arg Ala
                                         1                               5

aac gtt tat tca ccg ctt caa aat act gcc gtc tgg cta ggt gcg tgg 163
Asn Val Tyr Ser Pro Leu Gln Asn Thr Ala Val Trp Leu Gly Ala Trp
                        10                               15                               20

ctc tat gaa tta gtg ccc acc gaa gat gtc atc gat gcg ttc gtc gat 211
Leu Tyr Glu Leu Val Pro Thr Glu Asp Val Ile Asp Ala Phe Val Asp
                        25                               30                               35

ctc ggc ggc ccg cac acc ttc ggc gac ggc ggg ctg ctc gat atg ctg 259
Leu Gly Gly Pro His Thr Phe Gly Asp Gly Gly Leu Leu Asp Met Leu
                        40                               45                               50

cga act tta aaa gaa tta aca agc acg ctt atc gac gcc ccc ttc cac 307
Arg Thr Leu Lys Glu Leu Thr Ser Thr Leu Ile Asp Ala Pro Phe His
                        55                               60                               65

ggt ccg att tta act ctc gca ctc agc ggc cca ggc caa gtg ccg gcg 355
Gly Pro Ile Leu Thr Leu Ala Leu Ser Gly Pro Gly Gln Val Pro Ala
                        70                               75                               80                               85

ttg ccg gca ggt tca cgc gct gcg gtc ttg gcc tcc gcc tcg aag gag 403
Leu Pro Ala Gly Ser Arg Ala Ala Val Leu Ala Ser Ala Ser Lys Glu
                        90                               95                               100

ggg gcg ttg gtg ctg ggc ggc gtc gat aag cag cat tct tgg gcg ctt 451
Gly Ala Leu Val Leu Gly Gly Val Asp Lys Gln His Ser Trp Ala Leu
                        105                               110                               115

att cct acg cgc ggt aag gat gcc act gag tgg aat ttg gtg gag gtg 499
Ile Pro Thr Arg Gly Lys Asp Ala Thr Glu Trp Asn Leu Val Glu Val
                        120                               125                               130

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gag ggc ttt ttg ccg gcg att gcg act gtc tcg ccc ggt gag gcg gat 547
 Glu Gly Phe Leu Pro Ala Ile Ala Thr Val Ser Pro Gly Glu Ala Asp
 135 140 145
 cag ctg ctc cgt cag gcg aca gat cag gcg gca aat atc att gag tta 595
 Gln Leu Leu Arg Gln Ala Thr Asp Gln Ala Ala Asn Ile Ile Glu Leu
 150 155 160 165
 agt ggc tac gct tca ctt gcg ccg aaa tct ttg aag aat ccg cga cta 643
 Ser Gly Tyr Ala Ser Leu Ala Pro Lys Ser Leu Lys Asn Pro Arg Leu
 170 175 180
 acc gtg ggc atg ctg tca gat ttt tac gac acc ccg ggg ctt ccc tat 691
 Thr Val Gly Met Leu Ser Asp Phe Tyr Asp Thr Pro Gly Leu Pro Tyr
 185 190 195
 gca gtc cca gag agg tcg gcg aag ctt ttt gcg cgc gca gat cgc gtg 739
 Ala Val Pro Glu Arg Ser Ala Lys Leu Phe Ala Arg Ala Asp Arg Val
 200 205 210
 gct gcc atc gca gag acc gtg cag gaa acc atc ggc gat cac agc ctg 787
 Ala Ala Ile Ala Glu Thr Val Gln Glu Thr Ile Gly Asp His Ser Leu
 215 220 225
 gat cca cag ttg att ttc ctg tgg agc cat att cgg acc gcg cgc atg 835
 Asp Pro Gln Leu Ile Phe Leu Trp Ser His Ile Arg Thr Ala Arg Met
 230 235 240 245
 gct ggg gtg agt tat gcc ctc gca gag ttt gcg agg gac tat cac tcc 883
 Ala Gly Val Ser Tyr Ala Leu Ala Glu Phe Ala Arg Asp Tyr His Ser
 250 255 260
 tagttggcag ctggcgccgc tga 906

<210> 1618

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 1618

Met Glu Ile Arg Ala Asn Val Tyr Ser Pro Leu Gln Asn Thr Ala Val
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Trp Leu Gly Ala Trp Leu Tyr Glu Leu Val Pro Thr Glu Asp Val Ile
 20 25 30

Asp Ala Phe Val Asp Leu Gly Gly Pro His Thr Phe Gly Asp Gly Gly
 35 40 45

Leu Leu Asp Met Leu Arg Thr Leu Lys Glu Leu Thr Ser Thr Leu Ile
 50 55 60

Asp Ala Pro Phe His Gly Pro Ile Leu Thr Leu Ala Leu Ser Gly Pro
 65 70 75 80

Gly Gln Val Pro Ala Leu Pro Ala Gly Ser Arg Ala Ala Val Leu Ala
 85 90 95

Ser Ala Ser Lys Glu Gly Ala Leu Val Leu Gly Gly Val Asp Lys Gln
 100 105 110

His Ser Trp Ala Leu Ile Pro Thr Arg Gly Lys Asp Ala Thr Glu Trp
 115 120 125
 Asn Leu Val Glu Val Glu Gly Phe Leu Pro Ala Ile Ala Thr Val Ser
 130 135 140
 Pro Gly Glu Ala Asp Gln Leu Leu Arg Gln Ala Thr Asp Gln Ala Ala
 145 150 155 160
 Asn Ile Ile Glu Leu Ser Gly Tyr Ala Ser Leu Ala Pro Lys Ser Leu
 165 170 175
 Lys Asn Pro Arg Leu Thr Val Gly Met Leu Ser Asp Phe Tyr Asp Thr
 180 185 190
 Pro Gly Leu Pro Tyr Ala Val Pro Glu Arg Ser Ala Lys Leu Phe Ala
 195 200 205
 Arg Ala Asp Arg Val Ala Ala Ile Ala Glu Thr Val Gln Glu Thr Ile
 210 215 220
 Gly Asp His Ser Leu Asp Pro Gln Leu Ile Phe Leu Trp Ser His Ile
 225 230 235 240
 Arg Thr Ala Arg Met Ala Gly Val Ser Tyr Ala Leu Ala Glu Phe Ala
 245 250 255
 Arg Asp Tyr His Ser
 260

<210> 1619
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1282)
 <223> RXA00159

<400> 1619
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 Met Glu Asn Val Ser 5
 tcc gtc acg tcg gat ggt tcg gta gcg gat gtg cat gcc gaa cgg tgg 163
 Ser Val Thr Ser Asp Gly Ser Val Ala Asp Val His Ala Glu Arg Trp 20
 10 15
 caa gaa ttg ctc gca cgt ttg gat gcc gat gcg ccg gat att gcg gag 211
 Gln Glu Leu Leu Ala Arg Leu Asp Ala Asp Ala Pro Asp Ile Ala Glu 35
 25 30
 ggc acc gcc gca aag ttg ctc gct acg atc ccg ggc tat gag ctc gtt 259
 Gly Thr Ala Ala Lys Leu Leu Ala Thr Ile Pro Gly Tyr Glu Leu Val 50
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gac gcg ggg ccg atc agg gag tcg tcg ata cgc aat acg gcc ttg att Asp Ala Gly Pro Ile Arg Glu Ser Ser Ile Arg Asn Thr Ala Leu Ile 55 60 65	307
att cgc gtg att aac gcg ggc acc gag cca aag gcc gag gac ttg cct Ile Arg Val Ile Asn Ala Gly Thr Glu Pro Lys Ala Glu Asp Leu Pro 70 75 80 85	355
gag gct tta agg ctt gcc gac gaa cgt ata gcg caa aat gtg ccg ctg Glu Ala Leu Arg Leu Ala Asp Glu Arg Ile Ala Gln Asn Val Pro Leu 90 95 100	403
gga agt gtg ctg cac ggt ttt cgg atg tct ctg ggg gaa att ctg gag Gly Ser Val Leu His Gly Phe Arg Met Ser Leu Gly Glu Ile Leu Glu 105 110 115	451
cat ttg gtg cag ttg ggc ccg gaa tac aat att gat ccc ggc aga atg His Leu Val Gln Leu Gly Pro Glu Tyr Asn Ile Asp Pro Gly Arg Met 120 125 130	499
ctg cgc tgg tcc aca ctg atg tgg gcg gtc aat gat gcc ttt tct acg Leu Arg Trp Ser Thr Leu Met Trp Ala Val Asn Asp Ala Phe Ser Thr 135 140 145	547
cgt gcc aca agg gtg tac cgc gat cac gag gtc gcc acg gcg atc gcc Arg Ala Thr Arg Val Tyr Arg Asp His Glu Val Ala Thr Ala Ile Ala 150 155 160 165	595
gat tcg gtg cga agg tca gaa tgg atc ggc aaa gcg gtc tcg gaa ggc Asp Ser Val Arg Arg Ser Glu Trp Ile Gly Lys Ala Val Ser Glu Gly 170 175 180	643
tct gaa ctg tca gag ctt tta tgg ggt gct gcg atg tat gac gtt ccc Ser Glu Leu Ser Glu Leu Leu Trp Gly Ala Ala Met Tyr Asp Val Pro 185 190 195	691
gcc gac act cct cta aga gca ttg gca gcc acc tca cct gat cat gcg Ala Asp Thr Pro Leu Arg Ala Leu Ala Ala Thr Ser Pro Asp His Ala 200 205 210	739
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gtg ctg gca tcg gtg cag cca agc gtg atc gtg ggg atc gtg att ggg Val Leu Ala Ser Val Gln Pro Ser Val Ile Val Gly Ile Val Ile Gly 230 235 240 245	835
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agg gca gag gtg ctc tca aag ctg gcg gac tca tat aag gat gca tcc Arg Ala Glu Val Leu Ser Lys Leu Ala Asp Ser Tyr Lys Asp Ala Ser 265 270 275	931
ctt gta ttg aag gct gcc gat aat ctg aaa ctt aat gag gtg cag cgg Leu Val Leu Lys Ala Ala Asp Asn Leu Lys Leu Asn Glu Val Gln Arg 280 285 290	979
gca caa gat ttg tca tgg aag ttg gct atc cat gca agc cca cgg gtg	1027

Ala Gln Asp Leu Ser Trp Lys Leu Ala Ile His Ala Ser Pro Arg Val
 295 300 305

acg gag att ctt gcg cag aaa tat gtg aag cca cta agg gaa tct ggc 1075
 Thr Glu Ile Leu Ala Gln Lys Tyr Val Lys Pro Leu Arg Glu Ser Gly
 310 315 320 325

gag ttt gct cat gag atc gtg gaa tct ttg cgg gca tat gtg gac aac 1123
 Glu Phe Ala His Glu Ile Val Glu Ser Leu Arg Ala Tyr Val Asp Asn
 330 335 340

cag atg aat att cct gct gct gcg cgc agt att cct gtg cat gtg aat 1171
 Gln Met Asn Ile Pro Ala Ala Arg Ser Ile Pro Val His Val Asn
 345 350 355

acg ctt cgc tat cgg ttg cgc cgg ttt gag gag tta acg ggc tgc tat 1219
 Thr Leu Arg Tyr Arg Leu Arg Arg Phe Glu Glu Leu Thr Gly Cys Tyr
 360 365 370

ttg gag gat aca tcc acg gtc att gaa gtg tcg tgg gtg ctg gaa gtc 1267
 Leu Glu Asp Thr Ser Thr Val Ile Glu Val Ser Trp Val Leu Glu Val
 375 380 385

ttt ggc cgg gag ctg tagaaaattg cacctatata tat 1305
 Phe Gly Arg Glu Leu
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<210> 1620

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 1620

Met Glu Asn Val Ser Ser Val Thr Ser Asp Gly Ser Val Ala Asp Val
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His Ala Glu Arg Trp Gln Glu Leu Leu Ala Arg Leu Asp Ala Asp Ala
 20 25 30

Pro Asp Ile Ala Glu Gly Thr Ala Ala Lys Leu Leu Ala Thr Ile Pro
 35 40 45

Gly Tyr Glu Leu Val Asp Ala Gly Pro Ile Arg Glu Ser Ser Ile Arg
 50 55 60

Asn Thr Ala Leu Ile Ile Arg Val Ile Asn Ala Gly Thr Glu Pro Lys
 65 70 75 80

Ala Glu Asp Leu Pro Glu Ala Leu Arg Leu Ala Asp Glu Arg Ile Ala
 85 90 95

Gln Asn Val Pro Leu Gly Ser Val Leu His Gly Phe Arg Met Ser Leu
 100 105 110

Gly Glu Ile Leu Glu His Leu Val Gln Leu Gly Pro Glu Tyr Asn Ile
 115 120 125

Asp Pro Gly Arg Met Leu Arg Trp Ser Thr Leu Met Trp Ala Val Asn
 130 135 140

Asp Ala Phe Ser Thr Arg Ala Thr Arg Val Tyr Arg Asp His Glu Val
145 150 155 160

Ala Thr Ala Ile Ala Asp Ser Val Arg Arg Ser Glu Trp Ile Gly Lys
165 170 175

Ala Val Ser Glu Gly Ser Glu Leu Ser Glu Leu Leu Trp Gly Ala Ala
180 185 190

Met Tyr Asp Val Pro Ala Asp Thr Pro Leu Arg Ala Leu Ala Ala Thr
195 200 205

Ser Pro Asp His Ala Lys Ala Glu Thr Gln Ile Gln Lys Trp Thr Gln
210 215 220

Arg Ala Gly Val Arg Val Leu Ala Ser Val Gln Pro Ser Val Ile Val
225 230 235 240

Gly Ile Val Ile Gly Glu Pro Lys Arg Asn Val Asp Gly Pro Gly Phe
245 250 255

Ala Val Gly Leu Gly Arg Ala Glu Val Leu Ser Lys Leu Ala Asp Ser
260 265 270

Tyr Lys Asp Ala Ser Leu Val Leu Lys Ala Ala Asp Asn Leu Lys Leu
275 280 285

Asn Glu Val Gln Arg Ala Gln Asp Leu Ser Trp Lys Leu Ala Ile His
290 295 300

Ala Ser Pro Arg Val Thr Glu Ile Leu Ala Gln Lys Tyr Val Lys Pro
305 310 315 320

Leu Arg Glu Ser Gly Glu Phe Ala His Glu Ile Val Glu Ser Leu Arg
325 330 335

Ala Tyr Val Asp Asn Gln Met Asn Ile Pro Ala Ala Ala Arg Ser Ile
340 345 350

Pro Val His Val Asn Thr Leu Arg Tyr Arg Leu Arg Arg Phe Glu Glu
355 360 365

Leu Thr Gly Cys Tyr Leu Glu Asp Thr Ser Thr Val Ile Glu Val Ser
370 375 380

Trp Val Leu Glu Val Phe Gly Arg Glu Leu
385 390

<210> 1621

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> RXA00161

<400> 1621

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                Met Ser Glu Pro Gly
                1                    5

cca tcc ggg gtt aaa gaa aag aag aaa gta aag gca agt cac att gtc 163
Pro Ser Gly Val Lys Glu Lys Lys Lys Val Lys Ala Ser His Ile Val
                10                    15                    20

ttt ctt ctc att tgt ttt atc gca gcc tgc gcg ttg gcg tgg tgg cag 211
Phe Leu Leu Ile Cys Phe Ile Ala Ala Cys Ala Leu Ala Trp Trp Gln
                25                    30                    35

tgg tca aga ttc cag tcc ggg tct gga act ttc caa aac ctt ggc tat 259
Trp Ser Arg Phe Gln Ser Gly Ser Gly Thr Phe Gln Asn Leu Gly Tyr
                40                    45                    50

gcc ttc cag tgg cct ctt atc gga gca ttc ttt gtt tat gcc tac cgc 307
Ala Phe Gln Trp Pro Leu Ile Gly Ala Phe Phe Val Tyr Ala Tyr Arg
                55                    60                    65

aag tat ttg cag tat gag aat gag tcc att gag tta gaa aac atg gaa 355
Lys Tyr Leu Gln Tyr Glu Asn Glu Ser Ile Glu Leu Glu Asn Met Glu
                70                    75                    80                    85

gcc aaa atg atg gcg gag caa ggc aaa aca cca gtt gcg caa tca gag 403
Ala Lys Met Met Ala Glu Gln Gly Lys Thr Pro Val Ala Gln Ser Glu
                90                    95                    100

cag gaa gat agc ttc gtt cag ctc tct cac cgt ccg agc ctg gtg gaa 451
Gln Glu Asp Ser Phe Val Gln Leu Ser His Arg Pro Ser Leu Val Glu
                105                    110                    115

gat gac agc gtc aag gaa atc gac gaa tcc ttc ctg ccg tct cgc ccg 499
Asp Asp Ser Val Lys Glu Ile Asp Glu Ser Phe Leu Pro Ser Arg Pro
                120                    125                    130

acg atg gat gtg gaa gag ttc aac agg ttg aat gat ccg cat gca cgg 547
Thr Met Asp Val Glu Glu Phe Asn Arg Leu Asn Asp Pro His Ala Arg
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aga cgt cga aaa gca taaacctgga acttttccgg gcc 585
Arg Arg Arg Lys Ala
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<210> 1622

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 1622

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Met Ser Glu Pro Gly Pro Ser Gly Val Lys Glu Lys Lys Lys Val Lys
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Ala Ser His Ile Val Phe Leu Leu Ile Cys Phe Ile Ala Ala Cys Ala
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Leu Ala Trp Trp Gln Trp Ser Arg Phe Gln Ser Gly Ser Gly Thr Phe
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90										95					100					
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Asn	Tyr	His	Gly	Ile	Val	Tyr	Pro	His	Leu	Leu	Lys	Ala	Gly	Ile	Lys					
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tgt	ggg	att	agc	gag	tcg	att	cgg	gag	ttt	aac	aag	aac	ttc	aaa	cac	499				
Cys	Gly	Ile	Ser	Glu	Ser	Ile	Arg	Glu	Phe	Asn	Lys	Asn	Phe	Lys	His					
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att	tct	cgc	acg	ttc	ccc	agt	tac	gac	ctg	ctg	gtt	att	gat	gag	tac	547				
Ile	Ser	Arg	Thr	Phe	Pro	Ser	Tyr	Asp	Leu	Leu	Val	Ile	Asp	Glu	Tyr					
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cag	gac	atc	aat	gag	gac	tat	gca	gaa	ctg	ctg	cgc	aac	att	aag	tct	595				
Gln	Asp	Ile	Asn	Glu	Asp	Tyr	Ala	Glu	Leu	Leu	Arg	Asn	Ile	Lys	Ser					
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gtg	aat	ccg	ctt	atg	cag	att	gtc	atg	gtg	ggg	gat	ttg	gaa	caa	aaa	643				
Val	Asn	Pro	Leu	Met	Gln	Ile	Val	Met	Val	Gly	Asp	Leu	Glu	Gln	Lys					
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gtc	cgg	tct	gac	acc	acg	tta	gat	cca	caa	gaa	ttt	gca	gca	caa	ttg	691				
Val	Arg	Ser	Asp	Thr	Thr	Leu	Asp	Pro	Gln	Glu	Phe	Ala	Ala	Gln	Leu					
			185				190					195								
tgt	gaa	gat	cca	gtc	ttc	gcg	ccg	ttt	aca	cag	tcg	ttt	cga	att	ggc	739				
Cys	Glu	Asp	Pro	Val	Phe	Ala	Pro	Phe	Thr	Gln	Ser	Phe	Arg	Ile	Gly					
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gag	gct	atg	gca	gcg	ggg	ttg	gct	gat	gcc	tgg	aat	aaa	ccg	att	gtg	787				
Glu	Ala	Met	Ala	Ala	Gly	Leu	Ala	Asp	Ala	Trp	Asn	Lys	Pro	Ile	Val					
		215				220					225									
ggg	gcc	aat	acc	gca	cag	cag	att	gaa	tat	agg	tct	ttc	gct	gag	gca	835				
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Val	Val	Leu	Ile	Gln	Ser	Thr	Glu	Pro	Ser	Lys	Leu	Leu	Cys	Leu	Gly					
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Ser	Arg	Asn	Gly	Gln	Met	Ser	Asp	Ala	Leu	Asn	Val	Val	Glu	Arg	Lys					
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tcg	ccg	gca	aag	ttc	aat	aag	aaa	act	gtg	ttc	gcc	tct	att	cgc	gat	979				
Ser	Pro	Ala	Lys	Phe	Asn	Lys	Lys	Thr	Val	Phe	Ala	Ser	Ile	Arg	Asp					
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ttt	gat	tcc	agt	aaa	ggg	cta	gag	cgc	gat	acc	tgc	gtg	gtc	ttt	gac	1075				
Phe	Asp	Ser	Ser	Lys	Gly	Leu	Glu	Arg	Asp	Thr	Cys	Val	Val	Phe	Asp					
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Tyr	Asp	Glu	Glu	Phe	Trp	Asp	Met	Arg	Leu	Gly	Tyr	Pro	Asn	Val	Asp					
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cca	gtg	gtc	atg	cgc	aat	gtg	ttt	ttg	gtg	gca	gca	tca	cgc	ggg	aaa	1171
Pro	Val	Val	Met	Arg	Asn	Val	Phe	Leu	Val	Ala	Ala	Ser	Arg	Gly	Lys	
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aac	aag	gtt	gtt	ttt	gta	cgt	agc	gat	tct	ctt	caa	gca	gcg	tat	gag	1219
Asn	Lys	Val	Val	Phe	Val	Arg	Ser	Asp	Ser	Leu	Gln	Ala	Ala	Tyr	Glu	
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gct	ggg	gcg	gac	tgg	gct	gca	ggg	ctc	gct	gtg	ggg	gtg	gtg	gac	aac	1267
Ala	Gly	Ala	Asp	Trp	Ala	Ala	Gly	Leu	Ala	Val	Gly	Val	Val	Asp	Asn	
	375					380					385					
aat	act	gag	gtt	gca	cct	gag	gta	gat	gcc	cat	acg	ccg	gca	gaa	gaa	1315
Asn	Thr	Glu	Val	Ala	Pro	Glu	Val	Asp	Ala	His	Thr	Pro	Ala	Glu	Glu	
390					395					400					405	
agt	aag	ggg	gat	gtg	ggg	gag	gtt	cag	tca	cag	att	gag	cgc	atg	atg	1363
Ser	Lys	Gly	Asp	Val	Gly	Glu	Val	Gln	Ser	Gln	Ile	Glu	Arg	Met	Met	
				410				415						420		
ggg	ttt	atc	cct	gtt	tca	gtg	ttt	aaa	gaa	cta	cct	gag	ttg	gcg	ccg	1411
Gly	Phe	Ile	Pro	Val	Ser	Val	Phe	Lys	Glu	Leu	Pro	Glu	Leu	Ala	Pro	
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Ser	Glu	Tyr	Ala	Arg	Pro	Ile	Ser	Val	Thr	Glu	Ala	Phe	Asp	Phe	Lys	
		440					445					450				
tac	gca	gag	aat	gtc	gaa	gca	tgt	ttt	gac	ctg	ctt	gat	gtc	aag	cgt	1507
Tyr	Ala	Glu	Asn	Val	Glu	Ala	Cys	Phe	Asp	Leu	Leu	Asp	Val	Lys	Arg	
		455				460					465					
ctc	gac	aac	ggc	aag	ggg	gca	gcc	att	gag	gtc	aat	cgc	agt	gac	ggg	1555
Leu	Asp	Asn	Gly	Lys	Gly	Ala	Ala	Ile	Glu	Val	Asn	Arg	Ser	Asp	Gly	
470					475					480					485	
ctt	att	gat	ctc	tca	ccc	aca	gtg	gga	aac	ttt	cag	gaa	gca	gtg	ttc	1603
Leu	Ile	Asp	Leu	Ser	Pro	Thr	Val	Gly	Asn	Phe	Gln	Glu	Ala	Val	Phe	
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ttc	aag	gac	tac	aac	gtt	cat	aca	gca	cta	tcg	gcg	tac	ccg	agt	cag	1651
Phe	Lys	Asp	Tyr	Asn	Val	His	Thr	Ala	Leu	Ser	Ala	Tyr	Pro	Ser	Gln	
			505					510					515			
ttc	gcg	aaa	aat	ctt	aaa	cgt	ttg	gtg	aag	aaa	aac	aat	agc	gta	tgg	1699
Phe	Ala	Lys	Asn	Leu	Lys	Arg	Leu	Val	Lys	Lys	Asn	Asn	Ser	Val	Trp	
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cgt	aac	tgc	ctt	att	gtc	aca	gca	gcg	tcc	aca	gag	cag	atg	cgg	tat	1747
Arg	Asn	Cys	Leu	Ile	Val	Thr	Ala	Ala	Ser	Thr	Glu	Gln	Met	Arg	Tyr	
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gtc	gat	cag	gtg	cgc	agc	tct	atc	ccg	gtt	gct	gcg	gag	aag	gca	ttg	1795
Val	Asp	Gln	Val	Arg	Ser	Ser	Ile	Pro	Val	Ala	Ala	Glu	Lys	Ala	Leu	
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gtc	tca	cgg	ctg	agt	acg	agg	ctg	aat	gct	gat	tca	cgt	aat	cag	att	1843
Val	Ser	Arg	Leu	Ser	Thr	Arg	Leu	Asn	Ala	Asp	Ser	Arg	Asn	Gln	Ile	
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cca ctg atc ctt gac ggc gag gca gta cag agc aaa gta gtg cgc acg 1891
 Pro Leu Ile Leu Asp Gly Glu Ala Val Gln Ser Lys Val Val Arg Thr
 585 590 595

cca atg tct ttt gca ggt gtc gca gat gcg gtg cac aag ggt gtg ctt 1939
 Pro Met Ser Phe Ala Gly Val Ala Asp Ala Val His Lys Gly Val Leu
 600 605 610

tat gaa ttg aaa ttc gtc tct gag ttg aca cat ccg atg ttt ttg cag 1987
 Tyr Glu Leu Lys Phe Val Ser Glu Leu Thr His Pro Met Phe Leu Gln
 615 620 625

ctc gca atg tat ttg gtc atg tct ggg atg aag gac ggt att ttg tgg 2035
 Leu Ala Met Tyr Leu Val Met Ser Gly Met Lys Asp Gly Ile Leu Trp
 630 635 640 645

aac acc cgg aca gat gag gcg tgg cag gtg cgt gtt cct gac ccg aag 2083
 Asn Thr Arg Thr Asp Glu Ala Trp Gln Val Arg Val Pro Asp Pro Lys
 650 655 660

cgt ttt ctt aat gct gtg gtg ttg tgt gtc tcc aag cag gat tac cgg 2131
 Arg Phe Leu Asn Ala Val Val Leu Cys Val Ser Lys Gln Asp Tyr Arg
 665 670 675

gtc ggt aac ttt gat ctg ccg agc act ggt gga ggt gcg cgc 2173
 Val Gly Asn Phe Asp Leu Pro Ser Thr Gly Gly Gly Ala Arg
 680 685 690

taaatggtgt tgatgtgtgg ggt 2196

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<211> 691

<212> PRT

<213> Corynebacterium glutamicum

<400> 1624

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Gln Leu Ser Ser Glu Gln Gln Ala Met Ile Asp Tyr Val Leu Ala Gly
 35 40 45

Lys Asp Val Ile Val Asp Ala Thr Val Gly Ser Gly Lys Thr Thr Ala
 50 55 60

Ile Gln Arg Leu Cys Ser Ile Met Gly Ala Asp His Asp Val Leu Tyr
 65 70 75 80

Leu Thr Tyr Ser Lys Leu Leu Lys Val Asp Ala Gln Gln Arg Val Arg
 85 90 95

Gly Ala Lys Val Gln Asn Tyr His Gly Ile Val Tyr Pro His Leu Leu
 100 105 110

Lys Ala Gly Ile Lys Cys Gly Ile Ser Glu Ser Ile Arg Glu Phe Asn
 115 120 125

Lys Asn Phe Lys His Ile Ser Arg Thr Phe Pro Ser Tyr Asp Leu Leu
130 135 140

Val Ile Asp Glu Tyr Gln Asp Ile Asn Glu Asp Tyr Ala Glu Leu Leu
145 150 155 160

Arg Asn Ile Lys Ser Val Asn Pro Leu Met Gln Ile Val Met Val Gly
165 170 175

Asp Leu Glu Gln Lys Val Arg Ser Asp Thr Thr Leu Asp Pro Gln Glu
180 185 190

Phe Ala Ala Gln Leu Cys Glu Asp Pro Val Phe Ala Pro Phe Thr Gln
195 200 205

Ser Phe Arg Ile Gly Glu Ala Met Ala Ala Gly Leu Ala Asp Ala Trp
210 215 220

Asn Lys Pro Ile Val Gly Ala Asn Thr Ala Gln Gln Ile Glu Tyr Arg
225 230 235 240

Ser Phe Ala Glu Ala Val Val Leu Ile Gln Ser Thr Glu Pro Ser Lys
245 250 255

Leu Leu Cys Leu Gly Ser Arg Asn Gly Gln Met Ser Asp Ala Leu Asn
260 265 270

Val Val Glu Arg Lys Ser Pro Ala Lys Phe Asn Lys Lys Thr Val Phe
275 280 285

Ala Ser Ile Arg Asp Gly Asp Ser Gln Ile Ala His Pro Asn Asp Ala
290 295 300

Ala Val Phe Thr Thr Phe Asp Ser Ser Lys Gly Leu Glu Arg Asp Thr
305 310 315 320

Cys Val Val Phe Asp Tyr Asp Glu Glu Phe Trp Asp Met Arg Leu Gly
325 330 335

Tyr Pro Asn Val Asp Pro Val Val Met Arg Asn Val Phe Leu Val Ala
340 345 350

Ala Ser Arg Gly Lys Asn Lys Val Val Phe Val Arg Ser Asp Ser Leu
355 360 365

Gln Ala Ala Tyr Glu Ala Gly Ala Asp Trp Ala Ala Gly Leu Ala Val
370 375 380

Gly Val Val Asp Asn Asn Thr Glu Val Ala Pro Glu Val Asp Ala His
385 390 395 400

Thr Pro Ala Glu Glu Ser Lys Gly Asp Val Gly Glu Val Gln Ser Gln
405 410 415

Ile Glu Arg Met Met Gly Phe Ile Pro Val Ser Val Phe Lys Glu Leu
420 425 430

Pro Glu Leu Ala Pro Ser Glu Tyr Ala Arg Pro Ile Ser Val Thr Glu
435 440 445

Ala Phe Asp Phe Lys Tyr Ala Glu Asn Val Glu Ala Cys Phe Asp Leu

450 455 460
 Leu Asp Val Lys Arg Leu Asp Asn Gly Lys Gly Ala Ala Ile Glu Val
 465 470 475 480
 Asn Arg Ser Asp Gly Leu Ile Asp Leu Ser Pro Thr Val Gly Asn Phe
 485 490 495
 Gln Glu Ala Val Phe Phe Lys Asp Tyr Asn Val His Thr Ala Leu Ser
 500 505 510
 Ala Tyr Pro Ser Gln Phe Ala Lys Asn Leu Lys Arg Leu Val Lys Lys
 515 520 525
 Asn Asn Ser Val Trp Arg Asn Cys Leu Ile Val Thr Ala Ala Ser Thr
 530 535 540
 Glu Gln Met Arg Tyr Val Asp Gln Val Arg Ser Ser Ile Pro Val Ala
 545 550 555 560
 Ala Glu Lys Ala Leu Val Ser Arg Leu Ser Thr Arg Leu Asn Ala Asp
 565 570 575
 Ser Arg Asn Gln Ile Pro Leu Ile Leu Asp Gly Glu Ala Val Gln Ser
 580 585 590
 Lys Val Val Arg Thr Pro Met Ser Phe Ala Gly Val Ala Asp Ala Val
 595 600 605
 His Lys Gly Val Leu Tyr Glu Leu Lys Phe Val Ser Glu Leu Thr His
 610 615 620
 Pro Met Phe Leu Gln Leu Ala Met Tyr Leu Val Met Ser Gly Met Lys
 625 630 635 640
 Asp Gly Ile Leu Trp Asn Thr Arg Thr Asp Glu Ala Trp Gln Val Arg
 645 650 655
 Val Pro Asp Pro Lys Arg Phe Leu Asn Ala Val Val Leu Cys Val Ser
 660 665 670
 Lys Gln Asp Tyr Arg Val Gly Asn Phe Asp Leu Pro Ser Thr Gly Gly
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 Gly Ala Arg
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<210> 1625

<211> 1977

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1954)

<223> RXA00170

<400> 1625

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	Met Leu Leu Ala Ile	
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Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val Glu Asp Gln Phe Glu		
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ctt gta aaa gaa atc agt gat gag cag ttt gct gat gat ggt gtt gac	211	
Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala Asp Asp Gly Val Asp		
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Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys Glu Gln Leu Glu Asp		
	40 45 50	
ttc gaa tca gca cat cca gaa gta gtc att gag tat cac gag cac gtc	307	
Phe Glu Ser Ala His Pro Glu Val Val Ile Glu Tyr His Glu His Val		
	55 60 65	
aac gat agt aaa gac aat gtt gag gaa ctt ccg cta cct aag cgg gac	355	
Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro Leu Pro Lys Arg Asp		
	70 75 80 85	
atc gtt gca ggg gaa atg cgc tca gat gtc atc gag tta ccg gag ggg	403	
Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly		
	90 95 100	
gtg agc aag gac gaa gct gat cag gtg gag gtt gcg gaa gcg cga ctt	451	
Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val Ala Glu Ala Arg Leu		
	105 110 115	
aat gag ggc gca cga ttg atg gct gca act ggg tgt gag gct atg tgg	499	
Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly Cys Glu Ala Met Trp		
	120 125 130	
cca aca ggt ttc tca gtt tgt ggc cgg att ctt gac gct tat cgg cag	547	
Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu Asp Ala Tyr Arg Gln		
	135 140 145	
gtt gga ggt cag ttg tca tgg ctt ggg cca cca aag tca aac gag ttg	595	
Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu		
	150 155 160 165	
acc aat ccc gac ggt gtt ggc aaa aga agt gaa ttt gtt ggg ggt gcc	643	
Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu Phe Val Gly Gly Ala		
	170 175 180	
atc tat tgg cat cca gac aca ggc gct tat gca gtg acc ctg gac ggt	691	
Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly		
	185 190 195	
ttg agg cag tgg ggg acc ttg aac tgg gaa tca ggg cca ttg ggg tac	739	
Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr		
	200 205 210	
cca acc tct ggt ccg atg gat aca aac tat ccc ctt act cag cga cag	787	
Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln		
	215 220 225	
act ttt caa ggt ggt gac aac tat tac aac cca ttg act ggc ggt gct	835	

Thr 230	Phe	Gln	Gly	Gly	Asp 235	Asn	Tyr	Tyr	Asn	Pro 240	Leu	Thr	Gly	Gly	Ala 245	
gtg	tgg	ggc	gat	att	aaa	cag	cgc	tac	gaa	gaa	ctt	ggc	ggc	tcg	aat	883
Val	Trp	Gly	Asp	Ile 250	Lys	Gln	Arg	Tyr	Glu 255	Glu	Leu	Gly	Gly	Ser	Asn 260	
cat	gcc	att	ggc	atc	ccg	atc	act	aat	gag	cta	cct	agc	ggc	act	gag	931
His	Ala	Ile	Gly 265	Ile	Pro	Ile	Thr	Asn 270	Glu	Leu	Pro	Ser	Gly 275	Thr	Glu	
tat	ttt	tac	aat	aat	ttc	ttc	aat	gga	aca	att	tcg	tgg	cga	aat	gat	979
Tyr	Phe	Tyr	Asn 280	Asn	Phe	Phe	Asn 285	Gly	Thr	Ile	Ser	Trp 290	Arg	Asn	Asp	
cgt	cag	aca	cgg	ttt	atg	tat	ttg	gct	acg	cag	cgg	gtg	tgg	gat	gcg	1027
Arg	Gln	Thr	Arg	Phe 295	Met	Tyr 300	Leu	Ala	Thr	Gln	Arg 305	Val	Trp	Asp	Ala	
ttg	ggc	cgg	gag	acg	ggc	cgt	tta	ggc	ttt	cct	gaa	gca	gat	gaa	aca	1075
Leu	Gly	Arg	Glu	Thr 310	Gly 315	Arg	Leu	Gly	Phe	Pro 320	Glu	Ala	Asp	Glu	Thr 325	
cct	gag	gtt	tct	ggc	cta	ttc	cat	gtg	gtg	aat	ttt	gcg	gag	cgc	ggg	1123
Pro	Glu	Val	Ser 330	Gly	Leu	Phe	His	Val 335	Val	Asn	Phe	Ala	Glu	Arg 340	Gly	
gtg	att	gcg	tgg	aat	gga	atc	cta	ggc	gcc	aga	gag	ctg	tat	ggc	gat	1171
Val	Ile	Ala	Trp 345	Asn	Gly	Ile	Leu	Gly 350	Ala	Arg	Glu	Leu	Tyr 355	Gly	Asp	
gtt	tac	tcc	ctg	tgg	ctg	caa	tac	caa	aat	acc	gat	act	cct	tta	ggg	1219
Val	Tyr	Ser 360	Leu	Trp	Leu	Gln 365	Tyr	Gln	Asn	Thr	Asp 370	Thr	Pro	Leu	Gly	
tgg	ccg	ata	cca	tca	ttg	aca	tca	tta	aat	gag	tca	ctc	gaa	caa	gaa	1267
Trp	Pro	Ile	Pro	Ser	Leu 375	Thr 380	Ser	Leu	Asn	Glu	Ser 385	Leu	Glu	Gln	Glu	
ttc	acc	aga	ggc	gtt	gtt	tta	ggc	tca	ggc	gat	gca	ctg	aca	tgg	att	1315
Phe	Thr	Arg	Gly	Val 390	Val 395	Leu	Gly	Ser	Gly	Asp 400	Ala	Leu	Thr	Trp 405	Ile	
cct	gac	gat	gaa	gaa	aga	agt	ttg	gag	gat	ttc	ctc	cca	att	gga	agt	1363
Pro	Asp	Asp	Glu 410	Glu	Arg	Ser	Leu	Glu 415	Asp	Phe	Leu	Pro	Ile	Gly 420	Ser	
agc	ggc	tca	tcc	tca	tcg	agc	caa	gag	atg	acc	ctg	ttt	tcc	cag	cgt	1411
Ser	Gly	Ser	Ser 425	Ser	Ser	Ser	Gln	Glu 430	Met	Thr	Leu	Phe	Ser 435	Gln	Arg	
gca	caa	tac	gtg	gat	tgc	aag	aat	ctt	ccc	gat	tta	gat	gag	cag	aga	1459
Ala	Gln	Tyr 440	Val	Asp	Cys	Lys 445	Asn	Leu	Pro	Asp	Leu 450	Asp	Glu	Gln	Arg	
aaa	act	gaa	aac	aac	att	gaa	aag	aat	ggc	ggc	ccg	atc	aaa	aaa	gag	1507
Lys	Thr	Glu	Asn	Asn	Ile 455	Glu 460	Lys	Asn	Gly	Gly 465	Pro	Ile	Lys	Lys	Glu	
tat	agt	tcg	cga	ggc	ttc	ccc	acc	gag	ttc	aga	ttt	gtc	gtg	aga	aaa	1555
Tyr	Ser	Ser	Arg	Gly	Phe	Pro	Thr	Glu	Phe	Arg	Phe	Val	Val	Arg	Lys	

470 475 480 485
 ggg cat tat gac cgt tac agg aat gaa ggc tgg gga tat tta aaa aac 1603
 Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp Gly Tyr Leu Lys Asn
 490 495 500
 tat tgc aaa cac aac ttc gcc aac cac gct atg gct gag gcc gta gta 1651
 Tyr Cys Lys His Asn Phe Ala Asn His Ala Met Ala Glu Ala Val Val
 505 510 515
 gat aaa gcg gtg att gat tat ggc tca tcg cca gga acc agc tat tac 1699
 Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro Gly Thr Ser Tyr Tyr
 520 525 530
 aag ttc gag aaa acg gtg tac ttt cta gat tgc aga act tat aca ttc 1747
 Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys Arg Thr Tyr Thr Phe
 535 540 545
 aat aag aac tca gga tgt aaa gaa atg cac gct ccg caa tgg gtg act 1795
 Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala Pro Gln Trp Val Thr
 550 555 560 565
 att att tac aat cct cat act ttc act gga gca aat tcg aac aga ccc 1843
 Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala Asn Ser Asn Arg Pro
 570 575 580
 aag ggg gta att tca gca tgg tgt aat tca acc cca cct ggt gga atc 1891
 Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr Pro Pro Gly Gly Ile
 585 590 595
 gaa cac gag cct gaa att tcc caa tgt cct gat cat gtg aat ctt tat 1939
 Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp His Val Asn Leu Tyr
 600 605 610
 aat aag ctt cgc ata tgacagaacc ccatcaactg tgc 1977
 Asn Lys Leu Arg Ile
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<210> 1626

<211> 618

<212> PRT

<213> Corynebacterium glutamicum

<400> 1626

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 Glu Asp Gln Phe Glu Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala
 20 25 30
 Asp Asp Gly Val Asp Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys
 35 40 45
 Glu Gln Leu Glu Asp Phe Glu Ser Ala His Pro Glu Val Val Ile Glu
 50 55 60
 Tyr His Glu His Val Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro
 65 70 75 80
 Leu Pro Lys Arg Asp Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile

85								90				95			
Glu	Leu	Pro	Glu	Gly	Val	Ser	Lys	Asp	Glu	Ala	Asp	Gln	Val	Glu	Val
			100					105					110		
Ala	Glu	Ala	Arg	Leu	Asn	Glu	Gly	Ala	Arg	Leu	Met	Ala	Ala	Thr	Gly
		115					120					125			
Cys	Glu	Ala	Met	Trp	Pro	Thr	Gly	Phe	Ser	Val	Cys	Gly	Arg	Ile	Leu
	130					135					140				
Asp	Ala	Tyr	Arg	Gln	Val	Gly	Gly	Gln	Leu	Ser	Trp	Leu	Gly	Pro	Pro
145					150					155					160
Lys	Ser	Asn	Glu	Leu	Thr	Asn	Pro	Asp	Gly	Val	Gly	Lys	Arg	Ser	Glu
				165					170					175	
Phe	Val	Gly	Gly	Ala	Ile	Tyr	Trp	His	Pro	Asp	Thr	Gly	Ala	Tyr	Ala
			180					185					190		
Val	Thr	Leu	Asp	Gly	Leu	Arg	Gln	Trp	Gly	Thr	Leu	Asn	Trp	Glu	Ser
		195					200					205			
Gly	Pro	Leu	Gly	Tyr	Pro	Thr	Ser	Gly	Pro	Met	Asp	Thr	Asn	Tyr	Pro
	210					215					220				
Leu	Thr	Gln	Arg	Gln	Thr	Phe	Gln	Gly	Gly	Asp	Asn	Tyr	Tyr	Asn	Pro
225					230					235					240
Leu	Thr	Gly	Gly	Ala	Val	Trp	Gly	Asp	Ile	Lys	Gln	Arg	Tyr	Glu	Glu
				245					250					255	
Leu	Gly	Gly	Ser	Asn	His	Ala	Ile	Gly	Ile	Pro	Ile	Thr	Asn	Glu	Leu
			260					265					270		
Pro	Ser	Gly	Thr	Glu	Tyr	Phe	Tyr	Asn	Asn	Phe	Phe	Asn	Gly	Thr	Ile
		275					280					285			
Ser	Trp	Arg	Asn	Asp	Arg	Gln	Thr	Arg	Phe	Met	Tyr	Leu	Ala	Thr	Gln
	290					295					300				
Arg	Val	Trp	Asp	Ala	Leu	Gly	Arg	Glu	Thr	Gly	Arg	Leu	Gly	Phe	Pro
305					310					315					320
Glu	Ala	Asp	Glu	Thr	Pro	Glu	Val	Ser	Gly	Leu	Phe	His	Val	Val	Asn
				325					330					335	
Phe	Ala	Glu	Arg	Gly	Val	Ile	Ala	Trp	Asn	Gly	Ile	Leu	Gly	Ala	Arg
			340					345					350		
Glu	Leu	Tyr	Gly	Asp	Val	Tyr	Ser	Leu	Trp	Leu	Gln	Tyr	Gln	Asn	Thr
		355					360					365			
Asp	Thr	Pro	Leu	Gly	Trp	Pro	Ile	Pro	Ser	Leu	Thr	Ser	Leu	Asn	Glu
	370					375					380				
Ser	Leu	Glu	Gln	Glu	Phe	Thr	Arg	Gly	Val	Val	Leu	Gly	Ser	Gly	Asp
385					390					395					400
Ala	Leu	Thr	Trp	Ile	Pro	Asp	Asp	Glu	Glu	Arg	Ser	Leu	Glu	Asp	Phe
				405					410					415	

Leu Pro Ile Gly Ser Ser Gly Ser Ser Ser Ser Ser Gln Glu Met Thr
 420 425 430

Leu Phe Ser Gln Arg Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp
 435 440 445

Leu Asp Glu Gln Arg Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly
 450 455 460

Pro Ile Lys Lys Glu Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg
 465 470 475 480

Phe Val Val Arg Lys Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp
 485 490 495

Gly Tyr Leu Lys Asn Tyr Cys Lys His Asn Phe Ala Asn His Ala Met
 500 505 510

Ala Glu Ala Val Val Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro
 515 520 525

Gly Thr Ser Tyr Tyr Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys
 530 535 540

Arg Thr Tyr Thr Phe Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala
 545 550 555 560

Pro Gln Trp Val Thr Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala
 565 570 575

Asn Ser Asn Arg Pro Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr
 580 585 590

Pro Pro Gly Gly Ile Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp
 595 600 605

His Val Asn Leu Tyr Asn Lys Leu Arg Ile
 610 615

<210> 1627

<211> 456

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(433)

<223> RXA00173

<400> 1627

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gagagccgta aggcagctat tcgcgacgct attctgcct atg tca aca aca atc 115
 Met Ser Thr Thr Ile
 1 5

aag gct gct gca ccc tac agc ctt cat gcc cat gat ctc gaa cag ctt 163,
 Lys Ala Ala Ala Pro Tyr Ser Leu His Ala His Asp Leu Glu Gln Leu
 10 15 20

gct gta gat ctc act tta gtt acc acc ttt gat agc aat gct gca gtt 211
 Ala Val Asp Leu Thr Leu Val Thr Thr Phe Asp Ser Asn Ala Ala Val
 25 30 35

gat gtc acg cca aca cat aca gaa gca cct ggt ttt acc ctg cat gag 259
 Asp Val Thr Pro Thr His Thr Glu Ala Pro Gly Phe Thr Leu His Glu
 40 45 50

ggc acc gat act gcg cct atg gct cca acc ctg gtc gta cct att tcc 307
 Gly Thr Asp Thr Ala Pro Met Ala Pro Thr Leu Val Val Pro Ile Ser
 55 60 65

agc gac atc tcc aca gcc gtt tcg gaa ata tct aca tta gtg cag cag 355
 Ser Asp Ile Ser Thr Ala Val Ser Glu Ile Ser Thr Leu Val Gln Gln
 70 75 80 85

gct cgc acc gac gca gca agc gcc att cat gaa gca gaa gct gaa ttt 403
 Ala Arg Thr Asp Ala Ala Ser Ala Ile His Glu Ala Glu Ala Glu Phe
 90 95 100

tac aac caa ctt gct gcg gtc ctt gct cag tgatttaatg tggccgacac 453
 Tyr Asn Gln Leu Ala Ala Val Leu Ala Gln
 105 110

acc 456

<210> 1628

<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 1628

Met Ser Thr Thr Ile Lys Ala Ala Ala Pro Tyr Ser Leu His Ala His
 1 5 10 15

Asp Leu Glu Gln Leu Ala Val Asp Leu Thr Leu Val Thr Thr Phe Asp
 20 25 30

Ser Asn Ala Ala Val Asp Val Thr Pro Thr His Thr Glu Ala Pro Gly
 35 40 45

Phe Thr Leu His Glu Gly Thr Asp Thr Ala Pro Met Ala Pro Thr Leu
 50 55 60

Val Val Pro Ile Ser Ser Asp Ile Ser Thr Ala Val Ser Glu Ile Ser
 65 70 75 80

Thr Leu Val Gln Gln Ala Arg Thr Asp Ala Ala Ser Ala Ile His Glu
 85 90 95

Ala Glu Ala Glu Phe Tyr Asn Gln Leu Ala Ala Val Leu Ala Gln
 100 105 110

<210> 1629

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXA00174

<400> 1629

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taagccactg ggaatcataa aaaagaaagt agcactagct atg cct aat cac cca 115
Met Pro Asn His Pro
1 5
cct att tcc acc ttc gat gac cgt cgc tct gct atg cgc gaa ggc att 163
Pro Ile Ser Thr Phe Asp Asp Arg Arg Ser Ala Met Arg Glu Gly Ile
10 15 20
act gat tac ctt gcc aat aca aat gca aat ggg tta ggc ggt tac agc 211
Thr Asp Tyr Leu Ala Asn Thr Asn Ala Asn Gly Leu Gly Gly Tyr Ser
25 30 35
atc agc gac acc cac ctc gac aat ctt gct gag aaa ttc acc cgc aca 259
Ile Ser Asp Thr His Leu Asp Asn Leu Ala Glu Lys Phe Thr Arg Thr
40 45 50
cat ggt gaa gca cag tac gat gcc ggc ttt gat ccc aat gat ctt gaa 307
His Gly Glu Ala Gln Tyr Asp Ala Gly Phe Asp Pro Asn Asp Leu Glu
55 60 65
cca gag act ttt gtt cgt gac att gag atg agc tgg gat gag cgt gct 355
Pro Glu Thr Phe Val Arg Asp Ile Glu Met Ser Trp Asp Glu Arg Ala
70 75 80 85
att gat cgt gcc ctg atc cac aca caa ctg tgaagaaaga agccgcaatg 405
Ile Asp Arg Ala Leu Ile His Thr Gln Leu
90 95
tcc 408

<210> 1630

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1630

Met Pro Asn His Pro Pro Ile Ser Thr Phe Asp Asp Arg Arg Ser Ala
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Met Arg Glu Gly Ile Thr Asp Tyr Leu Ala Asn Thr Asn Ala Asn Gly
20 25 30
Leu Gly Gly Tyr Ser Ile Ser Asp Thr His Leu Asp Asn Leu Ala Glu
35 40 45
Lys Phe Thr Arg Thr His Gly Glu Ala Gln Tyr Asp Ala Gly Phe Asp
50 55 60
Pro Asn Asp Leu Glu Pro Glu Thr Phe Val Arg Asp Ile Glu Met Ser
65 70 75 80
Trp Asp Glu Arg Ala Ile Asp Arg Ala Leu Ile His Thr Gln Leu

85

90

95

<210> 1631

<211> 753

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(730)

<223> RXA00175

<400> 1631

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agcgaacatg ggcgggagcc catgtcgggg tgttgtgcga atg gct gtg tgt caa 115
                                         Met Ala Val Cys Gln
                                         1           5

cta cct cag cct gag aaa aca aca ctt ata aag aaa gac ctt tta ctc 163
Leu Pro Gln Pro Glu Lys Thr Thr Leu Ile Lys Lys Asp Leu Leu Leu
                        10                        15                        20

atg act tct aca act aac tcc acc gcc atg ttc aac gac cac ctt atc 211
Met Thr Ser Thr Thr Asn Ser Thr Ala Met Phe Asn Asp His Leu Ile
                        25                        30                        35

cct atg gca gag ctt gat gaa caa gct ctg cgc gac agc gtt ggt tct 259
Pro Met Ala Glu Leu Asp Glu Gln Ala Leu Arg Asp Ser Val Gly Ser
                        40                        45                        50

tgg gca cag tac aag cac ccg ctt gac cag cgc aaa gaa cca gag ctc 307
Trp Ala Gln Tyr Lys His Pro Leu Asp Gln Arg Lys Glu Pro Glu Leu
                        55                        60                        65

gtc ctt att cgt cgc gtc aac agc tca gag cgt gtg tgg gtc tta agt 355
Val Leu Ile Arg Arg Val Asn Ser Ser Glu Arg Val Trp Val Leu Ser
                        70                        75                        80                        85

ttc act gac ctg cgt gct gat gca ggt ctt gtg cct cgt agc aca ccg 403
Phe Thr Asp Leu Arg Ala Asp Ala Gly Leu Val Pro Arg Ser Thr Pro
                        90                        95                        100

aat gct gac ccc tcc aat atc cgc aat acc att ttc tct gtc gct gtc 451
Asn Ala Asp Pro Ser Asn Ile Arg Asn Thr Ile Phe Ser Val Ala Val
                        105                        110                        115

cgc gat ctt gtc ctt gat cgc tca ctt ccc cgg ctg ctt aac ctc aac 499
Arg Asp Leu Val Leu Asp Arg Ser Leu Pro Arg Leu Leu Asn Leu Asn
                        120                        125                        130

ggg caa cca cca gca ggt gaa tgg gaa gaa ggc ttt gtc tac gtc gat 547
Gly Gln Pro Pro Ala Gly Glu Trp Glu Glu Gly Phe Val Tyr Val Asp
                        135                        140                        145

tat gac cag agc gac acc gta gat ggc tac ctc att gag cac agc gaa 595
Tyr Asp Gln Ser Asp Thr Val Asp Gly Tyr Leu Ile Glu His Ser Glu
                        150                        155                        160                        165

cct gtc tcc att gaa agt caa acc acc ggt gaa atg cac tat ttc gat 643

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Pro Val Ser Ile Glu Ser Gln Thr Thr Gly Glu Met His Tyr Phe Asp
 170 175 180

aag gtg cca ggc ggt gtg gct gtt acc aac aat ccc gat ggc act gaa 691
 Lys Val Pro Gly Gly Val Ala Val Thr Asn Asn Pro Asp Gly Thr Glu
 185 190 195

caa ggt gat gca cgc cgc tgg gta agc cac tgg gaa tca taaaaaagaa 740
 Gln Gly Asp Ala Arg Arg Trp Val Ser His Trp Glu Ser
 200 205 210

agtagcacta gct 753

<210> 1632
 <211> 210
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1632
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Lys Asp Leu Leu Leu Met Thr Ser Thr Thr Asn Ser Thr Ala Met Phe
 20 25 30

Asn Asp His Leu Ile Pro Met Ala Glu Leu Asp Glu Gln Ala Leu Arg
 35 40 45

Asp Ser Val Gly Ser Trp Ala Gln Tyr Lys His Pro Leu Asp Gln Arg
 50 55 60

Lys Glu Pro Glu Leu Val Leu Ile Arg Arg Val Asn Ser Ser Glu Arg
 65 70 75 80

Val Trp Val Leu Ser Phe Thr Asp Leu Arg Ala Asp Ala Gly Leu Val
 85 90 95

Pro Arg Ser Thr Pro Asn Ala Asp Pro Ser Asn Ile Arg Asn Thr Ile
 100 105 110

Phe Ser Val Ala Val Arg Asp Leu Val Leu Asp Arg Ser Leu Pro Arg
 115 120 125

Leu Leu Asn Leu Asn Gly Gln Pro Pro Ala Gly Glu Trp Glu Glu Gly
 130 135 140

Phe Val Tyr Val Asp Tyr Asp Gln Ser Asp Thr Val Asp Gly Tyr Leu
 145 150 155 160

Ile Glu His Ser Glu Pro Val Ser Ile Glu Ser Gln Thr Thr Gly Glu
 165 170 175

Met His Tyr Phe Asp Lys Val Pro Gly Gly Val Ala Val Thr Asn Asn
 180 185 190

Pro Asp Gly Thr Glu Gln Gly Asp Ala Arg Arg Trp Val Ser His Trp
 195 200 205

Glu Ser
 210

<210> 1633
 <211> 582
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(559)
 <223> RXA00179

<400> 1633

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                                         Met Ile Ala Ile His
                                         1      5

gct att gca gca atc ctg ttc cta gga cca gca aca gta gct aac tct 163
Ala Ile Ala Ala Ile Leu Phe Leu Gly Pro Ala Thr Val Ala Asn Ser
                        10                        15                        20

cag ttc cac gtc cgc gcg tac gat gca cac aac ggc aac acc caa gcc 211
Gln Phe His Val Arg Ala Tyr Asp Ala His Asn Gly Asn Thr Gln Ala
                        25                        30                        35

gct ggc tcc gca aaa acc ctt ttc aag att tcc cag tcc tac ggc atg 259
Ala Gly Ser Ala Lys Thr Leu Phe Lys Ile Ser Gln Ser Tyr Gly Met
                        40                        45                        50

ctg tcc ctg ctc gtg cct ttg ctg ggt atc gcc atc atg ctt ctc gat 307
Leu Ser Leu Leu Val Pro Leu Leu Gly Ile Ala Ile Met Leu Leu Asp
                        55                        60                        65

tgg tct ttc tac aag tct gaa ggc cag ttc cac gca gca atc gct ctc 355
Trp Ser Phe Tyr Lys Ser Glu Gly Gln Phe His Ala Ala Ile Ala Leu
                        70                        75                        80                        85

agt gtt atc acc tgg gcg ctg ctt ctc ttc gtt atc ttc cca cgc cag 403
Ser Val Ile Thr Trp Ala Leu Leu Leu Phe Val Ile Phe Pro Arg Gln
                        90                        95                        100

aag aag atg atg ggt gct ctt gac ctt ctg gag gac gat gag cag gct 451
Lys Lys Met Met Gly Ala Leu Asp Leu Leu Glu Asp Asp Glu Gln Ala
                        105                        110                        115

gca aag act tac gag atc gaa aac tgg gac aag gcg aag agc cag ctg 499
Ala Lys Thr Tyr Glu Ile Glu Asn Trp Asp Lys Ala Lys Ser Gln Leu
                        120                        125                        130

tcc atg ttc ggc ggc atc tgg gct ctg ctg tgg gtc atc atc gct gtg 547
Ser Met Phe Gly Gly Ile Trp Ala Leu Leu Trp Val Ile Ile Ala Val
                        135                        140                        145

ctg atg ttc atc taacacatct caaattgccaa aaa 582
Leu Met Phe Ile
150

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<210> 1634

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 1634

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Met Ile Ala Ile His Ala Ile Ala Ala Ile Leu Phe Leu Gly Pro Ala
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Thr Val Ala Asn Ser Gln Phe His Val Arg Ala Tyr Asp Ala His Asn
          20             25             30

Gly Asn Thr Gln Ala Ala Gly Ser Ala Lys Thr Leu Phe Lys Ile Ser
          35             40             45

Gln Ser Tyr Gly Met Leu Ser Leu Leu Val Pro Leu Leu Gly Ile Ala
          50             55             60

Ile Met Leu Leu Asp Trp Ser Phe Tyr Lys Ser Glu Gly Gln Phe His
          65             70             75             80

Ala Ala Ile Ala Leu Ser Val Ile Thr Trp Ala Leu Leu Leu Phe Val
          85             90             95

Ile Phe Pro Arg Gln Lys Lys Met Met Gly Ala Leu Asp Leu Leu Glu
          100            105            110

Asp Asp Glu Gln Ala Ala Lys Thr Tyr Glu Ile Glu Asn Trp Asp Lys
          115            120            125

Ala Lys Ser Gln Leu Ser Met Phe Gly Gly Ile Trp Ala Leu Leu Trp
          130            135            140

Val Ile Ile Ala Val Leu Met Phe Ile
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<210> 1635

<211> 663

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(640)

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agaggggaacc aaacgccaaag gcgatgagtc taacccgagt atg aag aac ttt att 115
                                         Met Lys Asn Phe Ile
                                         1             5

cgg gta ctc atc gcc ttt agt gtt ttc ctc tgt ata tat acc gtt gct 163
Arg Val Leu Ile Ala Phe Ser Val Phe Leu Cys Ile Tyr Thr Val Ala
          10             15             20

ccc cac att ggc cga ggt cct gga gac ctc gca cca gtt aca gca atc 211
Pro His Ile Gly Arg Gly Pro Gly Asp Leu Ala Pro Val Thr Ala Ile_
          25             30             35

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ccc caa cga gcc aca gtc cta ggc tat gac aga gcc tcc atg ttt ggc 259
 Pro Gln Arg Ala Thr Val Leu Gly Tyr Asp Arg Ala Ser Met Phe Gly
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gga tgg ttg ggt ggc gtg cgg gaa ggc atc gtg gat gaa gcc ggc gac 307
 Gly Trp Leu Gly Gly Val Arg Glu Gly Ile Val Asp Glu Ala Gly Asp
 55 60 65

act gat cca tac tcc ggg aat cga tta gac ctc tct agt gcc gag gtg 355
 Thr Asp Pro Tyr Ser Gly Asn Arg Leu Asp Leu Ser Ser Ala Glu Val
 70 75 80 85

gat cat att ctc ccg ctc agc gcc gcc tgg gat cta ggc gca cac cgg 403
 Asp His Ile Leu Pro Leu Ser Ala Ala Trp Asp Leu Gly Ala His Arg
 90 95 100

tgg agc gct ggc gag aga atc agc ttt gcc aac gac ccc ctc aac ctc 451
 Trp Ser Ala Gly Glu Arg Ile Ser Phe Ala Asn Asp Pro Leu Asn Leu
 105 110 115

gtg ctc gtc tca aaa gct gag aac caa gaa aaa tcc gat caa ctt ccc 499
 Val Leu Val Ser Lys Ala Glu Asn Gln Glu Lys Ser Asp Gln Leu Pro
 120 125 130

agc gag tgg ctc ccc tct gat cga agt gca cga tgt tgg tac gtg gaa 547
 Ser Glu Trp Leu Pro Ser Asp Arg Ser Ala Arg Cys Trp Tyr Val Glu
 135 140 145

cgc ctt ttc gcc gtg gcc aac gca tac gaa ctt ccg tta cca gaa aac 595
 Arg Leu Phe Ala Val Ala Asn Ala Tyr Glu Leu Pro Leu Pro Glu Asn
 150 155 160 165

gac att cgg gtt gga cga aaa cag tgc ggg ttc gcc aaa cct tgg 640
 Asp Ile Arg Val Gly Arg Lys Gln Cys Gly Phe Ala Lys Pro Trp
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tgatctcggtt agtgtatgta tca 663

<210> 1636

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 1636

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Ile, Tyr Thr Val Ala Pro His Ile Gly Arg Gly Pro Gly Asp Leu Ala
 20 25 30

Pro Val Thr Ala Ile Pro Gln Arg Ala Thr Val Leu Gly Tyr Asp Arg
 35 40 45

Ala Ser Met Phe Gly Gly Trp Leu Gly Gly Val Arg Glu Gly Ile Val
 50 55 60

Asp Glu Ala Gly Asp Thr Asp Pro Tyr Ser Gly Asn Arg Leu Asp Leu
 65 70 75 80

Ser Ser Ala Glu Val Asp His Ile Leu Pro Leu Ser Ala Ala Trp Asp

	85		90		95
Leu Gly Ala His Arg Trp Ser Ala Gly Glu Arg Ile Ser Phe Ala Asn					
	100		105		110
Asp Pro Leu Asn Leu Val Leu Val Ser Lys Ala Glu Asn Gln Glu Lys					
	115		120		125
Ser Asp Gln Leu Pro Ser Glu Trp Leu Pro Ser Asp Arg Ser Ala Arg					
	130		135		140
Cys Trp Tyr Val Glu Arg Leu Phe Ala Val Ala Asn Ala Tyr Glu Leu					
	145		150		155
Pro Leu Pro Glu Asn Asp Ile Arg Val Gly Arg Lys Gln Cys Gly Phe					
	165		170		175
Ala Lys Pro Trp					
	180				

<210> 1637

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA00183

<400> 1637

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ttggctatgc tgatgagtta ccgcgaaaag gaggggtgcag atg act gaa tca cgc	115
Met Thr Glu Ser Arg	
1 5	

cgc gtg aaa atg gat aac gtt att tac gcc aat ttt ggc agc aaa cag	163
Arg Val Lys Met Asp Asn Val Ile Tyr Ala Asn Phe Gly Ser Lys Gln	
10 15 20	

cgc gta tct act cct gat gac cgc acc cag gtg att aat aaa tca cga	211
Arg Val Ser Thr Pro Asp Asp Arg Thr Gln Val Ile Asn Lys Ser Arg	
25 30 35	

cac aaa caa ttc agc cca gcg ggt act cgt acc gtg atg ttg acg gag	259
His Lys Gln Phe Ser Pro Ala Gly Thr Arg Thr Val Met Leu Thr Glu	
40 45 50	

aaa aac gcc gac agc gga cga cgg tcc cgc ggt gag cag tac tac cga	307
Lys Asn Ala Asp Ser Gly Arg Arg Ser Arg Gly Glu Gln Tyr Tyr Arg	
55 60 65	

aac ggc aat gtc acc ggc atg act gtg ctg gaa ggc cgc gtg gaa tgc	355
Asn Gly Asn Val Thr Gly Met Thr Val Leu Glu Gly Arg Val Glu Cys	
70 75 80 85	

act gtc gcg ggc tcc caa aac gag ccg ttt gtt acc aca gtg acc ttc	403
Thr Val Ala Gly Ser Gln Asn Glu Pro Phe Val Thr Thr Val Thr Phe	
90 95 100	

cca tac cga agc tcg gaa aaa ctc cgc gaa gcc tac gca gct att gcg 451
Pro Tyr Arg Ser Ser Glu Lys Leu Arg Glu Ala Tyr Ala Ala Ile Ala
105 110 115

gat act ccc aat ggc ctg cgg ctt gtg cgt gat ggc cat ctg acc tcc 499
Asp Thr Pro Asn Gly Leu Arg Leu Val Arg Asp Gly His Leu Thr Ser
120 125 130

tcc atg ctg gat cac ttg gtg gga agt cct gat gag tcg att tat ttt 547
Ser Met Leu Asp His Leu Val Gly Ser Pro Asp Glu Ser Ile Tyr Phe
135 140 145

gac tgc acc tgc ccc gac cga tcg ctt gtg tgt aaa cat gcc gtt gcc 595
Asp Cys Thr Cys Pro Asp Arg Ser Leu Val Cys Lys His Ala Val Ala
150 155 160 165

agc gcg tat cac gtt gcc gag aag atg acc gcg aac ccc ggt ctg atc 643
Ser Ala Tyr His Val Ala Glu Lys Met Thr Ala Asn Pro Gly Leu Ile
170 175 180

ttg gat att cgt ggt caa ggg atg gct gga tta gaa gca ctg att cgg 691
Leu Asp Ile Arg Gly Gln Gly Met Ala Gly Leu Glu Ala Leu Ile Arg
185 190 195

acc tat cac acc aag gtt gaa act gaa cct gaa gac aat gac agt ttt 739
Thr Tyr His Thr Lys Val Glu Thr Glu Pro Glu Asp Asn Asp Ser Phe
200 205 210

tgg aac ggc agg gaa ctt cct gct ttg cct gat cca aag att gcc cct 787
Trp Asn Gly Arg Glu Leu Pro Ala Leu Pro Asp Pro Lys Ile Ala Pro
215 220 225

gct atc gac gat tcc gat atc aac tac ctc cac aag gct tta agg atg 835
Ala Ile Asp Asp Ser Asp Ile Asn Tyr Leu His Lys Ala Leu Arg Met
230 235 240 245

gtc tca tac acc tcc ctg gag cag ctt cgt gcg gtc agt gat att gaa 883
Val Ser Tyr Thr Ser Leu Glu Gln Leu Arg Ala Val Ser Asp Ile Glu
250 255 260

gat atg tac gag att ttg gta gcc aac cac cct gat aac cag caa gtg 931
Asp Met Tyr Glu Ile Leu Val Ala Asn His Pro Asp Asn Gln Gln Val
265 270 275

tat gag gaa gaa gac act gat taaccagggc ttatggttgt ggt 975
Tyr Glu Glu Glu Asp Thr Asp
280

<210> 1638

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 1638

Met Thr Glu Ser Arg Arg Val Lys Met Asp Asn Val Ile Tyr Ala Asn
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Phe Gly Ser Lys Gln Arg Val Ser Thr Pro Asp Asp Arg Thr Gln Val
20 25 30

Ile Asn Lys Ser Arg His Lys Gln Phe Ser Pro Ala Gly Thr Arg Thr
35 40 45
Val Met Leu Thr Glu Lys Asn Ala Asp Ser Gly Arg Arg Ser Arg Gly
50 55 60
Glu Gln Tyr Tyr Arg Asn Gly Asn Val Thr Gly Met Thr Val Leu Glu
65 70 75 80
Gly Arg Val Glu Cys Thr Val Ala Gly Ser Gln Asn Glu Pro Phe Val
85 90 95
Thr Thr Val Thr Phe Pro Tyr Arg Ser Ser Glu Lys Leu Arg Glu Ala
100 105 110
Tyr Ala Ala Ile Ala Asp Thr Pro Asn Gly Leu Arg Leu Val Arg Asp
115 120 125
Gly His Leu Thr Ser Ser Met Leu Asp His Leu Val Gly Ser Pro Asp
130 135 140
Glu Ser Ile Tyr Phe Asp Cys Thr Cys Pro Asp Arg Ser Leu Val Cys
145 150 155 160
Lys His Ala Val Ala Ser Ala Tyr His Val Ala Glu Lys Met Thr Ala
165 170 175
Asn Pro Gly Leu Ile Leu Asp Ile Arg Gly Gln Gly Met Ala Gly Leu
180 185 190
Glu Ala Leu Ile Arg Thr Tyr His Thr Lys Val Glu Thr Glu Pro Glu
195 200 205
Asp Asn Asp Ser Phe Trp Asn Gly Arg Glu Leu Pro Ala Leu Pro Asp
210 215 220
Pro Lys Ile Ala Pro Ala Ile Asp Asp Ser Asp Ile Asn Tyr Leu His
225 230 235 240
Lys Ala Leu Arg Met Val Ser Tyr Thr Ser Leu Glu Gln Leu Arg Ala
245 250 255
Val Ser Asp Ile Glu Asp Met Tyr Glu Ile Leu Val Ala Asn His Pro
260 265 270
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275 280

<210> 1639

<211> 2751

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2728)

<223> RXA00185

<400> 1639

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Met Arg Ile His Glu
1 5

atc atc att gac aat ttc cga gcc atc gaa cat cta gaa ctt cgt gac 163
Ile Ile Ile Asp Asn Phe Arg Ala Ile Glu His Leu Glu Leu Arg Asp
10 15 20

att cct gac cag ggc gtt atc gtg atc cac ggt gac aat gag caa ggc 211
Ile Pro Asp Gln Gly Val Ile Val Ile His Gly Asp Asn Glu Gln Gly
25 30 35

aaa tct tca atc ctt gaa gcc ata aaa aca gtt ctg aat agt aaa cac 259
Lys Ser Ser Ile Leu Glu Ala Ile Lys Thr Val Leu Asn Ser Lys His
40 45 50

aga acc acc agc aag acg atc aag gcc att cag cct gtt gac cgt gat 307
Arg Thr Thr Ser Lys Thr Ile Lys Ala Ile Gln Pro Val Asp Arg Asp
55 60 65

gtt ccc atc agc atc acc ctc gag gca acc gta ggc acg gtt cga ttc 355
Val Pro Ile Ser Ile Thr Leu Glu Ala Thr Val Gly Thr Val Arg Phe
70 75 80 85

cgc ata cac aaa cgc ttc cta aaa tcc aca gcc gca gaa ctg caa gtc 403
Arg Ile His Lys Arg Phe Leu Lys Ser Thr Ala Ala Glu Leu Gln Val
90 95 100

atc gag cca cgt cca tcc aac cac cgt gga cta gaa gcc gaa gct gca 451
Ile Glu Pro Arg Pro Ser Asn His Arg Gly Leu Glu Ala Glu Ala Ala
105 110 115

ctg gca gaa ata ctg gaa agc cat ttg gac acc tct ttg ctt gac gca 499
Leu Ala Glu Ile Leu Glu Ser His Leu Asp Thr Ser Leu Leu Asp Ala
120 125 130

ttg ttt atg aaa cag ggt gaa gta gaa gca ggt atc agc gct gta gga 547
Leu Phe Met Lys Gln Gly Glu Val Glu Ala Gly Ile Ser Ala Val Gly
135 140 145

att cct acc ctg acc agc gct ttg aac gct caa aat ggc aat acc gaa 595
Ile Pro Thr Leu Thr Ser Ala Leu Asn Ala Gln Asn Gly Asn Thr Glu
150 155 160 165

gat gcc acc gaa gac acc gca ctc atg gag gct gta gaa aag gaa tac 643
Asp Ala Thr Glu Asp Thr Ala Leu Met Glu Ala Val Glu Lys Glu Tyr
170 175 180

cta aag ttc tac acc aac tcc gga aag gcg aat acg agg ttc cta cag 691
Leu Lys Phe Tyr Thr Asn Ser Gly Lys Ala Asn Thr Arg Phe Leu Gln
185 190 195

ttt tcc aaa cag gtg gaa acc ctt cgt act gat ttg gat gag gct aac 739
Phe Ser Lys Gln Val Glu Thr Leu Arg Thr Asp Leu Asp Glu Ala Asn
200 205 210

gct gaa gta gca aag ctc tcc tcc cat gtt gac cga gtt aaa cga ttg 787
Ala Glu Val Ala Lys Leu Ser Ser His Val Asp Arg Val Lys Arg Leu
215 220 225

gaa att gat cgg gat cag gcc aca gca cag tta ccc aag gca gag gaa Glu Ile Asp Arg Asp Gln Ala Thr Ala Gln Leu Pro Lys Ala Glu Glu 230 235 240 245	835
gaa ctc gca ggg agg aaa gca gaa ctg gag gaa gcc caa aag gtt aag Glu Leu Ala Gly Arg Lys Ala Glu Leu Glu Glu Ala Gln Lys Val Lys 250 255 260	883
gct caa gcc acg gaa atc ctt gcg cag ttt tcc cgg gcg gaa gaa cag Ala Gln Ala Thr Glu Ile Leu Ala Gln Phe Ser Arg Ala Glu Glu Gln 265 270 275	931
tta gag cag gca aca gga gct cag aaa cga cgt aaa gaa ctc cgc aat Leu Glu Gln Ala Thr Gly Ala Gln Lys Arg Arg Lys Glu Leu Arg Asn 280 285 290	979
aag ctg gaa tta gca cag aca gaa gtc gaa aag gct gaa gca ggg caa Lys Leu Glu Leu Ala Gln Thr Glu Val Glu Lys Ala Glu Ala Gly Gln 295 300 305	1027
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gaa aag gtg aaa gca gca cgt caa tcg gtt gct gga atc aaa aac cgt Glu Lys Val Lys Ala Ala Arg Gln Ser Val Ala Gly Ile Lys Asn Arg 345 350 355	1171
gac cgt aaa gaa cac ctc acg gtt atg ctt ggt gaa ctt gat cga att Asp Arg Lys Glu His Leu Thr Val Met Leu Gly Glu Leu Asp Arg Ile 360 365 370	1219
ggg cag cgc ctc tac gaa ttg cgc agc gtc cag cac tca tcg gtg cgt Gly Gln Arg Leu Tyr Glu Leu Arg Ser Val Gln His Ser Ser Val Arg 375 380 385	1267
gtg agc cag cgt gat att gat gct ctg caa aag gcg atc acc gag gtc Val Ser Gln Arg Asp Ile Asp Ala Leu Gln Lys Ala Ile Thr Glu Val 390 395 400 405	1315
gat atc caa agg acg ctc gtt gaa gcg cag cag gga agt att acc ctc Asp Ile Gln Arg Thr Leu Val Glu Ala Gln Gln Gly Ser Ile Thr Leu 410 415 420	1363
agt gct tcc aca ccc acc gac att caa cta ggt gat gac acc gtt tca Ser Ala Ser Thr Pro Thr Asp Ile Gln Leu Gly Asp Asp Thr Val Ser 425 430 435	1411
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caa cag cgc atg agc ggt ggg aca gaa aca aca gtt tta cgt gcc gag Gln Gln Arg Met Ser Gly Gly Thr Glu Thr Thr Val Leu Arg Ala Glu 520 525 530	1699
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Arg Phe Glu Ser Glu Gln Arg Arg Ala His Ala Ala Arg Arg Leu Tyr
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 Ala Leu Met Val Phe Tyr Arg Asp Glu Ser Arg Lys Arg Tyr Ala Ala
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 ccc ttc gcg gac aaa cta tcc agg ctg gca gca tcc gta ttt gga gaa 2371
 Pro Phe Ala Asp Lys Leu Ser Arg Leu Ala Ala Ser Val Phe Gly Glu
 745 750 755
 tca gca gac ttt gat ctt gat gat gag ctg aag atc tcc agt cgt tcc 2419
 Ser Ala Asp Phe Asp Leu Asp Asp Glu Leu Lys Ile Ser Ser Arg Ser
 760 765 770
 ata gga cca cga aca gtg gac ctt gcc aat ctt tct ggc ggc gca aag 2467
 Ile Gly Pro Arg Thr Val Asp Leu Ala Asn Leu Ser Gly Gly Ala Lys
 775 780 785
 gaa cag ctg gca atc ctc acc cgc ttt gct atc gca gaa ttg gta gca 2515
 Glu Gln Leu Ala Ile Leu Thr Arg Phe Ala Ile Ala Glu Leu Val Ala
 790 795 800 805
 gaa tcc tcc gcg caa ggt gct gtg cct gtg ttt att gat gat gca ttg 2563
 Glu Ser Ser Ala Gln Gly Ala Val Pro Val Phe Ile Asp Asp Ala Leu
 810 815 820
 ggg agc aca gac cca gag cga ctg acc cgc ata tct act ctg ttt agt 2611
 Gly Ser Thr Asp Pro Glu Arg Leu Thr Arg Ile Ser Thr Leu Phe Ser
 825 830 835
 gat gca ggc aag gac tct cag gtg ttt gtt ctc acc tgt gtt cca gac 2659
 Asp Ala Gly Lys Asp Ser Gln Val Phe Val Leu Thr Cys Val Pro Asp
 840 845 850
 cgg tac aac tat gta gag gtc acc caa aag cac agc atc gag tca ttg 2707
 Arg Tyr Asn Tyr Val Glu Val Thr Gln Lys His Ser Ile Glu Ser Leu
 855 860 865
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<210> 1640

<211> 876

<212> PRT

<213> Corynebacterium glutamicum

<400> 1640

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 Asp Asn Glu Gln Gly Lys Ser Ser Ile Leu Glu Ala Ile Lys Thr Val
 35 40 45
 Leu Asn Ser Lys His Arg Thr Thr Ser Lys Thr Ile Lys Ala Ile Gln
 50 55 60

Pro Val Asp Arg Asp Val Pro Ile Ser Ile Thr Leu Glu Ala Thr Val
 65 70 75 80
 Gly Thr Val Arg Phe Arg Ile His Lys Arg Phe Leu Lys Ser Thr Ala
 85 90 95
 Ala Glu Leu Gln Val Ile Glu Pro Arg Pro Ser Asn His Arg Gly Leu
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 Glu Ala Glu Ala Ala Leu Ala Glu Ile Leu Glu Ser His Leu Asp Thr
 115 120 125
 Ser Leu Leu Asp Ala Leu Phe Met Lys Gln Gly Glu Val Glu Ala Gly
 130 135 140
 Ile Ser Ala Val Gly Ile Pro Thr Leu Thr Ser Ala Leu Asn Ala Gln
 145 150 155 160
 Asn Gly Asn Thr Glu Asp Ala Thr Glu Asp Thr Ala Leu Met Glu Ala
 165 170 175
 Val Glu Lys Glu Tyr Leu Lys Phe Tyr Thr Asn Ser Gly Lys Ala Asn
 180 185 190
 Thr Arg Phe Leu Gln Phe Ser Lys Gln Val Glu Thr Leu Arg Thr Asp
 195 200 205
 Leu Asp Glu Ala Asn Ala Glu Val Ala Lys Leu Ser Ser His Val Asp
 210 215 220
 Arg Val Lys Arg Leu Glu Ile Asp Arg Asp Gln Ala Thr Ala Gln Leu
 225 230 235 240
 Pro Lys Ala Glu Glu Glu Leu Ala Gly Arg Lys Ala Glu Leu Glu Glu
 245 250 255
 Ala Gln Lys Val Lys Ala Gln Ala Thr Glu Ile Leu Ala Gln Phe Ser
 260 265 270
 Arg Ala Glu Glu Gln Leu Glu Gln Ala Thr Gly Ala Gln Lys Arg Arg
 275 280 285
 Lys Glu Leu Arg Asn Lys Leu Glu Leu Ala Gln Thr Glu Val Glu Lys
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 Ala Glu Ala Gly Gln Glu Asn Leu Ala Gln Glu Ala Ser Arg Glu Ala
 305 310 315 320
 Glu Glu Phe Leu Ala Leu Ser Glu Lys Phe Glu Ala Ala Arg Ala Ala
 325 330 335
 Glu Thr Leu Ala Val Glu Lys Val Lys Ala Ala Arg Gln Ser Val Ala
 340 345 350
 Gly Ile Lys Asn Arg Asp Arg Lys Glu His Leu Thr Val Met Leu Gly
 355 360 365
 Glu Leu Asp Arg Ile Gly Gln Arg Leu Tyr Glu Leu Arg Ser Val Gln
 370 375 380

His Ser Ser Val Arg Val Ser Gln Arg Asp Ile Asp Ala Leu Gln Lys
385 390 395 400

Ala Ile Thr Glu Val Asp Ile Gln Arg Thr Leu Val Glu Ala Gln Gln
405 410 415

Gly Ser Ile Thr Leu Ser Ala Ser Thr Pro Thr Asp Ile Gln Leu Gly
420 425 430

Asp Asp Thr Val Ser Ala Thr Asp Ala Gly Thr Thr Val Ala Leu Asp
435 440 445

Arg Glu Leu Thr Val Val Val Gly Asp Val Thr Leu Val Ile Asn Pro
450 455 460

Gly Lys Thr Ala Ala Glu Ser Arg Thr Asp Phe Glu Ser Ala Glu Ala
465 470 475 480

Ala Leu Ala Glu Leu Leu Asp Gln Leu Asp Val Ser Asp Leu Asp Gln
485 490 495

Leu Arg Glu Arg Phe Thr Ala Gln Glu Gln Arg Asp Ala Asp Ile Ala
500 505 510

Glu Leu Val Arg Glu Gln Gln Arg Met Ser Gly Gly Thr Glu Thr Thr
515 520 525

Val Leu Arg Ala Glu Leu Glu Gly Leu His Val Pro Glu Asp Leu Asp
530 535 540

Pro Ser Ile Ser Val Asp Asp Ala Gln Thr Gln Leu Asn Glu Ala Glu
545 550 555 560

Glu Ser Arg Glu Leu Ala Ala Glu Ala His Lys His Ala Asn Ala Ala
565 570 575

Leu Asp Gly Leu Arg Ser Arg Pro Val Asp Lys Ala Leu Thr Val Phe
580 585 590

Asn Ala Gln Leu Ala Ala Leu Gln Arg Asn Leu Ser Ser Ala Gln Val
595 600 605

Glu Leu Asp Arg Ala Val Ala Glu Thr Ser Asp Asp Glu Val Asp Ala
610 615 620

Ala Val Gln Arg Cys Ala Glu Ala Leu Ala Gly Val Arg Val Gln Lys
625 630 635 640

Gln Glu Ile Glu Gln Val Leu Ala Lys Thr Asn Pro Asp Met Ala Gln
645 650 655

Arg Leu Cys Asp Ala Ala Glu Ala Asn Val Arg Ser Tyr Lys Thr Ala
660 665 670

Val Ser Asp Ala Thr Thr Glu Leu Val Arg Leu Glu Gly Leu Ile Gly
675 680 685

Val Ala Ala Gly Ala Lys Glu Arg Leu Asp Lys Val Lys Ser Ala Leu
690 695 700

Thr Ala Ala Glu Asn Arg Phe Glu Ser Glu Gln Arg Arg Ala His Ala

tcg gag atc ggt aac ttt aat gtt gaa atg aac cac ccg cca cta tcc	307
Ser Glu Ile Gly Asn Phe Asn Val Glu Met Asn His Pro Pro Leu Ser	
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gtt aaa ggc gat gct tta cga cgc ctc gag caa ggc atc acc tcg cgt	355
Val Lys Gly Asp Ala Leu Arg Arg Leu Glu Gln Gly Ile Thr Ser Arg	
70 75 80 85	
cta ggt cgc gtg cgc gcg gcc gcc aca tcg gag aac gtg aac gtg gcg	403
Leu Gly Arg Val Arg Ala Ala Ala Thr Ser Glu Asn Val Asn Val Ala	
90 95 100	
atg atc ggc acg ctg ccc acc atc acc cca gaa ttc ctc gaa gat ccg	451
Met Ile Gly Thr Leu Pro Thr Ile Thr Pro Glu Phe Leu Glu Asp Pro	
105 110 115	
gca tgg atg acc caa gaa aac cgc tac cgt gcg ctg agc aat gcg gtg	499
Ala Trp Met Thr Gln Glu Asn Arg Tyr Arg Ala Leu Ser Asn Ala Val	
120 125 130	
atg gaa tcg cgt ggc gag tta gtg cac atc aac atc gcc gac cgt gaa	547
Met Glu Ser Arg Gly Glu Leu Val His Ile Asn Ile Ala Asp Arg Glu	
135 140 145	
caa atc atc cac gat ttc act gat ctc gcc ccc gaa tca act tgc acg	595
Gln Ile Ile His Asp Phe Thr Asp Leu Ala Pro Glu Ser Thr Cys Thr	
150 155 160 165	
tct att cag ttg cac ctg caa tta gca ccc aat aag ttt gct gca gcg	643
Ser Ile Gln Leu His Leu Gln Leu Ala Pro Asn Lys Phe Ala Ala Ala	
170 175 180	
tgg aat gcg tcg caa gca ata gct ggt gtt caa gca gct ctt tcc gcc	691
Trp Asn Ala Ser Gln Ala Ile Ala Gly Val Gln Ala Ala Leu Ser Ala	
185 190 195	
aac tcc cca ctt ttc cta ggc cgt cgg gtg tgg cat gaa agc cgc att	739
Asn Ser Pro Leu Phe Leu Gly Arg Arg Val Trp His Glu Ser Arg Ile	
200 205 210	
cca gtg ttt caa caa gct atc gat acg cgt act cct gaa ctt gtg aat	787
Pro Val Phe Gln Gln Ala Ile Asp Thr Arg Thr Pro Glu Leu Val Asn	
215 220 225	
caa gga gtc cgc ccc aga gta tgg ttc gcc gaa cga tgg atc acc agt	835
Gln Gly Val Arg Pro Arg Val Trp Phe Gly Glu Arg Trp Ile Thr Ser	
230 235 240 245	
gtt ttt gat ctt ttc gaa gaa aac gta cgc tac ttc tcc cct ctc atc	883
Val Phe Asp Leu Phe Glu Glu Asn Val Arg Tyr Phe Ser Pro Leu Ile	
250 255 260	
gca gaa tcc cgc gcc ctg tct ggc aca cca atg atg aag gga aaa tcc	931
Ala Glu Ser Arg Ala Leu Ser Gly Thr Pro Met Met Lys Gly Lys Ser	
265 270 275	
ccc gca ctc cac tac ctc aat ctc cac aac gga acg gtg tgg cgc tgg	979
Pro Ala Leu His Tyr Leu Asn Leu His Asn Gly Thr Val Trp Arg Trp	
280 285 290	

aac cga ccc att tac gca ccg ggg gaa gag cgc tct cat ctg cgt ttg 1027
 Asn Arg Pro Ile Tyr Ala Pro Gly Glu Glu Arg Ser His Leu Arg Leu
 295 300 305
 gaa aac cgt ctc cta cct gca ggt ccc acc ccc atc gac atc acc gcc 1075
 Glu Asn Arg Leu Leu Pro Ala Gly Pro Thr Pro Ile Asp Ile Thr Ala
 310 315 320 325
 gat gcc gct ttc tac tac ggt ttg gtt aaa tat ctg gcc gag gaa aac 1123
 Asp Ala Ala Phe Tyr Tyr Gly Leu Val Lys Tyr Leu Ala Glu Glu Asn
 330 335 340
 cgc cct gtc tgg tca cgt ctc cta ttc cct gat gcg gaa aag aac ttc 1171
 Arg Pro Val Trp Ser Arg Leu Leu Phe Pro Asp Ala Glu Lys Asn Phe
 345 350 355
 caa tcc ggt gca cgt tca ggg ctg ttc gcc cgc atg acc tgg cca acc 1219
 Gln Ser Gly Ala Arg Ser Gly Leu Phe Ala Arg Met Thr Trp Pro Thr
 360 365 370
 ctc gga caa gtc aac gtt gcg aat ctg gtc caa gag cac ctc atc cct 1267
 Leu Gly Gln Val Asn Val Ala Asn Leu Val Gln Glu His Leu Ile Pro
 375 380 385
 caa gcc aga atc gga ctg gaa cga ctc gaa gta aac aaa gac ctt atc 1315
 Gln Ala Arg Ile Gly Leu Glu Arg Leu Glu Val Asn Lys Asp Leu Ile
 390 395 400 405
 gac caa tac ctg ggc atc atc acc gaa cgc gcg aag tcc cgc caa aac 1363
 Asp Gln Tyr Leu Gly Ile Ile Thr Glu Arg Ala Lys Ser Arg Gln Asn
 410 415 420
 ggt gcc acc tgg cag ttg cgt agc ctc aac aag ctg gaa gca cac gga 1411
 Gly Ala Thr Trp Gln Leu Arg Ser Leu Asn Lys Leu Glu Ala His Gly
 425 430 435
 agc atg ccg ggt tcc gat gct cga aaa gca ggt ctt gca gca atg ttg 1459
 Ser Met Pro Gly Ser Asp Ala Arg Lys Ala Gly Leu Ala Ala Met Leu
 440 445 450
 caa cag tat tta cag aat caa gaa agc ggc caa cct gtc cac aca tgg 1507
 Gln Gln Tyr Leu Gln Asn Gln Glu Ser Gly Gln Pro Val His Thr Trp
 455 460 465
 gct att ggt tcg taaaacggca aggaaagata ata 1542
 Ala Ile Gly Ser
 470

<210> 1642

<211> 473

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1642

Met Glu Asp Leu Glu Ile Phe Asp Arg His Leu Gln His Ser Asp Phe
 1 5 10 15

Glu Asp Gln Gly Ser Ile Gly Leu Glu Leu Glu Leu Asn Leu Val Asp
 20 25 30

Lys His Met Gln Pro Ala Leu Ala Gly His Ala Val Leu Ser His Leu
35 40 45

Asp Asp Glu Tyr Gln Ser Glu Ile Gly Asn Phe Asn Val Glu Met Asn
50 55 60

His Pro Pro Leu Ser Val Lys Gly Asp Ala Leu Arg Arg Leu Glu Gln
65 70 75 80

Gly Ile Thr Ser Arg Leu Gly Arg Val Arg Ala Ala Ala Thr Ser Glu
85 90 95

Asn Val Asn Val Ala Met Ile Gly Thr Leu Pro Thr Ile Thr Pro Glu
100 105 110

Phe Leu Glu Asp Pro Ala Trp Met Thr Gln Glu Asn Arg Tyr Arg Ala
115 120 125

Leu Ser Asn Ala Val Met Glu Ser Arg Gly Glu Leu Val His Ile Asn
130 135 140

Ile Ala Asp Arg Glu Gln Ile Ile His Asp Phe Thr Asp Leu Ala Pro
145 150 155 160

Glu Ser Thr Cys Thr Ser Ile Gln Leu His Leu Gln Leu Ala Pro Asn
165 170 175

Lys Phe Ala Ala Ala Trp Asn Ala Ser Gln Ala Ile Ala Gly Val Gln
180 185 190

Ala Ala Leu Ser Ala Asn Ser Pro Leu Phe Leu Gly Arg Arg Val Trp
195 200 205

His Glu Ser Arg Ile Pro Val Phe Gln Gln Ala Ile Asp Thr Arg Thr
210 215 220

Pro Glu Leu Val Asn Gln Gly Val Arg Pro Arg Val Trp Phe Gly Glu
225 230 235 240

Arg Trp Ile Thr Ser Val Phe Asp Leu Phe Glu Glu Asn Val Arg Tyr
245 250 255

Phe Ser Pro Leu Ile Ala Glu Ser Arg Ala Leu Ser Gly Thr Pro Met
260 265 270

Met Lys Gly Lys Ser Pro Ala Leu His Tyr Leu Asn Leu His Asn Gly
275 280 285

Thr Val Trp Arg Trp Asn Arg Pro Ile Tyr Ala Pro Gly Glu Glu Arg
290 295 300

Ser His Leu Arg Leu Glu Asn Arg Leu Leu Pro Ala Gly Pro Thr Pro
305 310 315 320

Ile Asp Ile Thr Ala Asp Ala Ala Phe Tyr Tyr Gly Leu Val Lys Tyr
325 330 335

Leu Ala Glu Glu Asn Arg Pro Val Trp Ser Arg Leu Leu Phe Pro Asp
340 345 350

Ala Glu Lys Asn Phe Gln Ser Gly Ala Arg Ser Gly Leu Phe Ala Arg

355 360 365
 Met Thr Trp Pro Thr Leu Gly Gln Val Asn Val Ala Asn Leu Val Gln
 370 375 380
 Glu His Leu Ile Pro Gln Ala Arg Ile Gly Leu Glu Arg Leu Glu Val
 385 390 395 400
 Asn Lys Asp Leu Ile Asp Gln Tyr Leu Gly Ile Ile Thr Glu Arg Ala
 405 410 415
 Lys Ser Arg Gln Asn Gly Ala Thr Trp Gln Leu Arg Ser Leu Asn Lys
 420 425 430
 Leu Glu Ala His Gly Ser Met Pro Gly Ser Asp Ala Arg Lys Ala Gly
 435 440 445
 Leu Ala Ala Met Leu Gln Gln Tyr Leu Gln Asn Gln Glu Ser Gly Gln
 450 455 460
 Pro Val His Thr Trp Ala Ile Gly Ser
 465 470

<210> 1643

<211> 326

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(303)

<223> RXA00200

<400> 1643

cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac 48
 His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
 1 5 10 15
 cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc 96
 His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
 20 25 30
 gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg 144
 Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
 35 40 45
 tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc 192
 Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
 50 55 60
 tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac 240
 Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
 65 70 75 80
 atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat 288
 Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
 85 90 95
 atg aag gta gat gaa taagaccttc agtactggaa gtt 326
 Met Lys Val Asp Glu

100

<210> 1644

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 1644

His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
 1 5 10 15

His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
 20 25 30

Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
 35 40 45

Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
 50 55 60

Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
 65 70 75 80

Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
 85 90 95

Met Lys Val Asp Glu
 100

<210> 1645

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXA00207

<400> 1645

ctgcacaatt tttggtcgga cacatttttg cccccattgg gttgtcggat cagatcaaga 60

aaacccccgc ggaaaaattt tgtctctaga ctggctcacc atg gaa atg aaa ttg 115
 Met Glu Met Lys Leu
 1 5

aaa aag gca tcc cag gtc agc act gcc acc gtc gtc gca gca ggt ttg 163
 Lys Lys Ala Ser Gln Val Ser Thr Ala Thr Val Val Ala Ala Gly Leu
 10 15 20

atc ggc ggt tgg ttg act gcc cgt gaa tcc ggc att cgc cca ctg ggc 211
 Ile Gly Gly Trp Leu Thr Ala Arg Glu Ser Gly Ile Arg Pro Leu Gly
 25 30 35

acc att cca ttg gca gca tcc gga gcg ctt gct gca cga agc tgg aat 259
 Thr Ile Pro Leu Ala Ala Ser Gly Ala Leu Ala Ala Arg Ser Trp Asn
 40 45 50

gaa aag aag ggt cct gca gta gct act ggc ctg ctg gca acc tac gtt 307

Glu Lys Lys Gly Pro Ala Val Ala Thr Gly Leu Leu Ala Thr Tyr Val
 55 60 65
 ggt gca ttt ggc ctg tcc cac cca ctt gcc aag aag att ggc gcg tgg 355
 Gly Ala Phe Gly Leu Ser His Pro Leu Ala Lys Lys Ile Gly Ala Trp
 70 75 80 85
 cct gca gtt ctt act gtg acc gct ggc gct gct gcg att gct tac gca 403
 Pro Ala Val Leu Thr Val Thr Ala Gly Ala Ala Ile Ala Tyr Ala
 90 95 100
 gta tct gac tcc cag taataattac ggtaaaaaaa ctt 441
 Val Ser Asp Ser Gln
 105

<210> 1646

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1646

Met Glu Met Lys Leu Lys Lys Ala Ser Gln Val Ser Thr Ala Thr Val
 1 5 10 15
 Val Ala Ala Gly Leu Ile Gly Gly Trp Leu Thr Ala Arg Glu Ser Gly
 20 25 30
 Ile Arg Pro Leu Gly Thr Ile Pro Leu Ala Ala Ser Gly Ala Leu Ala
 35 40 45
 Ala Arg Ser Trp Asn Glu Lys Lys Gly Pro Ala Val Ala Thr Gly Leu
 50 55 60
 Leu Ala Thr Tyr Val Gly Ala Phe Gly Leu Ser His Pro Leu Ala Lys
 65 70 75 80
 Lys Ile Gly Ala Trp Pro Ala Val Leu Thr Val Thr Ala Gly Ala Ala
 85 90 95
 Ala Ile Ala Tyr Ala Val Ser Asp Ser Gln
 100 105

<210> 1647

<211> 786

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(763)

<223> RXA00211

<400> 1647

tgagccaaaa tcaataaggt gtttttcagc ctgaggtaaa aatacgggtgg tactgtcgaa 60
 accaatcatc ccctagtttt gaaaagaagg aagcgagcca atg tca ttc ctg atc 115
 Met Ser Phe Leu Ile
 1 5

cgc gtc ctg ttg tcc gac acc cca ggc agc ctc gcg tta ctc gct gaa 163
 Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu Ala Leu Leu Ala Glu
 10 15 20

gcc ctt ggg att gta gag gcc aat att caa tcc gtg gac gtg gtg gaa 211
 Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser Val Asp Val Val Glu
 25 30 35

cgc ttc ccc aat ggc acg gtc atg gac gat ctg gtg atc tcc atc cct 259
 Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu Val Ile Ser Ile Pro
 40 45 50

cgc gat gtc atg gca gac acc atc atc acc gca gct gaa gaa gtc gac 307
 Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala Ala Glu Glu Val Asp
 55 60 65

ggc gtg gag att gat tcc atc cgc cca ttc tcc ggg act gtt gac cgc 355
 Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser Gly Thr Val Asp Arg
 70 75 80 85

cgc gga cag atc caa atg ctg gct gct gtt gct cac caa cgc cgc gat 403
 Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala His Gln Arg Arg Asp
 90 95 100

atc acc gca gcg atg gaa gaa atg gtc gat gtc atc ccc cgc acc atg 451
 Ile Thr Ala Ala Met Glu Glu Met Val Asp Val Ile Pro Arg Thr Met
 105 110 115

acc tct ggt tgg gct ttg gtc att gat cta aaa gga ccc atc act cgc 499
 Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys Gly Pro Ile Thr Arg
 120 125 130

atc gct ggt tcc cta gca gcg ccc gaa gat gac ggc acc gtt ccg gag 547
 Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp Gly Thr Val Pro Glu
 135 140 145

aac atc gtt ctc aaa gaa gct cgc atg ctc aac ccg gaa aac gat ccg 595
 Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn Pro Glu Asn Asp Pro
 150 155 160 165

tgg att cca gag tcc tgg aca ctg ctt gat tct tcc ctt gcc atc gct 643
 Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser Ser Leu Ala Ile Ala
 170 175 180

ccg atc ggc aag cac ggc ctg gct ctg att atc ggt cgc cct ggt ggc 691
 Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile Gly Arg Pro Gly Gly
 185 190 195

cct gat ttc ttg gcc agc gaa gtg gag cac tta ggc caa gtc ggt gac 739
 Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu Gly Gln Val Gly Asp
 200 205 210

att atc gga gca atg ctt caa aaa taatctgagc tgtttaaaaa atg 786
 Ile Ile Gly Ala Met Leu Gln Lys
 215 220

<210> 1648

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 1648

Met Ser Phe Leu Ile Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu
 1 5 10 15
 Ala Leu Leu Ala Glu Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser
 20 25 30
 Val Asp Val Val Glu Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu
 35 40 45
 Val Ile Ser Ile Pro Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala
 50 55 60
 Ala Glu Glu Val Asp Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser
 65 70 75 80
 Gly Thr Val Asp Arg Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala
 85 90 95
 His Gln Arg Arg Asp Ile Thr Ala Ala Met Glu Glu Met Val Asp Val
 100 105 110
 Ile Pro Arg Thr Met Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys
 115 120 125
 Gly Pro Ile Thr Arg Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp
 130 135 140
 Gly Thr Val Pro Glu Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn
 145 150 155 160
 Pro Glu Asn Asp Pro Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser
 165 170 175
 Ser Leu Ala Ile Ala Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile
 180 185 190
 Gly Arg Pro Gly Gly Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu
 195 200 205
 Gly Gln Val Gly Asp Ile Ile Gly Ala Met Leu Gln Lys
 210 215 220

<210> 1649

<211> 1263

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1240)

<223> RXA00218

<400> 1649

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 gcattccgca aaccgcgacta gaccatccaa ggtgtcttct atg tca gct cgc aat 115
 Met Ser Ala Arg Asn
 1 5

ccg ttc cgc ccc act ttc gga gtt tcc ccc acc gta ctt gca ggc cga Pro Phe Arg Pro Thr Phe Gly Val Ser Pro Thr Val Leu Ala Gly Arg 10 15 20	163
gac tca ctt cta cag tct ttc aaa ctt ggt ctc gcg gaa ggc ccc gga Asp Ser Leu Leu Gln Ser Phe Lys Leu Gly Leu Ala Glu Gly Pro Gly 25 30 35	211
agc ccc ttt aga gca ttg ctg att tcg gga tct cgt ggc atg ggt aaa Ser Pro Phe Arg Ala Leu Leu Ile Ser Gly Ser Arg Gly Met Gly Lys 40 45 50	259
act gtg ttg ctc aat gaa ttt gaa gat gca gct gcg tct caa ggg tgg Thr Val Leu Leu Asn Glu Phe Glu Asp Ala Ala Ala Ser Gln Gly Trp 55 60 65	307
atc acg ctg cgc gcc tat ccg gat aat tcc atg gtg gat ggc tta gtt Ile Thr Leu Arg Ala Tyr Pro Asp Asn Ser Met Val Asp Gly Leu Val 70 75 80 85	355
aat tcc gcc atc ccg gag gcg cta cag aat ctt gac gga ccg cag tcc Asn Ser Ala Ile Pro Glu Ala Leu Gln Asn Leu Asp Gly Pro Gln Ser 90 95 100	403
aaa aga atg ctc agt ggt gtg gcc att cct ggt atc gct acg gtg acg Lys Arg Met Leu Ser Gly Val Ala Ile Pro Gly Ile Ala Thr Val Thr 105 110 115	451
gcc att gct gat cca acc aag aag gat ccc act ccc acg ctg att tcc Ala Ile Ala Asp Pro Thr Lys Lys Asp Pro Thr Pro Thr Leu Ile Ser 120 125 130	499
agg ctc cgc gag ttg gct act cgt ttg caa aag cac ggc tcc gga att Arg Leu Arg Glu Leu Ala Thr Arg Leu Gln Lys His Gly Ser Gly Ile 135 140 145	547
ttg atc acc ctt gat gaa ctc caa agc gcc aat gtg gat ctt ttg cat Leu Ile Thr Leu Asp Glu Leu Gln Ser Ala Asn Val Asp Leu Leu His 150 155 160 165	595
gtg ttg gcc act gcg gtc cag gat ctc cta cgg gat gat ttc gat atc Val Leu Ala Thr Ala Val Gln Asp Leu Leu Arg Asp Asp Phe Asp Ile 170 175 180	643
gca ttg gta gca gcg ggt ctg cca gag gga atc gat cgt ctt ctc cag Ala Leu Val Ala Ala Gly Leu Pro Glu Gly Ile Asp Arg Leu Leu Gln 185 190 195	691
cat gag ggc aca acc ttt atc cgc cga gcc gaa aga atc ctg ctc aat His Glu Gly Thr Thr Phe Ile Arg Arg Ala Glu Arg Ile Leu Leu Asn 200 205 210	739
cct gtc aac cat gaa gat tcg gtg gag atg ttc ctg gat acc gct gcg Pro Val Asn His Glu Asp Ser Val Glu Met Phe Leu Asp Thr Ala Ala 215 220 225	787
gaa ggc caa cgc cac atg act tcc gag gcc gcc gaa ctc gcg gcg cag Glu Gly Gln Arg His Met Thr Ser Glu Ala Ala Glu Leu Ala Ala Gln 230 235 240 245	835

atc agc aag ggc tac ccc tac tcc atg cag ctg act ggt tct ctg gca 883
 Ile Ser Lys Gly Tyr Pro Tyr Ser Met Gln Leu Thr Gly Ser Leu Ala
 250 255 260

tgg gcg cga agt act ctt gac aac tcc gat acc atc cag gcc gaa caa 931
 Trp Ala Arg Ser Thr Leu Asp Asn Ser Asp Thr Ile Gln Ala Glu Gln
 265 270 275

gta gat gct gtc cgc gac gag gtt gtg cgc cgc atg ggc atg caa gtc 979
 Val Asp Ala Val Arg Asp Glu Val Val Arg Arg Met Gly Met Gln Val
 280 285 290

cac gag cca agc ctg cac cag gtc cct gat ggt gag ctg acc att ttg 1027
 His Glu Pro Ser Leu His Gln Val Pro Asp Gly Glu Leu Thr Ile Leu
 295 300 305

tac gcg att gcc caa ctg tca aaa aac ggc gag atg gtg tct act gga 1075
 Tyr Ala Ile Ala Gln Leu Ser Lys Asn Gly Glu Met Val Ser Thr Gly
 310 315 320 325

gat atc gca cac ctc atg ggc gtc aag ccc aac gcc ttg tcg atg cag 1123
 Asp Ile Ala His Leu Met Gly Val Lys Pro Asn Ala Leu Ser Met Gln
 330 335 340

aga aag caa ctt ctc agc aga ggt ctc gta gag gtt ccc aag tac ggt 1171
 Arg Lys Gln Leu Leu Ser Arg Gly Leu Val Glu Val Pro Lys Tyr Gly
 345 350 355

ttc ctc aat ttc act ttg ccg tac atg cgc gag cac ctc ctc aac agc 1219
 Phe Leu Asn Phe Thr Leu Pro Tyr Met Arg Glu His Leu Leu Asn Ser
 360 365 370

ccg cac cac cga cca atc aca taagacacaa gcactaaaac agc 1263
 Pro His His Arg Pro Ile Thr
 375 380

<210> 1650

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 1650

Met Ser Ala Arg Asn Pro Phe Arg Pro Thr Phe Gly Val Ser Pro Thr
 1 5 10 15

Val Leu Ala Gly Arg Asp Ser Leu Leu Gln Ser Phe Lys Leu Gly Leu
 20 25 30

Ala Glu Gly Pro Gly Ser Pro Phe Arg Ala Leu Leu Ile Ser Gly Ser
 35 40 45

Arg Gly Met Gly Lys Thr Val Leu Leu Asn Glu Phe Glu Asp Ala Ala
 50 55 60

Ala Ser Gln Gly Trp Ile Thr Leu Arg Ala Tyr Pro Asp Asn Ser Met
 65 70 75 80

Val Asp Gly Leu Val Asn Ser Ala Ile Pro Glu Ala Leu Gln Asn Leu
 85 90 95

Asp Gly Pro Gln Ser Lys Arg Met Leu Ser Gly Val Ala Ile Pro Gly
 100 105 110
 Ile Ala Thr Val Thr Ala Ile Ala Asp Pro Thr Lys Lys Asp Pro Thr
 115 120 125
 Pro Thr Leu Ile Ser Arg Leu Arg Glu Leu Ala Thr Arg Leu Gln Lys
 130 135 140
 His Gly Ser Gly Ile Leu Ile Thr Leu Asp Glu Leu Gln Ser Ala Asn
 145 150 155 160
 Val Asp Leu Leu His Val Leu Ala Thr Ala Val Gln Asp Leu Leu Arg
 165 170 175
 Asp Asp Phe Asp Ile Ala Leu Val Ala Ala Gly Leu Pro Glu Gly Ile
 180 185 190
 Asp Arg Leu Leu Gln His Glu Gly Thr Thr Phe Ile Arg Arg Ala Glu
 195 200 205
 Arg Ile Leu Leu Asn Pro Val Asn His Glu Asp Ser Val Glu Met Phe
 210 215 220
 Leu Asp Thr Ala Ala Glu Gly Gln Arg His Met Thr Ser Glu Ala Ala
 225 230 235 240
 Glu Leu Ala Ala Gln Ile Ser Lys Gly Tyr Pro Tyr Ser Met Gln Leu
 245 250 255
 Thr Gly Ser Leu Ala Trp Ala Arg Ser Thr Leu Asp Asn Ser Asp Thr
 260 265 270
 Ile Gln Ala Glu Gln Val Asp Ala Val Arg Asp Glu Val Val Arg Arg
 275 280 285
 Met Gly Met Gln Val His Glu Pro Ser Leu His Gln Val Pro Asp Gly
 290 295 300
 Glu Leu Thr Ile Leu Tyr Ala Ile Ala Gln Leu Ser Lys Asn Gly Glu
 305 310 315 320
 Met Val Ser Thr Gly Asp Ile Ala His Leu Met Gly Val Lys Pro Asn
 325 330 335
 Ala Leu Ser Met Gln Arg Lys Gln Leu Leu Ser Arg Gly Leu Val Glu
 340 345 350
 Val Pro Lys Tyr Gly Phe Leu Asn Phe Thr Leu Pro Tyr Met Arg Glu
 355 360 365
 His Leu Leu Asn Ser Pro His His Arg Pro Ile Thr
 370 375 380

<210> 1651

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXA00220

<400> 1651

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tgatcgtgcc ggttttcctt gcgttggttag tcttggggct atg agc gca ttc cac 115
                                         Met Ser Ala Phe His
                                         1                               5

atc cga gcg gaa caa tcg cac gat atc agc gcg att cat gat gtt act 163
Ile Arg Ala Glu Gln Ser His Asp Ile Ser Ala Ile His Asp Val Thr
                        10                        15                        20

gaa gcg gcc ttt aca gga att gag cat tca gat gga aca gag caa gat 211
Glu Ala Ala Phe Thr Gly Ile Glu His Ser Asp Gly Thr Glu Gln Asp
                        25                        30                        35

ctc gtc gat aag ctt cgt gct gca aag gcg ctg agc ctt tcg ctc gtc 259
Leu Val Asp Lys Leu Arg Ala Ala Lys Ala Leu Ser Leu Ser Leu Val
                        40                        45                        50

gct gag gcg gat ggc gag gtc att ggg cat att gct gcc tct gag gtg 307
Ala Glu Ala Asp Gly Glu Val Ile Gly His Ile Ala Ala Ser Glu Val
                        55                        60                        65

ctg att ggc ggt ggg gtg cag ggc tgg ttt ggc att ggg cct gtc agt 355
Leu Ile Gly Gly Gly Val Gln Gly Trp Phe Gly Ile Gly Pro Val Ser
                        70                        75                        80                        85

gtt cgg ccc gat aag cag cag caa ggc gtg ggt att gcg ctg atg ggc 403
Val Arg Pro Asp Lys Gln Gln Gln Gly Val Gly Ile Ala Leu Met Gly
                        90                        95                        100

agc gcg ctt gat cag ttg cgt gcg gag ggt gct ggc ggc atc gtg ttg 451
Ser Ala Leu Asp Gln Leu Arg Ala Glu Gly Ala Gly Gly Ile Val Leu
                        105                        110                        115

ctg ggg gat ccg ggc tat tat cga cgc ttc ggt ttt gag gtc gtg ccc 499
Leu Gly Asp Pro Gly Tyr Tyr Arg Arg Phe Gly Phe Glu Val Val Pro
                        120                        125                        130

ggg ctg gtc tat ccg gac gcg cca gcg gaa ttt ttt atg gct gtg tgt 547
Gly Leu Val Tyr Pro Asp Ala Pro Ala Glu Phe Phe Met Ala Val Cys
                        135                        140                        145

ttg aat gct ccg gcg ttt ccg cag ggt gtt gtg gag tat cac tcg gca 595
Leu Asn Ala Pro Ala Phe Pro Gln Gly Val Val Glu Tyr His Ser Ala
                        150                        155                        160                        165

ttt gga ggg tagagacccc atcgtggcgg gcc 627
Phe Gly Gly

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<210> 1652

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 1652

Met Ser Ala Phe His Ile Arg Ala Glu Gln Ser His Asp Ile Ser Ala
 1 5 10 15
 Ile His Asp Val Thr Glu Ala Ala Phe Thr Gly Ile Glu His Ser Asp
 20 25 30
 Gly Thr Glu Gln Asp Leu Val Asp Lys Leu Arg Ala Ala Lys Ala Leu
 35 40 45
 Ser Leu Ser Leu Val Ala Glu Ala Asp Gly Glu Val Ile Gly His Ile
 50 55 60
 Ala Ala Ser Glu Val Leu Ile Gly Gly Gly Val Gln Gly Trp Phe Gly
 65 70 75 80
 Ile Gly Pro Val Ser Val Arg Pro Asp Lys Gln Gln Gln Gly Val Gly
 85 90 95
 Ile Ala Leu Met Gly Ser Ala Leu Asp Gln Leu Arg Ala Glu Gly Ala
 100 105 110
 Gly Gly Ile Val Leu Leu Gly Asp Pro Gly Tyr Tyr Arg Arg Phe Gly
 115 120 125
 Phe Glu Val Val Pro Gly Leu Val Tyr Pro Asp Ala Pro Ala Glu Phe
 130 135 140
 Phe Met Ala Val Cys Leu Asn Ala Pro Ala Phe Pro Gln Gly Val Val
 145 150 155 160
 Glu Tyr His Ser Ala Phe Gly Gly
 165

<210> 1653

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXA00230

<400> 1653

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 tcctatctat ctagtccac tagcacagat aggaactccg ttg att cat gag caa 115
 Leu Ile His Glu Gln
 1 5
 gac gtt cag aag ctg tta aac tac atc act tca cac ttt ggt gtt gac 163
 Asp Val Gln Lys Leu Leu Asn Tyr Ile Thr Ser His Phe Gly Val Asp
 10 15 20
 cct gaa aga tgg ttt cat cct gaa ggc tac caa agc att gcc cta gcg 211
 Pro Glu Arg Trp Phe His Pro Glu Gly Tyr Gln Ser Ile Ala Leu Ala
 25 30 35
 att ctt gac tcc att tac tcg act ggt aat cgc tat aca ggt gta ctc 259

Ile Leu Asp Ser Ile Tyr Ser Thr Gly Asn Arg Tyr Thr Gly Val Leu
 40 45 50
 aac ctt gtc aat cga tac tgc ggg ctg cgc gca aat gaa gga tca cac 307
 Asn Leu Val Asn Arg Tyr Cys Gly Leu Arg Ala Asn Glu Gly Ser His
 55 60 65
 cct gaa gcc gat act gcc act gat ctc atc gag aca ttc tac cgg tgg 355
 Pro Glu Ala Asp Thr Ala Thr Asp Leu Ile Glu Thr Phe Tyr Arg Trp
 70 75 80 85
 gga ggg gtc gac gaa ttt gtt ctc aaa acg aat aat cgg tgg aga act 403
 Gly Gly Val Asp Glu Phe Val Leu Lys Thr Asn Asn Arg Trp Arg Thr
 90 95 100
 tcc tcc aag att cac gca ccc tat aag gca tac gca gct ttg gaa gca 451
 Ser Ser Lys Ile His Ala Pro Tyr Lys Ala Tyr Ala Ala Leu Glu Ala
 105 110 115
 gca aag gta ctt gcg ggt cat tcc atc gaa tcc atc agc gat gtt gtc 499
 Ala Lys Val Leu Ala Gly His Ser Ile Glu Ser Ile Ser Asp Val Val
 120 125 130
 ggc agg ttc gat tcg cgc gaa agc cgt gaa cac tca gat atc gcg aga 547
 Gly Arg Phe Asp Ser Arg Glu Ser Arg Glu His Ser Asp Ile Ala Arg
 135 140 145
 gaa tgg ttg atg ata acc ggc caa agt agt gcg ttg acc tgg agt tac 595
 Glu Trp Leu Met Ile Thr Gly Gln Ser Ser Ala Leu Thr Trp Ser Tyr
 150 155 160 165
 ttc ctt atg ctc gta ggt gtc cca gga gtg aaa gca gac cga atg atc 643
 Phe Leu Met Leu Val Gly Val Pro Gly Val Lys Ala Asp Arg Met Ile
 170 175 180
 gtc cgt ttc gtc act cac gtg ctc gag cgt ccg aaa gag att tcc agg 691
 Val Arg Phe Val Thr His Val Leu Glu Arg Pro Lys Glu Ile Ser Arg
 185 190 195
 cac gaa gct tca cgg ttg att gag gaa gtt gcg gac att atg tgc gtc 739
 His Glu Ala Ser Arg Leu Ile Glu Glu Val Ala Asp Ile Met Cys Val
 200 205 210
 aac tac atc tac ctc gac cac acc atc tgg cgg ttc caa tca ggg cgc 787
 Asn Tyr Ile Tyr Leu Asp His Thr Ile Trp Arg Phe Gln Ser Gly Arg
 215 220 225
 ccc tac ctc caa gaa gac tcc tcc cct ttc gaa taaatccatc acatttcaca 840
 Pro Tyr Leu Gln Glu Asp Ser Ser Pro Phe Glu
 230 235 240
 gtc 843

<210> 1654

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 1654

Leu Ile His Glu Gln Asp Val Gln Lys Leu Leu Asn Tyr Ile Thr Ser

1	5	10	15
His Phe Gly Val Asp Pro Glu Arg Trp Phe His Pro Glu Gly Tyr Gln	20	25	30
Ser Ile Ala Leu Ala Ile Leu Asp Ser Ile Tyr Ser Thr Gly Asn Arg	35	40	45
Tyr Thr Gly Val Leu Asn Leu Val Asn Arg Tyr Cys Gly Leu Arg Ala	50	55	60
Asn Glu Gly Ser His Pro Glu Ala Asp Thr Ala Thr Asp Leu Ile Glu	65	70	75
Thr Phe Tyr Arg Trp Gly Gly Val Asp Glu Phe Val Leu Lys Thr Asn	85	90	95
Asn Arg Trp Arg Thr Ser Ser Lys Ile His Ala Pro Tyr Lys Ala Tyr	100	105	110
Ala Ala Leu Glu Ala Ala Lys Val Leu Ala Gly His Ser Ile Glu Ser	115	120	125
Ile Ser Asp Val Val Gly Arg Phe Asp Ser Arg Glu Ser Arg Glu His	130	135	140
Ser Asp Ile Ala Arg Glu Trp Leu Met Ile Thr Gly Gln Ser Ser Ala	145	150	155
Leu Thr Trp Ser Tyr Phe Leu Met Leu Val Gly Val Pro Gly Val Lys	165	170	175
Ala Asp Arg Met Ile Val Arg Phe Val Thr His Val Leu Glu Arg Pro	180	185	190
Lys Glu Ile Ser Arg His Glu Ala Ser Arg Leu Ile Glu Glu Val Ala	195	200	205
Asp Ile Met Cys Val Asn Tyr Ile Tyr Leu Asp His Thr Ile Trp Arg	210	215	220
Phe Gln Ser Gly Arg Pro Tyr Leu Gln Glu Asp Ser Ser Pro Phe Glu	225	230	235
			240

<210> 1655

<211> 517

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(517)

<223> RXA00233

<400> 1655

cgccctccagc agttgagggga gaagttccaa cacttgcacc aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa 115

Met Ser Val Asn Glu

1

5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163
 Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly
 10 15 20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211
 Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val
 25 30 35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259
 Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr
 40 45 50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307
 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val
 55 60 65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355
 Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu
 70 75 80 85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403
 Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg
 90 95 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct 451
 Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro
 105 110 115

gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499
 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu
 120 125 130

ggc cca cac cat ttc ctt 517
 Gly Pro His His Phe Leu
 135

<210> 1656

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 1656

Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly
 1 5 10 15

Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly
 20 25 30

Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
 35 40 45

Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala
 50 55 60

Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu
 65 70 75 80

Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His
 85 90 95

Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser
 100 105 110

Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp
 115 120 125

Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu
 130 135

<210> 1657

<211> 663

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(640)

<223> RXA00234

<400> 1657

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ttcagggtcta aataaaagcg cttttcgacg cccggtaacc tcaaggttgc cgggcgtcgt 60

tgccttacta ctgttactgg tgtgactatg atcgaggatt atg gca aag cag aag 115
                                     Met Ala Lys Gln Lys
                                     1      5

aaa act cat aaa ggc ctt gtt cct gtc tca agc agg gaa cgt gct tca 163
Lys Thr His Lys Gly Leu Val Pro Val Ser Ser Arg Glu Arg Ala Ser
                        10                        15                        20

gag tca gtt tct gct acc cgc gcc cca ttt aga ttg ggt gcc gtc ggc 211
Glu Ser Val Ser Ala Thr Arg Ala Pro Phe Arg Leu Gly Ala Val Gly
                        25                        30                        35

atc ggt gca atc gca ctc gta gtt ctt ctc atc ctg ttt gtc atc gcg 259
Ile Gly Ala Ile Ala Leu Val Val Leu Leu Ile Leu Phe Val Ile Ala
                        40                        45                        50

att cct gtg cgt aac tat ttt cag ctg cgc tcc gac atc gcc caa aca 307
Ile Pro Val Arg Asn Tyr Phe Gln Leu Arg Ser Asp Ile Ala Gln Thr
                        55                        60                        65

gag gct tcc att gaa gcc aaa gaa caa cag atc aaa caa ctg gaa tct 355
Glu Ala Ser Ile Glu Ala Lys Glu Gln Gln Ile Lys Gln Leu Glu Ser
70                        75                        80                        85

gac ctc aac agg tac caa tca gag gcg tac atc cgc gaa caa gca cgc 403
Asp Leu Asn Arg Tyr Gln Ser Glu Ala Tyr Ile Arg Glu Gln Ala Arg
                        90                        95                        100

ctg cgc cta ggc gtc att gaa cct gga gaa acc gcg ttc aga atc gtg 451
Leu Arg Leu Gly Val Ile Glu Pro Gly Glu Thr Ala Phe Arg Ile Val
105                        110                        115

gac cca gca cta gat acc gac acc tca gtc acc tct gac ggc aac gaa 499
Asp Pro Ala Leu Asp Thr Asp Thr Ser Val Thr Ser Asp Gly Asn Glu
120                        125                        130

gag aaa cca ctg gga gct tgg tat gaa aac ctc tgg gac tca gtc acc 547

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Glu Lys Pro Leu Gly Ala Trp Tyr Glu Asn Leu Trp Asp Ser Val Thr
 135 140 145
 aag cca gaa gca ctc ggc gaa gag gaa att gcg cct cca gca gtt gag 595
 Lys Pro Glu Ala Leu Gly Glu Glu Glu Ile Ala Pro Pro Ala Val Glu
 150 155 160 165
 gga gaa gtt cca aca ctt gca cca act gag gaa gca act gtg caa 640
 Gly Glu Val Pro Thr Leu Ala Pro Thr Glu Glu Ala Thr Val Gln
 170 175 180
 tagcgcttta gacacagact cat 663

<210> 1658

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 1658

Met Ala Lys Gln Lys Lys Thr His Lys Gly Leu Val Pro Val Ser Ser
 1 5 10 15
 Arg Glu Arg Ala Ser Glu Ser Val Ser Ala Thr Arg Ala Pro Phe Arg
 20 25 30
 Leu Gly Ala Val Gly Ile Gly Ala Ile Ala Leu Val Val Leu Leu Ile
 35 40 45
 Leu Phe Val Ile Ala Ile Pro Val Arg Asn Tyr Phe Gln Leu Arg Ser
 50 55 60
 Asp Ile Ala Gln Thr Glu Ala Ser Ile Glu Ala Lys Glu Gln Gln Ile
 65 70 75 80
 Lys Gln Leu Glu Ser Asp Leu Asn Arg Tyr Gln Ser Glu Ala Tyr Ile
 85 90 95
 Arg Glu Gln Ala Arg Leu Arg Leu Gly Val Ile Glu Pro Gly Glu Thr
 100 105 110
 Ala Phe Arg Ile Val Asp Pro Ala Leu Asp Thr Asp Thr Ser Val Thr
 115 120 125
 Ser Asp Gly Asn Glu Glu Lys Pro Leu Gly Ala Trp Tyr Glu Asn Leu
 130 135 140
 Trp Asp Ser Val Thr Lys Pro Glu Ala Leu Gly Glu Glu Glu Ile Ala
 145 150 155 160
 Pro Pro Ala Val Glu Gly Glu Val Pro Thr Leu Ala Pro Thr Glu Glu
 165 170 175
 Ala Thr Val Gln
 180

<210> 1659

<211> 501

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXA00237

<400> 1659

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ttacccaagg	acttaaacct	taaaaggagc	cctaaaaatc	atg	aag	ctt	tca	cac	115
				Met	Lys	Leu	Ser	His	
				1				5	

cgc	atc	gca	gca	atg	gca	gca	acc	gca	ggc	atc	aca	gtg	gca	gca	ttc	163
Arg	Ile	Ala	Ala	Met	Ala	Ala	Thr	Ala	Gly	Ile	Thr	Val	Ala	Ala	Phe	
				10					15					20		

gca	gca	cct	gct	tcc	gca	tcc	gac	ttc	gca	aac	cta	tcc	tcc	acc	aac	211
Ala	Ala	Pro	Ala	Ser	Ala	Ser	Asp	Phe	Ala	Asn	Leu	Ser	Ser	Thr	Asn	
			25					30					35			

aaa	gaa	ctg	tcc	cct	cag	tac	aac	tgg	gtt	gct	tgc	ggc	atc	ctt	gag	259
Lys	Glu	Leu	Ser	Pro	Gln	Tyr	Asn	Trp	Val	Ala	Cys	Gly	Ile	Leu	Glu	
		40					45					50				

ggc	ggc	ctc	aaa	gca	gct	ggc	gtc	ctt	gaa	gaa	ggc	cag	tac	aac	cgc	307
Gly	Gly	Leu	Lys	Ala	Ala	Gly	Val	Leu	Glu	Glu	Gly	Gln	Tyr	Asn	Arg	
		55				60					65					

gag	ctc	gca	gaa	gca	atc	gcc	gca	aag	ggc	gaa	ggc	ttc	tgg	acc	act	355
Glu	Leu	Ala	Glu	Ala	Ile	Ala	Ala	Lys	Gly	Glu	Gly	Phe	Trp	Thr	Thr	
	70				75					80					85	

cag	ttc	cca	caa	atc	ggc	gat	tgg	aac	gaa	gat	cag	gca	gca	gca	ctt	403
Gln	Phe	Pro	Gln	Ile	Gly	Asp	Trp	Asn	Glu	Asp	Gln	Ala	Ala	Ala	Leu	
			90					95					100			

gcc	gac	cgc	gca	caa	acc	tgt	ggc	cta	gtt	aag	gct	gac	acc	tac	ctt	451
Ala	Asp	Arg	Ala	Gln	Thr	Cys	Gly	Leu	Val	Lys	Ala	Asp	Thr	Tyr	Leu	
			105					110					115			

tct	gag	ctg	tcc	tcc	aac	ttc	tct	tcc	taaaagggttc	gggggtaacc	498
Ser	Glu	Leu	Ser	Ser	Asn	Phe	Ser	Ser			
		120				125					

cca	501
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<210> 1660

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 1660

Met	Lys	Leu	Ser	His	Arg	Ile	Ala	Ala	Met	Ala	Ala	Thr	Ala	Gly	Ile
1				5					10					15	

Thr	Val	Ala	Ala	Phe	Ala	Ala	Pro	Ala	Ser	Ala	Ser	Asp	Phe	Ala	Asn
		20					25					30			

Leu	Ser	Ser	Thr	Asn	Lys	Glu	Leu	Ser	Pro	Gln	Tyr	Asn	Trp	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Cys Gly Ile Leu Glu Gly Gly Leu Lys Ala Ala Gly Val Leu Glu Glu		
50	55	60
Gly Gln Tyr Asn Arg Glu Leu Ala Glu Ala Ile Ala Ala Lys Gly Glu		
65	70	75
Gly Phe Trp Thr Thr Gln Phe Pro Gln Ile Gly Asp Trp Asn Glu Asp		
85	90	95
Gln Ala Ala Ala Leu Ala Asp Arg Ala Gln Thr Cys Gly Leu Val Lys		
100	105	110
Ala Asp Thr Tyr Leu Ser Glu Leu Ser Ser Asn Phe Ser Ser		
115	120	125

<210> 1661

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> RXA00238

<400> 1661

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tttattttcat ttccatctca gtgatctctt aaggaaaccc atg aag aaa cta cgt	115
Met Lys Lys Leu Arg	
1 5	

ttc gcc acc atc gct gcc gct acc gtt gcc ctg act gcg agc ctt acc	163
Phe Ala Thr Ile Ala Ala Ala Thr Val Ala Leu Thr Ala Ser Leu Thr	
10 15 20	

ccc tca gct tcc gca cag gat ttc aac caa atc atc gac aac ttt gat	211
Pro Ser Ala Ser Ala Gln Asp Phe Asn Gln Ile Ile Asp Asn Phe Asp	
25 30 35	

tgc ggc atc ctt cag acc gct atc tac acc acc ggc ctg gct cac gag	259
Cys Gly Ile Leu Gln Thr Ala Ile Tyr Thr Thr Gly Leu Ala His Glu	
40 45 50	

aac tcc act cgc tca gag ctc gcc gct aat ctg cgc aac tcc gca gct	307
Asn Ser Thr Arg Ser Glu Leu Ala Ala Asn Leu Arg Asn Ser Ala Ala	
55 60 65	

gtc ggc caa cta gac ttc cca ttg aat atc gcg gct acc ggc tac tcc	355
Val Gly Gln Leu Asp Phe Pro Leu Asn Ile Ala Ala Thr Gly Tyr Ser	
70 75 80 85	

gag cgc atc gct aac cgc gca ctg acc tgc gga atc gtg aag gaa gat	403
Glu Arg Ile Ala Asn Arg Ala Leu Thr Cys Gly Ile Val Lys Glu Asp	
90 95 100	

cca cag gac ttc ctc tcc cag ctg cag ctt ctg tcc tct aac cta tct	451
Pro Gln Asp Phe Leu Ser Gln Leu Gln Leu Leu Ser Ser Asn Leu Ser	

105 110 115
tct tcc ttc ttc act gct tagtttctct tgggcttttc ctt 492
Ser Ser Phe Phe Thr Ala
120

<210> 1662
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 1662
Met Lys Lys Leu Arg Phe Ala Thr Ile Ala Ala Ala Thr Val Ala Leu
1 5 10 15
Thr Ala Ser Leu Thr Pro Ser Ala Ser Ala Gln Asp Phe Asn Gln Ile
20 25 30
Ile Asp Asn Phe Asp Cys Gly Ile Leu Gln Thr Ala Ile Tyr Thr Thr
35 40 45
Gly Leu Ala His Glu Asn Ser Thr Arg Ser Glu Leu Ala Ala Asn Leu
50 55 60
Arg Asn Ser Ala Ala Val Gly Gln Leu Asp Phe Pro Leu Asn Ile Ala
65 70 75 80
Ala Thr Gly Tyr Ser Glu Arg Ile Ala Asn Arg Ala Leu Thr Cys Gly
85 90 95
Ile Val Lys Glu Asp Pro Gln Asp Phe Leu Ser Gln Leu Gln Leu Leu
100 105 110
Ser Ser Asn Leu Ser Ser Ser Phe Phe Thr Ala
115 120

<210> 1663
<211> 708
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXA00239

<400> 1663
acaaagcgga tcagattaac aaggtccgtg acgctgtcga tgagcgcatt ggcaaaaaca 60
acggcggcga agagaatcca gccaaactagt attaggcgctc atg cgc gtc gta gtt 115
Met Arg Val Val Val
1 5
gtt gat cct aaa cac ccc gtc ctt cca gtc tct ttc ctc gag gct gtt 163
Val Asp Pro Lys His Pro Val Leu Pro Val Ser Phe Leu Glu Ala Val
10 15 20
ctt ggg cgg ggt gaa cct gtt tct atc gat ccc gat ttt cca ttt gat 211
Leu Gly Arg Gly Glu Pro Val Ser Ile Asp Pro Asp Phe Pro Phe Asp

25	30	35	
att gaa aaa tgg ggg atc aag acg tgc aca agc gcc tcc tgg ttt atc			259
Ile Glu Lys Trp Gly Ile Lys Thr Ser Thr Ser Ala Ser Trp Phe Ile			
40	45	50	
atc gca aaa ccg caa agc acg ctg ctt atc gac gcg ccc ctc aac cct			307
Ile Ala Lys Pro Gln Ser Thr Leu Leu Ile Asp Ala Pro Leu Asn Pro			
55	60	65	
ttg cat gag gcc gtc ggc gtc atg cgg gcg gcc gtg ggc cgc ggc gag			355
Leu His Glu Ala Val Gly Val Met Arg Ala Ala Val Gly Arg Gly Glu			
70	75	80	85
tgg gaa cgc acg caa acc cat gag agt ttg att ccg tat ctg gaa gaa			403
Trp Glu Arg Thr Gln Thr His Glu Ser Leu Ile Pro Tyr Leu Glu Glu			
90	95	100	
gaa tgc cag gag ttt att gaa gcg att cat ggt ggc gat gat gag cac			451
Glu Ser Gln Glu Phe Ile Glu Ala Ile His Gly Gly Asp Asp Glu His			
105	110	115	
atg aaa agc gaa ctg ggg gat gtt ttg ctg cag gtg ctt ttt cat gca			499
Met Lys Ser Glu Leu Gly Asp Val Leu Leu Gln Val Leu Phe His Ala			
120	125	130	
gaa atc gcc gcc cgt cag ggt cga ttc gac att ttt gac gtg gcg gcg			547
Glu Ile Ala Ala Arg Gln Gly Arg Phe Asp Ile Phe Asp Val Ala Ala			
135	140	145	
agt ttc gta gcc aag atg caa tct cgt tgc ccg tac ctg ttc gac ggc			595
Ser Phe Val Ala Lys Met Gln Ser Arg Ser Pro Tyr Leu Phe Asp Gly			
150	155	160	165
tct acc gga att gtg gac acc gac gag cag cag cgg ctg tgg gct caa			643
Ser Thr Gly Ile Val Asp Thr Asp Glu Gln Gln Arg Leu Trp Ala Gln			
170	175	180	
gga aaa gcc caa gag aaa cta agc agt gaa gaa gga aga aga			685
Gly Lys Ala Gln Glu Lys Leu Ser Ser Glu Glu Gly Arg Arg			
185	190	195	
taggttagag gacagaagct gca			708

<210> 1664

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 1664

Met Arg Val Val Val Val Asp Pro Lys His Pro Val Leu Pro Val Ser
1 5 10 15

Phe Leu Glu Ala Val Leu Gly Arg Gly Glu Pro Val Ser Ile Asp Pro
20 25 30

Asp Phe Pro Phe Asp Ile Glu Lys Trp Gly Ile Lys Thr Ser Thr Ser
35 40 45

Ala Ser Trp Phe Ile Ile Ala Lys Pro Gln Ser Thr Leu Leu Ile Asp

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<210> 1665
<211> 333
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(310)  
<223> RXA00240
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<400> 1665																		
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taatcaagtg cagatgaatt gtttagaaag gctggagacc atg ggt att ttt gac																		115
Met Gly Ile Phe Asp																		
1 5																		
gaa gct aag aag aag gca acc gaa ttc ctc gac tct gat tca ggc gag																		163
Glu	Ala	Lys	Lys	Lys	Ala	Thr	Glu	Phe	Leu	Asp	Ser	Asp	Ser	Gly	Glu			
10										15					20			
cag aag tcc gat gga ctg ctg gat aag gcc gca gac aaa gct aag ggt																		211
Gln	Lys	Ser	Asp	Gly	Leu	Leu	Asp	Lys	Ala	Ala	Asp	Lys	Ala	Lys	Gly			
25				30					35									
ctc ctc ggt gaa gac aaa gcg gat cag att aac aag gtc cgt gac gct																		259
Leu	Leu	Gly	Glu	Asp	Lys	Ala	Asp	Gln	Ile	Asn	Lys	Val	Arg	Asp	Ala			
40			45					50										
gtc gat gag cgc att ggc aaa aac aac ggc ggc gaa gag aat cca gcc																		307
Val	Asp	Glu	Arg	Ile	Gly	Lys	Asn	Asn	Gly	Gly	Glu	Glu	Asn	Pro	Ala			

55 60 65 333

aac tagtattagg cgatcatgcgc gtc
 Asn
 70

<210> 1666
 <211> 70
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1666
 Met Gly Ile Phe Asp Glu Ala Lys Lys Lys Ala Thr Glu Phe Leu Asp
 1 5 10 15
 Ser Asp Ser Gly Glu Gln Lys Ser Asp Gly Leu Leu Asp Lys Ala Ala
 20 25 30
 Asp Lys Ala Lys Gly Leu Leu Gly Glu Asp Lys Ala Asp Gln Ile Asn
 35 40 45
 Lys Val Arg Asp Ala Val Asp Glu Arg Ile Gly Lys Asn Asn Gly Gly
 50 55 60
 Glu Glu Asn Pro Ala Asn
 65 70

<210> 1667
 <211> 759
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(736)
 <223> RXA00244

<400> 1667
 agtgggaaag tgatgatgcc acacaccgcc ggcggattac aggatggcag ttcacaggg 60
 gtttaaacag tgaagatttg gcagaaagcg agatggataa atg aat gat cag ctg 115
 Met Asn Asp Gln Leu
 1 5
 tgg gaa ggc gac act gga acg ctg act ttt ggg tcc agg aaa gct ctg 163
 Trp Glu Gly Asp Thr Gly Thr Leu Thr Phe Gly Ser Arg Lys Ala Leu
 10 15 20
 gtg caa tta ctc aaa ggt ccc atg gtg aat gct ttg cag cat gtt gaa 211
 Val Gln Leu Leu Lys Gly Pro Met Val Asn Ala Leu Gln His Val Glu
 25 30 35
 gtg tgg cgg gct atc acc aca gat caa gat gcg ctc aat gct gtg ctt 259
 Val Trp Arg Ala Ile Thr Thr Asp Gln Asp Ala Leu Asn Ala Val Leu
 40 45 50
 aac aat ttg ttc ctc gag ttg gtt ctt gat gag gat gcg ggt gtt gca 307
 Asn Asn Leu Phe Leu Glu Leu Val Leu Asp Glu Asp Ala Gly Val Ala
 55 60 65

ttt act cgg cct gcc aat ggt aga caa gaa gta ttg gtt gga aat aac 355
 Phe Thr Arg Pro Ala Asn Gly Arg Gln Glu Val Leu Val Gly Asn Asn
 70 75 80 85
 aaa act gaa gcg atg ccc aaa gtg ctg cgc acg gag acg ctg tcg cat 403
 Lys Thr Glu Ala Met Pro Lys Val Leu Arg Thr Glu Thr Leu Ser His
 90 95 100
 ttt gat acg ttg atc att ttg att ctg cgc caa gaa ctc acc atg gcg 451
 Phe Asp Thr Leu Ile Ile Leu Ile Leu Arg Gln Glu Leu Thr Met Ala
 105 110 115
 cca ccg ggg gaa cga gtc att gtg gat cgt gaa gaa atc cgc gaa caa 499
 Pro Pro Gly Glu Arg Val Ile Val Asp Arg Glu Glu Ile Arg Glu Gln
 120 125 130
 gtg ttg ctc tac cgc gtt gat gaa gag cga gat gaa gcc aaa cta gct 547
 Val Leu Leu Tyr Arg Val Asp Glu Glu Arg Asp Glu Ala Lys Leu Ala
 135 140 145
 aag cga ttc gac gct gca ttt agg cgc atc gtg gat tat tca tta gct 595
 Lys Arg Phe Asp Ala Ala Phe Arg Arg Ile Val Asp Tyr Ser Leu Ala
 150 155 160 165
 aaa aag aca gag aca cct gaa cgt ttt gag gtc tca cca gca ctg cgc 643
 Lys Lys Thr Glu Thr Pro Glu Arg Phe Glu Val Ser Pro Ala Leu Arg
 170 175 180
 cag att ttt gat gcc gac act gtg gca ggt gtg cgc gct gag tac gaa 691
 Gln Ile Phe Asp Ala Asp Thr Val Ala Gly Val Arg Ala Glu Tyr Glu
 185 190 195
 aaa ttt aac aaa gca gcc cat gat gga aat gaa gag gaa cag aag 736
 Lys Phe Asn Lys Ala Ala His Asp Gly Asn Glu Glu Glu Gln Lys
 200 205 210
 tgaccagcga acaagcttta gat 759

<210> 1668

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 1668

Met Asn Asp Gln Leu Trp Glu Gly Asp Thr Gly Thr Leu Thr Phe Gly
 1 5 10 15
 Ser Arg Lys Ala Leu Val Gln Leu Leu Lys Gly Pro Met Val Asn Ala
 20 25 30
 Leu Gln His Val Glu Val Trp Arg Ala Ile Thr Thr Asp Gln Asp Ala
 35 40 45
 Leu Asn Ala Val Leu Asn Asn Leu Phe Leu Glu Leu Val Leu Asp Glu
 50 55 60
 Asp Ala Gly Val Ala Phe Thr Arg Pro Ala Asn Gly Arg Gln Glu Val
 65 70 75 80

ccg aaa agc ccg tcg gat tat gtg agt gat tgg gtg aag tcc ccg tgg	355
Pro Lys Ser Pro Ser Asp Tyr Val Ser Asp Trp Val Lys Ser Arg Trp	
70 75 80 85	
ttt gtg cgt cgt ccg ggt agt tcg cag act ggt gag acc gtg gaa ccg	403
Phe Val Arg Arg Pro Gly Ser Ser Gln Thr Gly Glu Thr Val Glu Pro	
90 95 100	
agt gaa gag ctg ttg gcg gtg ctg gat tcg gtg cag cgg tgg gat aac	451
Ser Glu Glu Leu Leu Ala Val Leu Asp Ser Val Gln Arg Trp Asp Asn	
105 110 115	
ccg cat cga agc att tcg gcg tct cga att gaa tcg ttg acg cag gcg	499
Pro His Arg Ser Ile Ser Ala Ser Arg Ile Glu Ser Leu Thr Gln Ala	
120 125 130	
ttg cag act ttg gcg ttg gaa tcg gac ccc agc aca gcg aaa cgt tta	547
Leu Gln Thr Leu Ala Leu Glu Ser Asp Pro Ser Thr Ala Lys Arg Leu	
135 140 145	
gct gag tta gag cgt gaa cgc gac agg att gaa cgc cag att gaa gcg	595
Ala Glu Leu Glu Arg Glu Arg Asp Arg Ile Glu Arg Gln Ile Glu Ala	
150 155 160 165	
gtc cac gct ggt gaa ttt gaa gtc ctc acc acc gtg cag att ggt gat	643
Val His Ala Gly Glu Phe Glu Val Leu Thr Thr Val Gln Ile Gly Asp	
170 175 180	
cgg gta gca gat att ttg gat cta gca gca tct att cct gca gat ttc	691
Arg Val Ala Asp Ile Leu Asp Leu Ala Ala Ser Ile Pro Ala Asp Phe	
185 190 195	
gcc agg gta agg cat gag ctg agc gat ctg aac cgg aag ctg cgc agg	739
Ala Arg Val Arg His Glu Leu Ser Asp Leu Asn Arg Lys Leu Arg Arg	
200 205 210	
cag ttg ctt gat cct gaa gat tcc cgt ggt gat gtt ttg gaa gag atc	787
Gln Leu Leu Asp Pro Glu Asp Ser Arg Gly Asp Val Leu Glu Glu Ile	
215 220 225	
ttc agg gga gtt gat ctg att ggg gat tcc gat gcg ggg cgc agc ttc	835
Phe Arg Gly Val Asp Leu Ile Gly Asp Ser Asp Ala Gly Arg Ser Phe	
230 235 240 245	
aat agt ttc ttt gat gtt ttg ctc gat cgg gaa cgc tca agt ctg att	883
Asn Ser Phe Phe Asp Val Leu Leu Asp Arg Glu Arg Ser Ser Leu Ile	
250 255 260	
gat cga tgg atc aga gaa gtt ctg gga cgc gat gag gct att gat ctg	931
Asp Arg Trp Ile Arg Glu Val Leu Gly Arg Asp Glu Ala Ile Asp Leu	
265 270 275	
gat tca aaa tta agg aca ggg ctg tac cga att ttc cgg gat atg gag	979
Asp Ser Lys Leu Arg Thr Gly Leu Tyr Arg Ile Phe Arg Asp Met Glu	
280 285 290	
gat gcc agc ttc gag gtc aac ggg gaa atg aca ggg ctg gct cga agt	1027
Asp Ala Ser Phe Glu Val Asn Gly Glu Met Thr Gly Leu Ala Arg Ser	
295 300 305	
ttg cgt cac tat gtc act acc gag gag ttc gca gag agc cga cgc atg	1075

Leu Arg His Tyr Val Thr Thr Glu Glu Phe Ala Glu Ser Arg Arg Met
 310 315 320 325
 att cag ttg ctt cgc gat acc cgc agt gcc gct gct aag gcc gcc gag 1123
 Ile Gln Leu Leu Arg Asp Thr Arg Ser Ala Ala Ala Lys Ala Ala Glu
 330 335 340
 gct ggt gaa gtg acc tca ctc aat cac atg gac aca cca ctc gtg cgc 1171
 Ala Gly Glu Val Thr Ser Leu Asn His Met Asp Thr Pro Leu Val Arg
 345 350 355
 att ggt atg gat gtt cgc tcg att gcg ggg ttg aaa ctg aag aac cca 1219
 Ile Gly Met Asp Val Arg Ser Ile Ala Gly Leu Lys Leu Lys Asn Pro
 360 365 370
 ggt gaa gaa cgc gtc gaa gat ttg cct gag cca gtt gaa gaa caa gaa 1267
 Gly Glu Glu Arg Val Glu Asp Leu Pro Glu Pro Val Glu Glu Gln Glu
 375 380 385
 cta gac act gaa gtc ttg atg gaa caa att cgg gca agc gag att gat 1315
 Leu Asp Thr Glu Val Leu Met Glu Gln Ile Arg Ala Ser Glu Ile Asp
 390 395 400 405
 ttt gag gaa ttg gaa gag gct gtt tct tta gtt ctt gcc gag caa tcg 1363
 Phe Glu Glu Leu Glu Glu Ala Val Ser Leu Val Leu Ala Glu Gln Ser
 410 415 420
 cac gcc acg atc acc gag gta cta gaa cat ttc ccg gca acg caa ggt 1411
 His Ala Thr Ile Thr Glu Val Leu Glu His Phe Pro Ala Thr Gln Gly
 425 430 435
 ctc gcc agc att gtt gga ttg tta tac ctg gcg atg cgt gat ggt gtt 1459
 Leu Ala Ser Ile Val Gly Leu Leu Tyr Leu Ala Met Arg Asp Gly Val
 440 445 450
 ccc aca ggt cgc gcg caa ata gtg gag tgg gaa agt gat gat gcc aca 1507
 Pro Thr Gly Arg Ala Gln Ile Val Glu Trp Glu Ser Asp Asp Ala Thr
 455 460 465
 cac cgc cgg cgg att aca gga tgg cag ttc atc agg ggt tta aac agt 1555
 His Arg Arg Arg Ile Thr Gly Trp Gln Phe Ile Arg Gly Leu Asn Ser
 470 475 480 485
 gaa gat ttg gca gaa agc gag atg gat aaa tgaatgatca gctgtgggaa 1605
 Glu Asp Leu Ala Glu Ser Glu Met Asp Lys
 490 495
 ggc 1608
 <210> 1670
 <211> 495
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1670
 Met Thr Val Val Ser His Ala Leu Gly Phe Lys Arg Phe Arg Gln Glu
 1 5 10 15
 Ser Leu Glu Leu Ser Leu Leu Arg Ser Asp Asn Phe Pro Val Val Leu
 20 25 30

Ala Val Val Ala Gln Tyr Phe Pro Gln Gly Ala Ile Ala Lys Pro Ala
 35 40 45
 Ser Glu Leu Tyr Gln Leu Leu Ser Asp Asp Phe Arg Val Leu Arg Glu
 50 55 60
 Glu Gly Phe Glu Leu Pro Lys Ser Pro Ser Asp Tyr Val Ser Asp Trp
 65 70 75 80
 Val Lys Ser Arg Trp Phe Val Arg Arg Pro Gly Ser Ser Gln Thr Gly
 85 90 95
 Glu Thr Val Glu Pro Ser Glu Glu Leu Leu Ala Val Leu Asp Ser Val
 100 105 110
 Gln Arg Trp Asp Asn Pro His Arg Ser Ile Ser Ala Ser Arg Ile Glu
 115 120 125
 Ser Leu Thr Gln Ala Leu Gln Thr Leu Ala Leu Glu Ser Asp Pro Ser
 130 135 140
 Thr Ala Lys Arg Leu Ala Glu Leu Glu Arg Glu Arg Asp Arg Ile Glu
 145 150 155 160
 Arg Gln Ile Glu Ala Val His Ala Gly Glu Phe Glu Val Leu Thr Thr
 165 170 175
 Val Gln Ile Gly Asp Arg Val Ala Asp Ile Leu Asp Leu Ala Ala Ser
 180 185 190
 Ile Pro Ala Asp Phe Ala Arg Val Arg His Glu Leu Ser Asp Leu Asn
 195 200 205
 Arg Lys Leu Arg Arg Gln Leu Leu Asp Pro Glu Asp Ser Arg Gly Asp
 210 215 220
 Val Leu Glu Glu Ile Phe Arg Gly Val Asp Leu Ile Gly Asp Ser Asp
 225 230 235 240
 Ala Gly Arg Ser Phe Asn Ser Phe Phe Asp Val Leu Leu Asp Arg Glu
 245 250 255
 Arg Ser Ser Leu Ile Asp Arg Trp Ile Arg Glu Val Leu Gly Arg Asp
 260 265 270
 Glu Ala Ile Asp Leu Asp Ser Lys Leu Arg Thr Gly Leu Tyr Arg Ile
 275 280 285
 Phe Arg Asp Met Glu Asp Ala Ser Phe Glu Val Asn Gly Glu Met Thr
 290 295 300
 Gly Leu Ala Arg Ser Leu Arg His Tyr Val Thr Thr Glu Glu Phe Ala
 305 310 315 320
 Glu Ser Arg Arg Met Ile Gln Leu Leu Arg Asp Thr Arg Ser Ala Ala
 325 330 335
 Ala Lys Ala Ala Glu Ala Gly Glu Val Thr Ser Leu Asn His Met Asp
 340 345 350

Thr Pro Leu Val Arg Ile Gly Met Asp Val Arg Ser Ile Ala Gly Leu
 355 360 365
 Lys Leu Lys Asn Pro Gly Glu Glu Arg Val Glu Asp Leu Pro Glu Pro
 370 375 380
 Val Glu Glu Gln Glu Leu Asp Thr Glu Val Leu Met Glu Gln Ile Arg
 385 390 395 400
 Ala Ser Glu Ile Asp Phe Glu Glu Leu Glu Glu Ala Val Ser Leu Val
 405 410 415
 Leu Ala Glu Gln Ser His Ala Thr Ile Thr Glu Val Leu Glu His Phe
 420 425 430
 Pro Ala Thr Gln Gly Leu Ala Ser Ile Val Gly Leu Leu Tyr Leu Ala
 435 440 445
 Met Arg Asp Gly Val Pro Thr Gly Arg Ala Gln Ile Val Glu Trp Glu
 450 455 460
 Ser Asp Asp Ala Thr His Arg Arg Arg Ile Thr Gly Trp Gln Phe Ile
 465 470 475 480
 Arg Gly Leu Asn Ser Glu Asp Leu Ala Glu Ser Glu Met Asp Lys
 485 490 495

<210> 1671

<211> 846

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(823)

<223> RXA00248

<400> 1671

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 tagaccagtg tcttaggcaa gaccccattht aggacacctc atg att ccc ctg att 115
 Met Ile Pro Leu Ile
 1 5
 acg ctt tcc cac ggt tcc cgc aaa aag tcc gca gct gca ggc att act 163
 Thr Leu Ser His Gly Ser Arg Lys Lys Ser Ala Ala Ala Gly Ile Thr
 10 15 20
 gcg ctg act cat gag gcc gga cga atg ctg gaa aca cca gcc gtg gaa 211
 Ala Leu Thr His Glu Ala Gly Arg Met Leu Glu Thr Pro Ala Val Glu
 25 30 35
 gcg cat tta gag ctt gct gaa cct tcc ctt gat cag gtt gtg gca acg 259
 Ala His Leu Glu Leu Ala Glu Pro Ser Leu Asp Gln Val Val Ala Thr
 40 45 50
 ctc agt gcg gaa ggt gta acc agg gca gcg ttg gtt cct ttg ctg ttt 307
 Leu Ser Ala Glu Gly Val Thr Arg Ala Ala Leu Val Pro Leu Leu Phe
 55 60 65

agc aat gcg tat cac gca aag att gac gtt cct gag gca gta aaa gat 355
 Ser Asn Ala Tyr His Ala Lys Ile Asp Val Pro Glu Ala Val Lys Asp
 70 75 80 85

gct tca gaa aag tat ggt gtg gaa ctt ctc gtg ggt ccg cat ttg ggc 403
 Ala Ser Glu Lys Tyr Gly Val Glu Leu Leu Val Gly Pro His Leu Gly
 90 95 100

act ggc tcc gat gta gcc agc gtg ctt gcg cag cgg ttg agt gcg gac 451
 Thr Gly Ser Asp Val Ala Ser Val Leu Ala Gln Arg Leu Ser Ala Asp
 105 110 115

gcc ccc aca gat gcc cat gtg att ttg tat tcc gtt ggc agc tca cac 499
 Ala Pro Thr Asp Ala His Val Ile Leu Tyr Ser Val Gly Ser Ser His
 120 125 130

gtg tcc gcc aat gaa tca gtc atc gat ctt gcc cac acc att gct ctc 547
 Val Ser Ala Asn Glu Ser Val Ile Asp Leu Ala His Thr Ile Ala Leu
 135 140 145

ctc act ggc ttt tcg gtt gag gtg gtg ccc gct acc ggt ggg cca ggt 595
 Leu Thr Gly Phe Ser Val Glu Val Val Pro Ala Thr Gly Gly Pro Gly
 150 155 160 165

gcc ggc ggc gcc gga gta ata gag gtg gcc tcg aaa cac aag gcc gtc 643
 Ala Gly Gly Ala Gly Val Ile Glu Val Ala Ser Lys His Lys Ala Val
 170 175 180

cac atc ctg ccg ctg ttt gtt acg gaa ggt ttg ctg ctg gat cgg gct 691
 His Ile Leu Pro Leu Phe Val Thr Glu Gly Leu Leu Leu Asp Arg Ala
 185 190 195

att gat caa tcc gcc aac atc gca gct gcc acc ggc aca aac ttc acc 739
 Ile Asp Gln Ser Ala Asn Ile Ala Ala Thr Gly Thr Asn Phe Thr
 200 205 210

tat tcc gaa ccc cta act act gac ctc gca cca ctt gtt gca gcc cgt 787
 Tyr Ser Glu Pro Leu Thr Thr Asp Leu Ala Pro Leu Val Ala Ala Arg
 215 220 225

tac cac gct gca ttg agc gca ctg ctg gca cat atc taagaccgct 833
 Tyr His Ala Ala Leu Ser Ala Leu Leu Ala His Ile
 230 235 240

aaggaaatca gct 846

<210> 1672

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 1672

Met Ile Pro Leu Ile Thr Leu Ser His Gly Ser Arg Lys Lys Ser Ala
 1 5 10 15

Ala Ala Gly Ile Thr Ala Leu Thr His Glu Ala Gly Arg Met Leu Glu
 20 25 30

Thr Pro Ala Val Glu Ala His Leu Glu Leu Ala Glu Pro Ser Leu Asp
 35 40 45

Gln Val Val Ala Thr Leu Ser Ala Glu Gly Val Thr Arg Ala Ala Leu
 50 55 60
 Val Pro Leu Leu Phe Ser Asn Ala Tyr His Ala Lys Ile Asp Val Pro
 65 70 75 80
 Glu Ala Val Lys Asp Ala Ser Glu Lys Tyr Gly Val Glu Leu Leu Val
 85 90 95
 Gly Pro His Leu Gly Thr Gly Ser Asp Val Ala Ser Val Leu Ala Gln
 100 105 110
 Arg Leu Ser Ala Asp Ala Pro Thr Asp Ala His Val Ile Leu Tyr Ser
 115 120 125
 Val Gly Ser Ser His Val Ser Ala Asn Glu Ser Val Ile Asp Leu Ala
 130 135 140
 His Thr Ile Ala Leu Leu Thr Gly Phe Ser Val Glu Val Val Pro Ala
 145 150 155 160
 Thr Gly Gly Pro Gly Ala Gly Gly Ala Gly Val Ile Glu Val Ala Ser
 165 170 175
 Lys His Lys Ala Val His Ile Leu Pro Leu Phe Val Thr Glu Gly Leu
 180 185 190
 Leu Leu Asp Arg Ala Ile Asp Gln Ser Ala Asn Ile Ala Ala Ala Thr
 195 200 205
 Gly Thr Asn Phe Thr Tyr Ser Glu Pro Leu Thr Thr Asp Leu Ala Pro
 210 215 220
 Leu Val Ala Ala Arg Tyr His Ala Ala Leu Ser Ala Leu Leu Ala His
 225 230 235 240
 Ile

<210> 1673

<211> 239

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(216)

<223> RXA00250

<400> 1673

gct ttg ggt gct gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att 48
 Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile
 1 5 10 15

gat ctg att ttc ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg 96
 Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu
 20 25 30

gtc ggc atg gcc cgc aag ctg gct gac ggc cac aag caa gcc aac acc 144

Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr
35 40 45

gag cca caa gaa aac ccc gca gtc cag aca gcc cca gta aaa acc cag 192
Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln
50 55 60

gaa gcc cag gaa gcc ccc cag aac taatctttcc ggtcgcgcag ttc 239
Glu Ala Gln Glu Ala Pro Gln Asn
65 70

<210> 1674

<211> 72

<212> PRT

<213> Corynebacterium glutamicum

<400> 1674

Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile
1 5 10 15

Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu
20 25 30

Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr
35 40 45

Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln
50 55 60

Glu Ala Gln Glu Ala Pro Gln Asn
65 70

<210> 1675

<211> 366

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

 $\langle 222 \rangle \quad (101) \dots (343)$

<223> RXA00252

<400> 1675

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cttcttcttt gcggaaggcg tcggcgagtc cgcggagggc gtg ttt gct ggc ggc 115
Val Phe Ala Gly Gly
1 5

gta gat ggt gtt gcc ggg gtg tgg tcc gtt gcc ggc gcc gga gtt gat 163
Val Asp Gly Val Ala Gly Val Trp Ser Val Ala Gly Ala Gly Val Asp
10 15 20

gta gat gac gca gcc gga tgc cgc gcg gag ggc ggg caa gag ttg gcg 211
Val Asp Asp Ala Ala Gly Cys Arg Ala Glu Gly Gly Gln Glu Leu Ala
25 30 35

act caa ctc ggc cgg gac aat gac gtt gag atc aag gtg tgc gtg cca 259
Thr Gln Leu Gly Arg Asp Asn Asp Val Glu Ile Lys Val Cys Val Pro

25	30	35	
acc act gtt gaa caa gta cgt ctc agc gat ctt tac ggt gag cag tgg			259
Thr Thr Val Glu Gln Val Arg Leu Ser Asp Leu Tyr Gly Glu Gln Trp			
40	45	50	
acc gag ttc gct ctt gtc tgc ccc tac acc aca aaa gac gag gta aaa			307
Thr Glu Phe Ala Leu Val Cys Pro Tyr Thr Thr Lys Asp Glu Val Lys			
55	60	65	
gaa gag ctt ggt ata aaa ata aac acc tac ctc acc gat tcg acc gat			355
Glu Glu Leu Gly Ile Lys Ile Asn Thr Tyr Leu Thr Asp Ser Thr Asp			
70	75	80	85
gac agt agt aac gat att gtg ctc agg gat aaa gac ggt tca tat gat			403
Asp Ser Ser Asn Asp Ile Val Leu Arg Asp Lys Asp Gly Ser Tyr Asp			
90	95	100	
tgg atc tat ttc aac aga ttc gac att gtg tac ctc tgc aac ggc tca			451
Trp Ile Tyr Phe Asn Arg Phe Asp Ile Val Tyr Leu Cys Asn Gly Ser			
105	110	115	
gcg gaa aat cta aaa atc tac ccc att gat tca gtt cta gaa ttt gag			499
Ala Glu Asn Leu Lys Ile Tyr Pro Ile Asp Ser Val Leu Glu Phe Glu			
120	125	130	
cat aga gac gac tac ggt acc tgg aaa ctg agc gct atc aca gag ccg			547
His Arg Asp Asp Tyr Gly Thr Trp Lys Leu Ser Ala Ile Thr Glu Pro			
135	140	145	
ggt aat caa taataacgcg gacacttaag tac			579
Gly Asn Gln			
150			

<210> 1678

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1678

Met	Lys	Ile	Lys	Lys	Phe	Ser	Ile	Thr	Ala	Leu	Ala	Ser	Val	Leu	Met
1				5					10					15	

Leu	Thr	Gly	Cys	Ala	Thr	Asn	His	Ser	Ser	Pro	Leu	Tyr	Ser	Tyr	Leu
			20					25					30		

Asn	Ala	Ser	Thr	Ser	Thr	Thr	Val	Glu	Gln	Val	Arg	Leu	Ser	Asp	Leu
	35						40					45			

Tyr	Gly	Glu	Gln	Trp	Thr	Glu	Phe	Ala	Leu	Val	Cys	Pro	Tyr	Thr	Thr
	50					55					60				

Lys	Asp	Glu	Val	Lys	Glu	Glu	Leu	Gly	Ile	Lys	Ile	Asn	Thr	Tyr	Leu
65					70					75					80

Thr	Asp	Ser	Thr	Asp	Asp	Ser	Ser	Asn	Asp	Ile	Val	Leu	Arg	Asp	Lys
				85					90					95	

Asp	Gly	Ser	Tyr	Asp	Trp	Ile	Tyr	Phe	Asn	Arg	Phe	Asp	Ile	Val	Tyr
			100					105					110		

Leu Cys Asn Gly Ser Ala Glu Asn Leu Lys Ile Tyr Pro Ile Asp Ser
 115 120 125

Val Leu Glu Phe Glu His Arg Asp Asp Tyr Gly Thr Trp Lys Leu Ser
 130 135 140

Ala Ile Thr Glu Pro Gly Asn Gln
 145 150

<210> 1679

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(772)

<223> RXA00258

<400> 1679

taattaatat aattaatgta gtttattaac ctattatgca atgacatttt ttaataatta 60

accacgtcac aacattctct cagatcacag aggttcgctc atg cgc cac acc acg 115
 Met Arg His Thr Thr
 1 5

tca gcc aca tca act aca tct att att aag cgt gct atg acc att agt 163
 Ser Ala Thr Ser Thr Thr Ser Ile Ile Lys Arg Ala Met Thr Ile Ser
 10 15 20

gcc gct gtt ctt att gcc agc gct gtt ggt ctc aca acc agc gca agt 211
 Ala Ala Val Leu Ile Ala Ser Ala Val Gly Leu Thr Thr Ser Ala Ser
 25 30 35

tcg ctc aat act ctc agc gct aca tca cct gaa tca ccc gat cag gca 259
 Ser Leu Asn Thr Leu Ser Ala Thr Ser Pro Glu Ser Pro Asp Gln Ala
 40 45 50

gcc act gtg tca cag gct gaa tca gat agt gaa tta gat gac ggc atg 307
 Ala Thr Val Ser Gln Ala Glu Ser Asp Ser Glu Leu Asp Asp Gly Met
 55 60 65

aaa aag ctt gca acc aag atc ctt aat cgc gct gac aac gct gaa aat 355
 Lys Lys Leu Ala Thr Lys Ile Leu Asn Arg Ala Asp Asn Ala Glu Asn
 70 75 80 85

aat gat gac acc ggc aaa aac ctc aac aat gat gat aag aag ctc aac 403
 Asn Asp Asp Thr Gly Lys Asn Leu Asn Asn Asp Asp Lys Lys Leu Asn
 90 95 100

acg aag cag ccg cag cgc cct gct gaa aaa gtt gcc cag gcg atc gag 451
 Thr Lys Gln Pro Gln Arg Pro Ala Glu Lys Val Ala Gln Ala Ile Glu
 105 110 115

cta agc ctt gat acc acc acg aat gca gaa aag cct gat aaa agt ttt 499
 Leu Ser Leu Asp Thr Thr Thr Asn Ala Glu Lys Pro Asp Lys Ser Phe
 120 125 130

cac cat gaa aaa ccc gta aac gcc tat gtc aca agt gtc agc tac aac 547

His His Glu Lys Pro Val Asn Ala Tyr Val Thr Ser Val Ser Tyr Asn
 135 140 145
 aaa agc aat gac acc tgg act atc aaa cca tca gac agc gcg gtg aat 595
 Lys Ser Asn Asp Thr Trp Thr Ile Lys Pro Ser Asp Ser Ala Val Asn
 150 155 160 165
 aca ccg acc aat gat gct gag cgc atc agc aat atc atc caa gaa gct 643
 Thr Pro Thr Asn Asp Ala Glu Arg Ile Ser Asn Ile Ile Gln Glu Ala
 170 175 180
 cgc gac ctc ggt ctc agc gac gat gaa tcc ttg acg caa cag atc gca 691
 Arg Asp Leu Gly Leu Ser Asp Asp Glu Ser Leu Thr Gln Gln Ile Ala
 185 190 195
 ttt cac gct cat gct gct aat tat tta gtc acc gaa tgg gta ctt cgc 739
 Phe His Ala His Ala Ala Asn Tyr Leu Val Thr Glu Trp Val Leu Arg
 200 205 210
 ggc tat cag ctt gct aac ccg aag gtg ctt cca tgagaaaaca acgacgcatg 792
 Gly Tyr Gln Leu Ala Asn Pro Lys Val Leu Pro
 215 220
 atg 795

<210> 1680

<211> 224.

<212> PRT

<213> Corynebacterium glutamicum

<400> 1680

Met Arg His Thr Thr Ser Ala Thr Ser Thr Thr Ser Ile Ile Lys Arg
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 Ala Met Thr Ile Ser Ala Ala Val Leu Ile Ala Ser Ala Val Gly Leu
 20 25 30
 Thr Thr Ser Ala Ser Ser Leu Asn Thr Leu Ser Ala Thr Ser Pro Glu
 35 40 45
 Ser Pro Asp Gln Ala Ala Thr Val Ser Gln Ala Glu Ser Asp Ser Glu
 50 55 60
 Leu Asp Asp Gly Met Lys Lys Leu Ala Thr Lys Ile Leu Asn Arg Ala
 65 70 75 80
 Asp Asn Ala Glu Asn Asn Asp Asp Thr Gly Lys Asn Leu Asn Asn Asp
 85 90 95
 Asp Lys Lys Leu Asn Thr Lys Gln Pro Gln Arg Pro Ala Glu Lys Val
 100 105 110
 Ala Gln Ala Ile Glu Leu Ser Leu Asp Thr Thr Thr Asn Ala Glu Lys
 115 120 125
 Pro Asp Lys Ser Phe His His Glu Lys Pro Val Asn Ala Tyr Val Thr
 130 135 140
 Ser Val Ser Tyr Asn Lys Ser Asn Asp Thr Trp Thr Ile Lys Pro Ser
 145 150 155 160

Asp Ser Ala Val Asn Thr Pro Thr Asn Asp Ala Glu Arg Ile Ser Asn
 165 170 175

Ile Ile Gln Glu Ala Arg Asp Leu Gly Leu Ser Asp Asp Glu Ser Leu
 180 185 190

Thr Gln Gln Ile Ala Phe His Ala His Ala Ala Asn Tyr Leu Val Thr
 195 200 205

Glu Trp Val Leu Arg Gly Tyr Gln Leu Ala Asn Pro Lys Val Leu Pro
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<210> 1681

<211> 1299

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1276)

<223> RXA00260

<400> 1681

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tcagcaggtg attgcagatc gctatgggcc gttggtgaat atg cat agc gac gct 115
 Met His Ser Asp Ala
 1 5

gtg cta gcg ggt gct tca ata aga gca aaa ata ggt gct ctc gca act 163
 Val Leu Ala Gly Ala Ser Ile Arg Ala Lys Ile Gly Ala Leu Ala Thr
 10 15 20

att tac ggt gct caa aac tta gag aat gtc att cac tca gtt agt ttt 211
 Ile Tyr Gly Ala Gln Asn Leu Glu Asn Val Ile His Ser Val Ser Phe
 25 30 35

act gac aga cgt att tct ccc gat gga caa ctg tcg aaa gaa tta ttt 259
 Thr Asp Arg Arg Ile Ser Pro Asp Gly Gln Leu Ser Lys Glu Leu Phe
 40 45 50

cgc gaa gct tgg agc gca aac ctt ctt atc cct gat cca tct tct gat 307
 Arg Glu Ala Trp Ser Ala Asn Leu Leu Ile Pro Asp Pro Ser Ser Asp
 55 60 65

gtg gaa gcg ttt gcg tgg agc gaa aag aat tcc act gag cta gcg gga 355
 Val Glu Ala Phe Ala Trp Ser Glu Lys Asn Ser Thr Glu Leu Ala Gly
 70 75 80 85

ggc ata ttc gtt gag aaa atg cta ttt act gtc ccg gac aca ggc cgc 403
 Gly Ile Phe Val Glu Lys Met Leu Phe Thr Val Pro Asp Thr Gly Arg
 90 95 100

tcc aat aac cgt gtc cag agc ttc tca gaa gaa ctt cgt aac cac att 451
 Ser Asn Asn Arg Val Gln Ser Phe Ser Glu Glu Leu Arg Asn His Ile
 105 110 115

tct ttg aaa gat atg tat tct aca caa cgt gaa gag cta tta gac ctt 499
 Ser Leu Lys Asp Met Tyr Ser Thr Gln Arg Glu Glu Leu Leu Asp Leu

120	125	130	
gcc tac gag ctc atg gtg ggg gaa gca gta cgt ttt gct aac ttc cgc Ala Tyr Glu Leu Met Val Gly Glu Ala Val Arg Phe Ala Asn Phe Arg 135 140 145			547
ctt tat gat cag aat ctc cca cca ctt act gaa gca aat ata gac aaa Leu Tyr Asp Gln Asn Leu Pro Pro Leu Thr Glu Ala Asn Ile Asp Lys 150 155 160 165			595
ttg aga gcc cat cta cgt gag gcc gca gct agt gcg tca cta gga gtg Leu Arg Ala His Leu Arg Glu Ala Ala Ala Ser Ala Ser Leu Gly Val 170 175 180			643
tta tat cta atg gtg tgg cga tct gta aaa gac gca gct gca gcg cac Leu Tyr Leu Met Val Trp Arg Ser Val Lys Asp Ala Ala Ala His 185 190 195			691
act aaa cat aca aga atg agc aaa gaa aat gcg aca acg cat agt gtt Thr Lys His Thr Arg Met Ser Lys Glu Asn Ala Thr Thr His Ser Val 200 205 210			739
aca aaa gtt tct atc ttt gtt gac caa tta tta agc gga aca ttc cct Thr Lys Val Ser Ile Phe Val Asp Gln Leu Leu Ser Gly Thr Phe Pro 215 220 225			787
tgt tca aag cct ttt cac gaa tct tca caa gtc cca ctg agt gaa gcc Cys Ser Lys Pro Phe His Glu Ser Ser Gln Val Pro Leu Ser Glu Ala 230 235 240 245			835
acc aag ata gtt ttt aat ttg att atg gag tca ccg ccg atg gaa act Thr Lys Ile Val Phe Asn Leu Ile Met Glu Ser Pro Pro Met Glu Thr 250 255 260			883
gag ccg agt gtg ctg cga aat tcc ctc caa gaa cac tcg gat tgg gag Glu Pro Ser Val Leu Arg Asn Ser Leu Gln Glu His Ser Asp Trp Glu 265 270 275			931
cta ttg caa cag tgt gat gag aag att cct gat cgg gag ttt ctg atg Leu Leu Gln Gln Cys Asp Glu Lys Ile Pro Asp Arg Glu Phe Leu Met 280 285 290			979
gag tgg tta tat caa gaa cag acg tgg act gca gag caa ttt ttt gat Glu Trp Leu Tyr Gln Glu Gln Thr Trp Thr Ala Glu Gln Phe Phe Asp 295 300 305			1027
gct cta gct atg gtt tct tct agc gag ttt cgt ata tgt gca cct gga Ala Leu Ala Met Val Ser Ser Ser Glu Phe Arg Ile Cys Ala Pro Gly 310 315 320 325			1075
tgt gcg cat caa gta agt gca gac atc gct aca caa gtc tta gaa ttc Cys Ala His Gln Val Ser Ala Asp Ile Ala Thr Gln Val Leu Glu Phe 330 335 340			1123
cac gat cga gtg tct ttc cat gac gat cgt aaa agc gcc atg ctt gct His Asp Arg Val Ser Phe His Asp Asp Arg Lys Ser Ala Met Leu Ala 345 350 355			1171
gct gaa gca act att att ggt aac aaa att ggt tca caa gca cgg gcc Ala Glu Ala Thr Ile Ile Gly Asn Lys Ile Gly Ser Gln Ala Arg Ala 360 365 370			1219

gga gac ttt gtt tta ggt gaa gta atc acc aag ctg cag aac ata cct 1267
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ggt gag gta taacttctgc gtcgtccaat tag 1299
 Gly Glu Val
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<210> 1682

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 1682

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His Ser Val Ser Phe Thr Asp Arg Arg Ile Ser Pro Asp Gly Gln Leu
 35 40 45

Ser Lys Glu Leu Phe Arg Glu Ala Trp Ser Ala Asn Leu Leu Ile Pro
 50 55 60

Asp Pro Ser Ser Asp Val Glu Ala Phe Ala Trp Ser Glu Lys Asn Ser
 65 70 75 80

Thr Glu Leu Ala Gly Gly Ile Phe Val Glu Lys Met Leu Phe Thr Val
 85 90 95

Pro Asp Thr Gly Arg Ser Asn Asn Arg Val Gln Ser Phe Ser Glu Glu
 100 105 110

Leu Arg Asn His Ile Ser Leu Lys Asp Met Tyr Ser Thr Gln Arg Glu
 115 120 125

Glu Leu Leu Asp Leu Ala Tyr Glu Leu Met Val Gly Glu Ala Val Arg
 130 135 140

Phe Ala Asn Phe Arg Leu Tyr Asp Gln Asn Leu Pro Pro Leu Thr Glu
 145 150 155 160

Ala Asn Ile Asp Lys Leu Arg Ala His Leu Arg Glu Ala Ala Ala Ser
 165 170 175

Ala Ser Leu Gly Val Leu Tyr Leu Met Val Trp Arg Ser Val Lys Asp
 180 185 190

Ala Ala Ala Ala His Thr Lys His Thr Arg Met Ser Lys Glu Asn Ala
 195 200 205

Thr Thr His Ser Val Thr Lys Val Ser Ile Phe Val Asp Gln Leu Leu
 210 215 220

Ser Gly Thr Phe Pro Cys Ser Lys Pro Phe His Glu Ser Ser Gln Val
 225 230 235 240

Asp	Pro	Val	Thr	Gly	Asp	Ile	Thr	Phe	His	Phe	Thr	Asp	Gly	Thr	Phe	
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gtc	acc	ctc	aag	gcg	ggg	gtt	gat	ggc	aag	gat	ggg	acc	gat	ggc	caa	355
Val	Thr	Leu	Lys	Ala	Gly	Val	Asp	Gly	Lys	Asp	Gly	Thr	Asp	Gly	Gln	
70					75				80						85	
gat	ggg	gtg	atc	ggc	aag	gac	gca	acc	att	gtt	gat	gtc	gct	acg	gag	403
Asp	Gly	Val	Ile	Gly	Lys	Asp	Ala	Thr	Ile	Val	Asp	Val	Ala	Thr	Glu	
				90					95					100		
tcc	aat	ggg	gat	gtc	aag	ctc	acc	tcc	tct	gat	ggc	acc	gtc	gtc	acc	451
Ser	Asn	Gly	Asp	Val	Lys	Leu	Thr	Phe	Ser	Asp	Gly	Thr	Val	Val	Thr	
			105					110					115			
att	cct	gca	gct	aag	gac	ggg	gtg	gat	ggg	gaa	gat	ggc	aag	gat	ggc	499
Ile	Pro	Ala	Ala	Lys	Asp	Gly	Val	Asp	Gly	Glu	Asp	Gly	Lys	Asp	Gly	
		120					125					130				
gag	gac	gct	act	gtg	gtg	tct	act	gcg	act	gac	gcc	aac	ggc	aat	atc	547
Glu	Asp	Ala	Thr	Val	Val	Ser	Thr	Ala	Thr	Asp	Ala	Asn	Gly	Asn	Ile	
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gtc	att	acg	tcc	tct	gat	ggc	tct	gtg	ctt	gtt	gtt	gct	aac	ggg	aag	595
Val	Ile	Thr	Phe	Ser	Asp	Gly	Ser	Val	Leu	Val	Val	Ala	Asn	Gly	Lys	
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gac	ggc	aac	gat	ggc	tca	gac	ggc	cag	gat	ggg	gct	gat	ggg	gaa	aat	643
Asp	Gly	Asn	Asp	Gly	Ser	Asp	Gly	Gln	Asp	Gly	Ala	Asp	Gly	Glu	Asn	
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ggc	aag	gat	ggg	gag	aac	ggc	gct	aac	gcg	acc	att	gtc	gat	cag	att	691
Gly	Lys	Asp	Gly	Glu	Asn	Gly	Ala	Asn	Ala	Thr	Ile	Val	Asp	Gln	Ile	
			185					190					195			
gcc	aat	gac	gat	ggg	tcc	att	acc	att	gtg	tcc	tcc	gat	ggg	tct	gag	739
Ala	Asn	Asp	Asp	Gly	Ser	Ile	Thr	Ile	Val	Phe	Ser	Asp	Gly	Ser	Glu	
		200					205					210				
gtc	act	atc	cca	gcg	cca	gct	aag	ggg	gcc	acc	gat	gag	ctg	gca	cag	787
Val	Thr	Ile	Pro	Ala	Pro	Ala	Lys	Gly	Ala	Thr	Asp	Glu	Leu	Ala	Gln	
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tgt	ctg	ctg	aac	ccg	aag	atg	ttg	ctg	ctg	gca	gca	att	cct	gct	gca	835
Cys	Leu	Leu	Asn	Pro	Lys	Met	Leu	Leu	Leu	Ala	Ala	Ile	Pro	Ala	Ala	
230					235				240						245	
ggg	gct	att	gct	aac	gct	gtg	gca	ccg	gcg	atc	cca	cgt	gtt	gtt	gaa	883
Gly	Ala	Ile	Ala	Asn	Ala	Val	Ala	Pro	Ala	Ile	Pro	Arg	Val	Val	Glu	
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gat	gtg	cgt	gca	cag	tcc	aat	ctt	cca	agc	ctc	aac	ccc	cag	ttt	gat	931
Asp	Val	Arg	Ala	Gln	Phe	Asn	Leu	Pro	Ser	Leu	Asn	Pro	Gln	Phe	Asp	
			265					270					275			
cag	tgg	ctc	tac	aac	gcg	acc	aag	gat	att	gat	gca	ggg	ttg	ttg	atc	979
Gln	Trp	Leu	Tyr	Asn	Ala	Thr	Lys	Asp	Ile	Asp	Ala	Gly	Leu	Leu	Ile	
		280					285					290				
tct	ggg	gct	acc	ggc	ctt	gct	gtg	ctg	tcg	gtg	ctc	gct	gat	gat	ttc	1027
Ser	Gly	Ala	Thr	Gly	Leu	Ala	Val	Leu	Ser	Val	Leu	Ala	Asp	Asp	Phe	

295	300	305	
tgt ggc gac att gat gcc gat gac aac gca gat ggt gac gtg gcg gca			1075
Cys Gly Asp Ile Asp Ala Asp Asp Asn Ala Asp Gly Asp Val Ala Ala			
310	315	320	325
gaa aag cca act ggc tct tct ggg ctt gga tca tct gaa cag agt gaa			1123
Glu Lys Pro Thr Gly Ser Ser Gly Leu Gly Ser Ser Glu Gln Ser Glu			
	330	335	340
aag gtt gat ggt gac gac gat agt gtg atc gac act gaa act gat gca			1171
Lys Val Asp Gly Asp Asp Asp Ser Val Ile Asp Thr Glu Thr Asp Ala			
	345	350	355
gat ctc gaa gta gaa gaa gac cct gag ctt gtt aac gca ggt			1213
Asp Leu Glu Val Glu Glu Asp Pro Glu Leu Val Asn Ala Gly			
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taacgccagt gtaatgctgg att			1236
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Thr Ala Gln Gln Val Gly Ala Gly Thr Pro Ile His Val Val Asn Leu			
	35	40	45
Asp Arg Thr Val Val Asp Pro Val Thr Gly Asp Ile Thr Phe His Phe			
	50	55	60
Thr Asp Gly Thr Phe Val Thr Leu Lys Ala Gly Val Asp Gly Lys Asp			
	65	70	75
Gly Thr Asp Gly Gln Asp Gly Val Ile Gly Lys Asp Ala Thr Ile Val			
	85	90	95
Asp Val Ala Thr Glu Ser Asn Gly Asp Val Lys Leu Thr Phe Ser Asp			
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Gly Thr Val Val Thr Ile Pro Ala Ala Lys Asp Gly Val Asp Gly Glu			
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Asp Gly Lys Asp Gly Glu Asp Ala Thr Val Val Ser Thr Ala Thr Asp			
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Ala Asn Gly Asn Ile Val Ile Thr Phe Ser Asp Gly Ser Val Leu Val			
	145	150	155
Val Ala Asn Gly Lys Asp Gly Asn Asp Gly Ser Asp Gly Gln Asp Gly			
	165	170	175
Ala Asp Gly Glu Asn Gly Lys Asp Gly Glu Asn Gly Ala Asn Ala Thr			

180	185	190
Ile Val Asp Gln Ile Ala Asn Asp Asp Gly Ser Ile Thr Ile Val Phe 195	200	205
Ser Asp Gly Ser Glu Val Thr Ile Pro Ala Pro Ala Lys Gly Ala Thr 210	215	220
Asp Glu Leu Ala Gln Cys Leu Leu Asn Pro Lys Met Leu Leu Leu Ala 225	230	235
Ala Ile Pro Ala Ala Gly Ala Ile Ala Asn Ala Val Ala Pro Ala Ile 245	250	255
Pro Arg Val Val Glu Asp Val Arg Ala Gln Phe Asn Leu Pro Ser Leu 260	265	270
Asn Pro Gln Phe Asp Gln Trp Leu Tyr Asn Ala Thr Lys Asp Ile Asp 275	280	285
Ala Gly Leu Leu Ile Ser Gly Ala Thr Gly Leu Ala Val Leu Ser Val 290	295	300
Leu Ala Asp Asp Phe Cys Gly Asp Ile Asp Ala Asp Asp Asn Ala Asp 305	310	315
Gly Asp Val Ala Ala Glu Lys Pro Thr Gly Ser Ser Gly Leu Gly Ser 325	330	335
Ser Glu Gln Ser Glu Lys Val Asp Gly Asp Asp Asp Ser Val Ile Asp 340	345	350
Thr Glu Thr Asp Ala Asp Leu Glu Val Glu Glu Asp Pro Glu Leu Val 355	360	365
Asn Ala Gly 370		

<210> 1685

<211> 2733

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2710)

<223> RXA00274

<400> 1685

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Leu Ser Leu Asn Leu	
1	5

aag aag aat tct gcg cgt tct att acc gcg ctg act gtt gct ggt ctg	163
Lys Lys Asn Ser Ala Arg Ser Ile Thr Ala Leu Thr Val Ala Gly Leu	
10	20

ggt ctg tct att gtt cct gcg gca tct gca cag gat gtt gcg gat gac	211
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Gly	Leu	Ser	Ile	Val	Pro	Ala	Ala	Ser	Ala	Gln	Asp	Val	Ala	Asp	Asp		
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Thr	Thr	Asn	Ser	Asp	Ser	Thr	Arg	Asp	Ala	Ile	Cys	Ala	Ala	Ala	Pro		
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ctt	gtt	gca	ggc	gca	gca	gtg	ggg	gtt	ggg	ctg	ctg	tct	cag	cag	cca	307	
Leu	Val	Ala	Gly	Ala	Ala	Val	Gly	Val	Gly	Leu	Leu	Ser	Gln	Gln	Pro		
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gaa	ttc	cag	cat	atg	gtg	tcc	cag	att	cag	tct	gac	gca	cag	cgc	att	355	
Glu	Phe	Gln	His	Met	Val	Ser	Gln	Ile	Gln	Ser	Asp	Ala	Gln	Arg	Ile		
	70				75				80						85		
ggg	cag	gat	ctc	agc	aat	cag	ttc	aac	aac	tct	ctt	gaa	tcg	ctc	aac	403	
Gly	Gln	Asp	Leu	Ser	Asn	Gln	Phe	Asn	Asn	Ser	Leu	Glu	Ser	Leu	Asn		
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att	ggc	ctc	ggg	aac	ggc	gtg	cac	ggc	cca	cag	cag	aac	gct	gtg	cag	451	
Ile	Gly	Leu	Gly	Asn	Gly	Val	His	Gly	Pro	Gln	Gln	Asn	Ala	Val	Gln		
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Gly	Ile	Asp	Leu	Thr	Glu	Ala	Ala	Arg	Thr	Met	Ala	Gly	Trp	Asn	Asp		
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ctg	gcg	gca	cag	gtg	ggc	cag	act	gca	ggc	cct	gct	atc	ggc	gct	gtt	547	
Leu	Ala	Ala	Gln	Val	Gly	Gln	Thr	Ala	Gly	Pro	Ala	Ile	Gly	Ala	Val		
	135					140					145						
gct	ggg	act	gcc	ggc	ctg	atc	gca	ctg	gtt	gac	tac	tgc	tgg	ctg	gaa	595	
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	150				155					160					165		
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Val	Asp	Gly	Gln	Asp	Gly	Thr	Ser	Ile	Thr	Ile	Thr	Glu	Ile	Lys	Thr		
			185					190					195				
gat	gat	gac	ggc	aat	acc	att	gtt	gtc	ttt	tcc	gat	ggg	tct	gaa	atc	739	
Asp	Asp	Asp	Gly	Asn	Thr	Ile	Val	Val	Phe	Ser	Asp	Gly	Ser	Glu	Ile		
		200					205					210					
acc	atc	acc	aat	ggg	aaa	gac	ggc	gct	gct	atc	acc	att	gtt	aat	act	787	
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Tyr	Arg	Asp	Asp	Glu	Gly	Asn	Thr	Val	Val	Glu	Phe	Ser	Asp	Gly	Ser		
	230				235					240				245			
acc	att	gtt	atc	gac	aag	ggg	gaa	gac	ggg	aaa	gat	gga	gaa	gac	ggc	883	
Thr	Ile	Val	Ile	Asp	Lys	Gly	Glu	Asp	Gly	Lys	Asp	Gly	Glu	Asp	Gly		
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aag	gac	ggc	gaa	gac	ggg	aag	gac	ctt	acc	gta	act	gat	acc	tac	atc	931	
Lys	Asp	Gly	Glu	Asp	Gly	Lys	Asp	Leu	Thr	Val	Thr	Asp	Thr	Tyr	Ile		

265	270	275	
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gac ggc aac act gtt gtc gaa ttc tcc gat ggc tcc aat gtg acc atc Asp Gly Asn Thr Val Val Glu Phe Ser Asp Gly Ser Asn Val Thr Ile 330 335 340			1123
aac aag ggt gag aag ggc gac aag ggt gac gct ggc gcc gat ggc gaa Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Ala Gly Ala Asp Gly Glu 345 350 355			1171
gac ggc gca gat ggt gaa tca att act gtt gtt aac acc agc aac gat Asp Gly Ala Asp Gly Glu Ser Ile Thr Val Val Asn Thr Ser Asn Asp 360 365 370			1219
gct gaa ggc aac act ctt gtt gag ctc tcc gat ggc act gtt att acc Ala Glu Gly Asn Thr Leu Val Glu Leu Ser Asp Gly Thr Val Ile Thr 375 380 385			1267
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gat gcg gac ggc aac act gtt gtg gtg ttc tcg aac ggc act gaa atc Asp Ala Asp Gly Asn Thr Val Val Phe Ser Asn Gly Thr Glu Ile 425 430 435			1411
acc atc aac aag ggt gag aag ggc gac aag gga gat acc ggc gaa gac Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Thr Gly Glu Asp 440 445 450			1459
ggt aag gac gga ctg acc ccg tac atc ggc cca gat ggt aac tgg tgg Gly Lys Asp Gly Leu Thr Pro Tyr Ile Gly Pro Asp Gly Asn Trp Trp 455 460 465			1507
atc ggt gag aac aac acc tgt act gct gca cgt ggc aat gac ggt aaa Ile Gly Glu Asn Asn Thr Cys Thr Ala Ala Arg Gly Asn Asp Gly Lys 470 475 480 485			1555
gac ggt gac acc cca cgc atc ggt gat aat ggt aat tgg tgg atc ggc Asp Gly Asp Thr Pro Arg Ile Gly Asp Asn Gly Asn Trp Trp Ile Gly 490 495 500			1603
atc gtt gat acc ggc gtt cct gct cgt ggt cag gat ggc gcc aac gga Ile Val Asp Thr Gly Val Pro Ala Arg Gly Gln Asp Gly Ala Asn Gly 505 510 515			1651

gcc gat ggt gct aac acc gtt gag atc att aat ggc tac tgg tac atc Ala Asp Gly Ala Asn Thr Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile 520 525 530	1699
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gga gcc gat gga caa gac ggt gaa aat gga acc aac ggt gct aac acc Gly Ala Asp Gly Gln Asp Gly Glu Asn Gly Thr Asn Gly Ala Asn Thr 550 555 560 565	1795
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gtc aag gcg cag ggt cca aag ggc gat aag ggt gac act ggt gac acg Val Lys Ala Gln Gly Pro Lys Gly Asp Lys Gly Asp Thr Gly Asp Thr 585 590 595	1891
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ttt gaa tat gaa atc ccg cac act gtt att ggt gac aac ggt aac tgg Phe Glu Tyr Glu Ile Pro His Thr Val Ile Gly Asp Asn Gly Asn Trp 630 635 640 645	2035
tac atc ggt gaa aag gat act ggt atc cca gct cag ggt ggc act gga Tyr Ile Gly Glu Lys Asp Thr Gly Ile Pro Ala Gln Gly Gly Thr Gly 650 655 660	2083
aca cct ggt gag gat ggc ctc aca cca cac att ggc gac aac ggt aac Thr Pro Gly Glu Asp Gly Leu Thr Pro His Ile Gly Asp Asn Gly Asn 665 670 675	2131
tgg tgg atc ggt gat acc gat aca ggt gtc tct gca agc ccg acc ccc Trp Trp Ile Gly Asp Thr Asp Thr Gly Val Ser Ala Ser Pro Thr Pro 680 685 690	2179
gtt ggt gag gcg gta gcg ggt gtc act gat gtg gtc ttc aac act agt Val Gly Glu Ala Val Ala Gly Val Thr Asp Val Val Phe Asn Thr Ser 695 700 705	2227
gat gaa ccc aag acc att act gca acg atc aat ggt gaa gaa tat gat Asp Glu Pro Lys Thr Ile Thr Ala Thr Ile Asn Gly Glu Glu Tyr Asp 710 715 720 725	2275
tac acc ctt cca cca cat agt gct gtt gtg ttc tac gct aca ggt tca Tyr Thr Leu Pro Pro His Ser Ala Val Val Phe Tyr Ala Thr Gly Ser 730 735 740	2323
cca atg gca tat tct cta ccg aat gca tcg ggc ctc act gtt ata ggt Pro Met Ala Tyr Ser Leu Pro Asn Ala Ser Gly Leu Thr Val Ile Gly 745 750 755	2371

act gaa gag act cct ggt ttc acc act att cga ttc agt gac cat tcc 2419
 Thr Glu Glu Thr Pro Gly Phe Thr Thr Ile Arg Phe Ser Asp His Ser
 760 765 770

act gtg acc att cca cat gga cga gat ggc acc aac ggt act aac gaa 2467
 Thr Val Thr Ile Pro His Gly Arg Asp Gly Thr Asn Gly Thr Asn Glu
 775 780 785

ctg acg gta agg atg gtc tca ccc cgc aca tcg gtg aga acg gaa act 2515
 Leu Thr Val Arg Met Val Ser Pro Arg Thr Ser Val Arg Thr Glu Thr
 790 795 800 805

ggt gga tcg gcg aaa agg aca ctg gta ttt cga caa cct ttg gcg gtg 2563
 Gly Gly Ser Ala Lys Arg Thr Leu Val Phe Arg Gln Pro Leu Ala Val
 810 815 820

gcg gca acc ctg gta ccg gca atg act gca tca cgg tcc cag gtg atg 2611
 Ala Ala Thr Leu Val Pro Ala Met Thr Ala Ser Arg Ser Gln Val Met
 825 830 835

atc ttg gat tcc cag atg atg ctg agg ccg gtg cag aga ccg gtg cag 2659
 Ile Leu Asp Ser Gln Met Met Leu Arg Pro Val Gln Arg Pro Val Gln
 840 845 850

atg ccg aag gta cta ttg act aaa ggt cat aga gca acg acc atg act 2707
 Met Pro Lys Val Leu Leu Thr Lys Gly His Arg Ala Thr Thr Met Thr
 855 860 865

gat taaagtcgga acacaacccc tag 2733
 Asp
 870

<210> 1686

<211> 870

<212> PRT

<213> Corynebacterium glutamicum

<400> 1686

Leu Ser Leu Asn Leu Lys Lys Asn Ser Ala Arg Ser Ile Thr Ala Leu
 1 5 10 15

Thr Val Ala Gly Leu Gly Leu Ser Ile Val Pro Ala Ala Ser Ala Gln
 20 25 30

Asp Val Ala Asp Asp Thr Thr Asn Ser Asp Ser Thr Arg Asp Ala Ile
 35 40 45

Cys Ala Ala Ala Pro Leu Val Ala Gly Ala Ala Val Gly Val Gly Leu
 50 55 60

Leu Ser Gln Gln Pro Glu Phe Gln His Met Val Ser Gln Ile Gln Ser
 65 70 75 80

Asp Ala Gln Arg Ile Gly Gln Asp Leu Ser Asn Gln Phe Asn Asn Ser
 85 90 95

Leu Glu Ser Leu Asn Ile Gly Leu Gly Asn Gly Val His Gly Pro Gln
 100 105 110

Gln Asn Ala Val Gln Gly Ile Asp Leu Thr Glu Ala Ala Arg Thr Met

115	120	125
Ala Gly Trp Asn Asp Leu Ala Ala Gln Val Gly Gln Thr Ala Gly Pro		
130	135	140
Ala Ile Gly Ala Val Ala Gly Thr Ala Gly Leu Ile Ala Leu Val Asp		
145	150	155 160
Tyr Cys Trp Leu Glu Gly Phe Asp Phe Ala Gly Gly Ser Ser Gly Thr		
165	170	175
Asp Gly Glu Asn Gly Val Asp Gly Gln Asp Gly Thr Ser Ile Thr Ile		
180	185	190
Thr Glu Ile Lys Thr Asp Asp Asp Gly Asn Thr Ile Val Val Phe Ser		
195	200	205
Asp Gly Ser Glu Ile Thr Ile Thr Asn Gly Lys Asp Gly Ala Ala Ile		
210	215	220
Thr Ile Val Asn Thr Tyr Arg Asp Asp Glu Gly Asn Thr Val Val Glu		
225	230	235 240
Phe Ser Asp Gly Ser Thr Ile Val Ile Asp Lys Gly Glu Asp Gly Lys		
245	250	255
Asp Gly Glu Asp Gly Lys Asp Gly Glu Asp Gly Lys Asp Leu Thr Val		
260	265	270
Thr Asp Thr Tyr Ile Asn Asp Asp Gly Asp Thr Val Val Glu Leu Ser		
275	280	285
Asp Gly Ser Thr Ile Ile Val Lys Lys Gly Thr Asp Gly Lys Asp Gly		
290	295	300
Ala Asp Gly Ser Asp Gly Ala Asp Gly Val Ser Ile Thr Val Glu Asn		
305	310	315 320
Ser Tyr Val Asp Ala Asp Gly Asn Thr Val Val Glu Phe Ser Asp Gly		
325	330	335
Ser Asn Val Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly Asp Ala		
340	345	350
Gly Ala Asp Gly Glu Asp Gly Ala Asp Gly Glu Ser Ile Thr Val Val		
355	360	365
Asn Thr Ser Asn Asp Ala Glu Gly Asn Thr Leu Val Glu Leu Ser Asp		
370	375	380
Gly Thr Val Ile Thr Ile Asn Lys Gly Asp Lys Gly Asp Ala Gly Ala		
385	390	395 400
Asp Gly Glu Asp Gly Ser Asn Gly Ala Asp Gly Glu Ser Ile Thr Val		
405	410	415
Ile Glu Thr Arg Phe Asp Ala Asp Gly Asn Thr Val Val Val Phe Ser		
420	425	430
Asn Gly Thr Glu Ile Thr Ile Asn Lys Gly Glu Lys Gly Asp Lys Gly		
435	440	445

Asp Thr Gly Glu Asp Gly Lys Asp Gly Leu Thr Pro Tyr Ile Gly Pro
 450 455 460
 Asp Gly Asn Trp Trp Ile Gly Glu Asn Asn Thr Cys Thr Ala Ala Arg
 465 470 475 480
 Gly Asn Asp Gly Lys Asp Gly Asp Thr Pro Arg Ile Gly Asp Asn Gly
 485 490 495
 Asn Trp Trp Ile Gly Ile Val Asp Thr Gly Val Pro Ala Arg Gly Gln
 500 505 510
 Asp Gly Ala Asn Gly Ala Asp Gly Ala Asn Thr Val Glu Ile Ile Asn
 515 520 525
 Gly Tyr Trp Tyr Ile Asn Gly Glu Asn Thr Gly Val Lys Ala Val Gly
 530 535 540
 Glu Asn Gly Thr Asn Gly Ala Asp Gly Gln Asp Gly Glu Asn Gly Thr
 545 550 555 560
 Asn Gly Ala Asn Thr Val Glu Ile Ile Asn Gly Tyr Trp Tyr Ile Asn
 565 570 575
 Gly Glu Asn Thr Gly Val Lys Ala Gln Gly Pro Lys Gly Asp Lys Gly
 580 585 590
 Asp Thr Gly Asp Thr Gly Ala Pro Gly Glu Gly Ser Gly Asn Val Asp
 595 600 605
 Ile Glu Ile Arg Glu Ser Ser Tyr Pro Gly Gly Gly Gln Ala Thr Ile
 610 615 620
 Ile Ile Leu Asp Gln Phe Glu Tyr Glu Ile Pro His Thr Val Ile Gly
 625 630 635 640
 Asp Asn Gly Asn Trp Tyr Ile Gly Glu Lys Asp Thr Gly Ile Pro Ala
 645 650 655
 Gln Gly Gly Thr Gly Thr Pro Gly Glu Asp Gly Leu Thr Pro His Ile
 660 665 670
 Gly Asp Asn Gly Asn Trp Trp Ile Gly Asp Thr Asp Thr Gly Val Ser
 675 680 685
 Ala Ser Pro Thr Pro Val Gly Glu Ala Val Ala Gly Val Thr Asp Val
 690 695 700
 Val Phe Asn Thr Ser Asp Glu Pro Lys Thr Ile Thr Ala Thr Ile Asn
 705 710 715 720
 Gly Glu Glu Tyr Asp Tyr Thr Leu Pro Pro His Ser Ala Val Val Phe
 725 730 735
 Tyr Ala Thr Gly Ser Pro Met Ala Tyr Ser Leu Pro Asn Ala Ser Gly
 740 745 750
 Leu Thr Val Ile Gly Thr Glu Glu Thr Pro Gly Phe Thr Thr Ile Arg
 755 760 765

Phe Ser Asp His Ser Thr Val Thr Ile Pro His Gly Arg Asp Gly Thr
 770 775 780
 Asn Gly Thr Asn Glu Leu Thr Val Arg Met Val Ser Pro Arg Thr Ser
 785 790 795 800
 Val Arg Thr Glu Thr Gly Gly Ser Ala Lys Arg Thr Leu Val Phe Arg
 805 810 815
 Gln Pro Leu Ala Val Ala Ala Thr Leu Val Pro Ala Met Thr Ala Ser
 820 825 830
 Arg Ser Gln Val Met Ile Leu Asp Ser Gln Met Met Leu Arg Pro Val
 835 840 845
 Gln Arg Pro Val Gln Met Pro Lys Val Leu Leu Thr Lys Gly His Arg
 850 855 860
 Ala Thr Thr Met Thr Asp
 865 870

<210> 1687

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXA00275

<400> 1687

ctgacgcaga cggtgcacag ctcgcaaccg ctattgacga acagaaccgc cccacaaaga 60
 gctgttccct acggcagatc gcaaggaact attcgcctgg ttg gat aag cgt cgc 115
 Leu Asp Lys Arg Arg
 1 5
 cca gaa tta agc gac gat ttc atc aaa gct ttt gat gat ttc ctt cat 163
 Pro Glu Leu Ser Asp Asp Phe Ile Lys Ala Phe Asp Asp Phe Leu His
 10 15 20
 tct ttt gcg tgc ctg gac aaa aca acg atc acc cta ttg gcg caa tca 211
 Ser Phe Ala Cys Leu Asp Lys Thr Thr Ile Thr Leu Leu Ala Gln Ser
 25 30 35
 ccg gtg cgc aca tcc act ggc tat aca ggt act ttt atc ggc atc ccc 259
 Pro Val Arg Thr Ser Thr Gly Tyr Thr Gly Thr Phe Ile Gly Ile Pro
 40 45 50
 aat aat gaa cca ctg tcc gaa gag ccc acc ccc acc att tac att gtg 307
 Asn Asn Glu Pro Leu Ser Glu Glu Pro Thr Pro Thr Ile Tyr Ile Val
 55 60 65
 cac gat aat cac aca ggg ata atc cac agt tac ccc gca cga atg att 355
 His Asp Asn His Thr Gly Ile Ile His Ser Tyr Pro Ala Arg Met Ile
 70 75 80 85
 aat ctt aaa tct gag ctc ggt tcc gct gag atg att cac gag gca atc 403
 Asn Leu Lys Ser Glu Leu Gly Ser Ala Glu Met Ile His Glu Ala Ile

90	95	100	
tgg ggg tca ccc cat caa cag cag tta atc tca tgg tat gag act tac			451
Trp Gly Ser Pro His Gln Gln Gln Leu Ile Ser Trp Tyr Glu Thr Tyr			
105	110	115	
tac acc aac atc tac tat ggt ttt aac cca ccc act gaa cca cat aag			499
Tyr Thr Asn Ile Tyr Tyr Gly Phe Asn Pro Pro Thr Glu Pro His Lys			
120	125	130	
agt ctt gag att ttt gct caa gac ttc tgt ctg acc cca cca gag aaa			547
Ser Leu Glu Ile Phe Ala Gln Asp Phe Cys Leu Thr Pro Pro Glu Lys			
135	140	145	
cct cct ttt ttc taaggcaagg cccgtggcac aca			582
Pro Pro Phe Phe			
150			
..			
<210> 1688			
<211> 153			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1688			
Leu Asp Lys Arg Arg Pro Glu Leu Ser Asp Asp Phe Ile Lys Ala Phe			
1	5	10	15
Asp Asp Phe Leu His Ser Phe Ala Cys Leu Asp Lys Thr Thr Ile Thr			
20	25	30	
Leu Leu Ala Gln Ser Pro Val Arg Thr Ser Thr Gly Tyr Thr Gly Thr			
35	40	45	
Phe Ile Gly Ile Pro Asn Asn Glu Pro Leu-Ser Glu Glu Pro Thr Pro			
50	55	60	
Thr Ile Tyr Ile Val His Asp Asn His Thr Gly Ile Ile His Ser Tyr			
65	70	75	80
Pro Ala Arg Met Ile Asn Leu Lys Ser Glu Leu Gly Ser Ala Glu Met			
85	90	95	
Ile His Glu Ala Ile Trp Gly Ser Pro His Gln Gln Gln Leu Ile Ser			
100	105	110	
Trp Tyr Glu Thr Tyr Tyr Thr Asn Ile Tyr Tyr Gly Phe Asn Pro Pro			
115	120	125	
Thr Glu Pro His Lys Ser Leu Glu Ile Phe Ala Gln Asp Phe Cys Leu			
130	135	140	
Thr Pro Pro Glu Lys Pro Pro Phe Phe			
145	150		

<210> 1689

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>.

<221> CDS

<222> (101)..(442)

<223> RXA00276

<400> 1689

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ggcacactac cctatgacta caccgcaacc cagcaaacct gcgccatggc cgcttgcccta 60

taagtatcaa gccatcagca atgatgattt tgacaaccat atg gat gac ctc agc 115
                                         Met Asp Asp Leu Ser
                                         1 5

agt cgc caa gac cat gaa gcc tac ggc acg tac aac ccc gat aac ggt 163
Ser Arg Gln Asp His Glu Ala Tyr Gly Thr Tyr Asn Pro Asp Asn Gly
                        10 15 20

gtc atg ccc gat cat gtc atc gtg cct tca ccc tat gaa cca tat gat 211
Val Met Pro Asp His Val Ile Val Pro Ser Pro Tyr Glu Pro Tyr Asp
                        25 30 35

gat gct gcg ccg att gat cct ttc gac tac gac gaa gat ctt ctc gat 259
Asp Ala Ala Pro Ile Asp Pro Phe Asp Tyr Asp Glu Asp Leu Leu Asp
                        40 45 50

gag att aaa gaa gag cgc gct gca cat gcg gtt gac gca caa gta aca 307
Glu Ile Lys Glu Glu Arg Ala Ala His Ala Val Asp Ala Gln Val Thr
                        55 60 65

gaa aca act aaa gct gac gca gac gtt gca cag ctc gca acc gct att 355
Glu Thr Thr Lys Ala Asp Ala Asp Val Ala Gln Leu Ala Thr Ala Ile
                        70 75 80 85

gac gaa cag aac cgc ccc aca aag agc tgt tcc cta cgg cag atc gca 403
Asp Glu Gln Asn Arg Pro Thr Lys Ser Cys Ser Leu Arg Gln Ile Ala
                        90 95 100

agg aac tat tcg cct ggt tgg ata agc gtc gcc cag aat taagcgacga 452
Arg Asn Tyr Ser Pro Gly Trp Ile Ser Val Ala Gln Asn
                        105 110

tttcatcaaaa gct 465

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<210> 1690

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 1690

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Met Asp Asp Leu Ser Ser Arg Gln Asp His Glu Ala Tyr Gly Thr Tyr
 1 5 10 15

Asn Pro Asp Asn Gly Val Met Pro Asp His Val Ile Val Pro Ser Pro
20 25 30

Tyr Glu Pro Tyr Asp Asp Ala Ala Pro Ile Asp Pro Phe Asp Tyr Asp
35 40 45

Glu Asp Leu Leu Asp Glu Ile Lys Glu Glu Arg Ala Ala His Ala Val
50 55 60

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Asp Ala Gln Val Thr Glu Thr Thr Lys Ala Asp Ala Asp Val Ala Gln
65 70 75 80

Leu Ala Thr Ala Ile Asp Glu Gln Asn Arg Pro Thr Lys Ser Cys Ser
85 90 95

Leu Arg Gln Ile Ala Arg Asn Tyr Ser Pro Gly Trp Ile Ser Val Ala
100 105 110

Gln Asn

<210> 1691

<211> 1509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1486)

<223> RXA00279

<400> 1691

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acattcagcc ccacattcag ctcggaccgc gttggagttt ttg gat acc gat gac 115
Leu Asp Thr Asp Asp
1 5

tcg cct gat cat tgg ctt gat ccg tta acg gag aag gat act tct aag 163
Ser Pro Asp His Trp Leu Asp Pro Leu Thr Glu Lys Asp Thr Ser Lys
10 15 20

cgc act ctc gtt aat tcg att gtt cag gaa act ttc ggc cag cct att 211
Arg Thr Leu Val Asn Ser Ile Val Gln Glu Thr Phe Gly Gln Pro Ile
25 30 35

ttt gtt gcc cgc aag att tgg gct ttc gtc aat acg tcg ccg ggc cgg 259
Phe Val Ala Arg Lys Ile Trp Ala Phe Val Asn Thr Ser Pro Gly Arg
40 45 50

atg acg ttg atg acg att atc att tcg atc gcc att ttt gct gct ggt 307
Met Thr Leu Met Thr Ile Ile Ile Ser Ile Ala Ile Phe Ala Ala Gly
55 60 65

tac gcc atg tcg gtg tct tcg gat act agg cag tcc aat ttg gat gat 355
Tyr Ala Met Ser Val Ser Ser Asp Thr Arg Gln Ser Asn Leu Asp Asp
70 75 80 85

ttg atc act aat gcg gag cct gtt tcc tat aac gcg cat gtg ctg tat 403
Leu Ile Thr Asn Ala Glu Pro Val Ser Tyr Asn Ala His Val Leu Tyr
90 95 100

aca tca ttg tcg gtt gct gat acc act gct acc act ggt ttt gtt cag 451
Thr Ser Leu Ser Val Ala Asp Thr Thr Ala Thr Thr Gly Phe Val Gln
105 110 115

gct ggt gtg gag ggc ccg gtg aat cgg gtg aag tat cac act gct att 499
Ala Gly Val Glu Gly Pro Val Asn Arg Val Lys Tyr His Thr Ala Ile
120 125 130

gat cgt gct gcg gtt gct gct act cat act gcg gcg tct gcg gat agt Asp Arg Ala Ala Val Ala Ala Thr His Thr Ala Ala Ser Ala Asp Ser 135 140 145	547
agt aat gag cat ttg atg gag ttg gtg ctg gag att cag cgt cag ttg Ser Asn Glu His Leu Met Glu Leu Val Leu Glu Ile Gln Arg Gln Leu 150 155 160 165	595
ccg gtg tat acg ggg ttg gtg gaa act gct cgg act aat aac cgt gcg Pro Val Tyr Thr Gly Leu Val Glu Thr Ala Arg Thr Asn Asn Arg Ala 170 175 180	643
ggt aat ccc gtg ggt gtg gcc tat atg tct gag gcc agc gcg atg atg Gly Asn Pro Val Gly Val Ala Tyr Met Ser Glu Ala Ser Ala Met Met 185 190 195	691
cgt aat gaa att ttg ccg atg gcg tct gag ctt tac aac ctg acg agt Arg Asn Glu Ile Leu Pro Met Ala Ser Glu Leu Tyr Asn Leu Thr Ser 200 205 210	739
cgt gcg gtg tct gat cag cag cgt tcg gtg acg ggt ccg cag tgg ttt Arg Ala Val Ser Asp Gln Gln Arg Ser Val Thr Gly Pro Gln Trp Phe 215 220 225	787
ccg ctg tct gga ttg ctt gcg gct ctt gcc atg ttg att gtt gcg cag Pro Leu Ser Gly Leu Leu Ala Ala Leu Ala Met Leu Ile Val Ala Gln 230 235 240 245	835
tgg tgg ttg atg cgg att acg cgc agg cgc atc aac aag ggg ttt gcc Trp Trp Leu Met Arg Ile Thr Arg Arg Arg Ile Asn Lys Gly Phe Ala 250 255 260	883
ctg gcc acg gtg atg atg atg acg gca acg tta tgg gtg tca gct gca Leu Ala Thr Val Met Met Met Thr Ala Thr Leu Trp Val Ser Ala Ala 265 270 275	931
aac tgg gcg acg tgg cag gct ggc acg aag ggt ttt gag gaa gcg tcg Asn Trp Ala Thr Trp Gln Ala Gly Thr Lys Gly Phe Glu Glu Ala Ser 280 285 290	979
ggg ccg ttg aat tcc atg act acg gct cgt att tat gcg cag cag acc Gly Pro Leu Asn Ser Met Thr Thr Ala Arg Ile Tyr Ala Gln Gln Thr 295 300 305	1027
cgc acg acg gag acg ttg tcg ttg gtg cgt agg cag tcg att cag ggc Arg Thr Thr Glu Thr Leu Ser Leu Val Arg Arg Gln Ser Ile Gln Gly 310 315 320 325	1075
agt ggc act ggt ttt acc gca acg att aat cag att aag cgt gcg ctg Ser Gly Thr Gly Phe Thr Ala Thr Ile Asn Gln Ile Lys Arg Ala Leu 330 335 340	1123
gat gag tat gaa acc act gcg cag tca cag act ccg gag cat cag cag Asp Glu Tyr Glu Thr Thr Ala Gln Ser Gln Thr Pro Glu His Gln Gln 345 350 355	1171
ttg att acg gcg att cgt aat gcg att gct gca tgg act gcc gat cac Leu Ile Thr Ala Ile Arg Asn Ala Ile Ala Ala Trp Thr Ala Asp His 360 365 370	1219

gat gag ttc acg gtg ttg ttg gcg tct ggt gat tac aac ggt gcg gtc 1267
 Asp Glu Phe Thr Val Leu Leu Ala Ser Gly Asp Tyr Asn Gly Ala Val
 375 380 385

aat gcg gtg ctc aac aaa gat gag gag ggc cag acc agc ttt gat gag 1315
 Asn Ala Val Leu Asn Lys Asp Glu Glu Gly Gln Thr Ser Phe Asp Glu
 390 395 400 405

ctc gat act gcg ctg gct gag ctg atc gcg gat tct cgc agc tcc atg 1363
 Leu Asp Thr Ala Leu Ala Glu Leu Ile Ala Asp Ser Arg Ser Ser Met
 410 415 420

cgt tcc tat atc cag tcg ggc ctg cag gcc acg gag ttg gtg tcc gtc 1411
 Arg Ser Tyr Ile Gln Ser Gly Leu Gln Ala Thr Glu Leu Val Ser Val
 425 430 435

atg gtg atg att ctg tct gtc gtt tct gtg ttg gct ttg tgg gtc ggc 1459
 Met Val Met Ile Leu Ser Val Val Ser Val Leu Ala Leu Trp Val Gly
 440 445 450

atc cgc ccc cgt ttg cag gag tac tta taaatgcacg ctttttcgacg 1506
 Ile Arg Pro Arg Leu Gln Glu Tyr Leu
 455 460

ccc 1509

<210> 1692

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 1692

Leu Asp Thr Asp Asp Ser Pro Asp His Trp Leu Asp Pro Leu Thr Glu
 1 5 10 15

Lys Asp Thr Ser Lys Arg Thr Leu Val Asn Ser Ile Val Gln Glu Thr
 20 25 30

Phe Gly Gln Pro Ile Phe Val Ala Arg Lys Ile Trp Ala Phe Val Asn
 35 40 45

Thr Ser Pro Gly Arg Met Thr Leu Met Thr Ile Ile Ile Ser Ile Ala
 50 55 60

Ile Phe Ala Ala Gly Tyr Ala Met Ser Val Ser Ser Asp Thr Arg Gln
 65 70 75 80

Ser Asn Leu Asp Asp Leu Ile Thr Asn Ala Glu Pro Val Ser Tyr Asn
 85 90 95

Ala His Val Leu Tyr Thr Ser Leu Ser Val Ala Asp Thr Thr Ala Thr
 100 105 110

Thr Gly Phe Val Gln Ala Gly Val Glu Gly Pro Val Asn Arg Val Lys
 115 120 125

Tyr His Thr Ala Ile Asp Arg Ala Ala Val Ala Ala Thr His Thr Ala
 130 135 140

Ala Ser Ala Asp Ser Ser Asn Glu His Leu Met Glu Leu Val Leu Glu

145 150 155 160
Ile Gln Arg Gln Leu Pro Val Tyr Thr Gly Leu Val Glu Thr Ala Arg
 165 170 175
Thr Asn Asn Arg Ala Gly Asn Pro Val Gly Val Ala Tyr Met Ser Glu
 180 185 190
Ala Ser Ala Met Met Arg Asn Glu Ile Leu Pro Met Ala Ser Glu Leu
 195 200 205
Tyr Asn Leu Thr Ser Arg Ala Val Ser Asp Gln Gln Arg Ser Val Thr
 210 215 220
Gly Pro Gln Trp Phe Pro Leu Ser Gly Leu Leu Ala Ala Leu Ala Met
225 230 235 240
Leu Ile Val Ala Gln Trp Trp Leu Met Arg Ile Thr Arg Arg Arg Ile
 245 250 255
Asn Lys Gly Phe Ala Leu Ala Thr Val Met Met Met Thr Ala Thr Leu
 260 265 270
Trp Val Ser Ala Ala Asn Trp Ala Thr Trp Gln Ala Gly Thr Lys Gly
 275 280 285
Phe Glu Glu Ala Ser Gly Pro Leu Asn Ser Met Thr Thr Ala Arg Ile
290 295 300
Tyr Ala Gln Gln Thr Arg Thr Thr Glu Thr Leu Ser Leu Val Arg Arg
305 310 315 320
Gln Ser Ile Gln Gly Ser Gly Thr Gly Phe Thr Ala Thr Ile Asn Gln
 325 330 335
Ile Lys Arg Ala Leu Asp Glu Tyr Glu Thr Thr Ala Gln Ser Gln Thr
 340 345 350
Pro Glu His Gln Gln Leu Ile Thr Ala Ile Arg Asn Ala Ile Ala Ala
 355 360 365
Trp Thr Ala Asp His Asp Glu Phe Thr Val Leu Leu Ala Ser Gly Asp
370 375 380
Tyr Asn Gly Ala Val Asn Ala Val Leu Asn Lys Asp Glu Glu Gly Gln
385 390 395 400
Thr Ser Phe Asp Glu Leu Asp Thr Ala Leu Ala Glu Leu Ile Ala Asp
 405 410 415
Ser Arg Ser Ser Met Arg Ser Tyr Ile Gln Ser Gly Leu Gln Ala Thr
 420 425 430
Glu Leu Val Ser Val Met Val Met Ile Leu Ser Val Val Ser Val Leu
435 440 445
Ala Leu Trp Val Gly Ile Arg Pro Arg Leu Gln Glu Tyr Leu
450 455 460

<211> 789

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(789)

<223> RXA00282

<400> 1693

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tcg cgc gag cag tcc tgg gat caa tcc tgg cag aac cta aat aag gat	96
Ser Arg Glu Gln Ser Trp Asp Gln Ser Trp Gln Asn Leu Asn Lys Asp	
20 25 30	
tcc cag tac ggt ccg acc tcg cat ccg gag gac gcg ccg gga gga ttc	144
Ser Gln Tyr Gly Pro Thr Ser His Pro Glu Asp Ala Pro Gly Gly Phe	
35 40 45	
cag gga aac ggc cag ggt aac agc ccg ggc aac gct cag ggc aat ggt	192
Gln Gly Asn Gly Gln Gly Asn Ser Arg Gly Asn Ala Gln Gly Asn Gly	
50 55 60	
cag ggc aat ggt cag ggc ttt ggc ccg ggt aat gct tcg gga tat gga	240
Gln Gly Asn Gly Gln Gly Phe Gly Pro Gly Asn Ala Ser Gly Tyr Gly	
65 70 75 80	
ggc tac ggt cag cca tac ccg cag act ccg tac cag aat tcc tac caa	288
Gly Tyr Gly Gln Pro Tyr Pro Gln Thr Pro Tyr Gln Asn Ser Tyr Gln	
85 90 95	
ggc tat ggc gct act tca ccg cag aac gac gtg gcg ctg gaa gcg agc	336
Gly Tyr Gly Ala Thr Ser Pro Gln Asn Asp Val Ala Leu Glu Ala Ser	
100 105 110	
aac ggc aaa gtc gac atc atg ccg gcg att ccg ttc gga ttc aaa gcc	384
Asn Gly Lys Val Asp Ile Met Arg Ala Ile Arg Phe Gly Phe Lys Ala	
115 120 125	
acg ttt gcc aat cca gca gtg tgg att ttg ggc acc gtc ggt ctt ggc	432
Thr Phe Ala Asn Pro Ala Val Trp Ile Leu Gly Thr Val Gly Leu Gly	
130 135 140	
ctt gcg ttc atg att gtg agt ggg ttg ctt ggc tac tta tca ttt ttg	480
Leu Ala Phe Met Ile Val Ser Gly Leu Leu Gly Tyr Leu Ser Phe Leu	
145 150 155 160	
atc gac cct aat gcg ggc acg acg act tct ggt ttt tcg gtt tcc gag	528
Ile Asp Pro Asn Ala Gly Thr Thr Thr Ser Gly Phe Ser Val Ser Glu	
165 170 175	
acc ctg ttg aac gta gct atc gga atc atc acc ttc gca ata acc att	576
Thr Leu Leu Asn Val Ala Ile Gly Ile Ile Thr Phe Ala Ile Thr Ile	
180 185 190	
tgc gtc atg cgc ggt gca ctg ctt tct gtt gat gga cac aaa gtt cgc	624
Cys Val Met Arg Gly Ala Leu Leu Ser Val Asp Gly His Lys Val Arg	
195 200 205	

ttc ggt gat ttc ttt aaa ccc atc aat gtt ggt caa aca gtg att ctg 672
 Phe Gly Asp Phe Phe Lys Pro Ile Asn Val Gly Gln Thr Val Ile Leu
 210 215 220

atg gtg ggg ctg ggt atc ttc ggc atc atc ctg ggc acc ttc acc act 720
 Met Val Gly Leu Gly Ile Phe Gly Ile Ile Leu Gly Thr Phe Thr Thr
 225 230 235 240

ttt ctc act caa aat ctg gtg tcg ttt aat gac gct gcc ggt acc gtt 768
 Phe Leu Thr Gln Asn Leu Val Ser Phe Asn Asp Ala Ala Gly Thr Val
 245 250 255

gag gtc aat aac agc ggt tta 789
 Glu Val Asn Asn Ser Gly Leu
 260

<210> 1694

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 1694

Met Ser Arg Asp Asp Gln Thr Asn Asn Asn Gly Glu Gly Asp Asp Thr
 1 5 10 15

Ser Arg Glu Gln Ser Trp Asp Gln Ser Trp Gln Asn Leu Asn Lys Asp
 20 25 30

Ser Gln Tyr Gly Pro Thr Ser His Pro Glu Asp Ala Pro Gly Gly Phe
 35 40 45

Gln Gly Asn Gly Gln Gly Asn Ser Arg Gly Asn Ala Gln Gly Asn Gly
 50 55 60

Gln Gly Asn Gly Gln Gly Phe Gly Pro Gly Asn Ala Ser Gly Tyr Gly
 65 70 75 80

Gly Tyr Gly Gln Pro Tyr Pro Gln Thr Pro Tyr Gln Asn Ser Tyr Gln
 85 90 95

Gly Tyr Gly Ala Thr Ser Pro Gln Asn Asp Val Ala Leu Glu Ala Ser
 100 105 110

Asn Gly Lys Val Asp Ile Met Arg Ala Ile Arg Phe Gly Phe Lys Ala
 115 120 125

Thr Phe Ala Asn Pro Ala Val Trp Ile Leu Gly Thr Val Gly Leu Gly
 130 135 140

Leu Ala Phe Met Ile Val Ser Gly Leu Leu Gly Tyr Leu Ser Phe Leu
 145 150 155 160

Ile Asp Pro Asn Ala Gly Thr Thr Thr Ser Gly Phe Ser Val Ser Glu
 165 170 175

Thr Leu Leu Asn Val Ala Ile Gly Ile Ile Thr Phe Ala Ile Thr Ile
 180 185 190

Cys Val Met Arg Gly Ala Leu Leu Ser Val Asp Gly His Lys Val Arg

195	200	205
Phe Gly Asp Phe Phe Lys Pro Ile Asn Val Gly Gln Thr Val Ile Leu		
210	215	220
Met Val Gly Leu Gly Ile Phe Gly Ile Ile Leu Gly Thr Phe Thr Thr		
225	230	235 240
Phe Leu Thr Gln Asn Leu Val Ser Phe Asn Asp Ala Ala Gly Thr Val		
245	250	255
Glu Val Asn Asn Ser Gly Leu		
260		

<210> 1695

<211> 536

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(513)

<223> RXA00285

<400> 1695

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Gly Thr Glu Leu Gly Ala Leu Leu Leu Arg Val Leu Asn Arg Glu Glu	
1 5 10 15	
atg atg gac aga ttc gca cgg gag ctg ggt ttt ttc gtc gac aag cag	96
Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln	
20 25 30	
ctt gaa gag gtc gag cgc atc aac tgt cac cat aac tac acg gtc cag	144
Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln	
35 40 45	
gag gag cac tac ggc gag acc att tgg ctc acc cgt aag ggt gcc gtg	192
Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val	
50 55 60	
ttg gcg gac gaa ggc acg ccg gcg ttg att ccg ggg tcg atg ggc acc	240
Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr	
65 70 75 80	
gcg tcg tac gtg ggc agt ggc aag ggc aac gcc gag gca ctg cgg tcg	288
Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser	
85 90 95	
gcg ccg cat ggg gcg ggc cgg agg atg tac cgc aac cag gct aaa aag	336
Ala Pro His Gly Ala Gly Arg Arg Met Tyr Arg Asn Gln Ala Lys Lys	
100 105 110	
cgc ttc tcg acg gcc gac ctg gat tct cgg atg gcg ggc atc gtc tac	384
Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr	
115 120 125	
cgg ccc ggc aag gag tgg atc gat gaa att ccc gac gct tac aaa gac	432
Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp	
130 135 140	

atc gat cag gtg atg gcc gat gct gcc gat ttg gtg aca att cgc cat 480
Ile Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His
145 150 155 160

aaa ttg cgc cag atc gtc aac gtg aaa ggc acc taaagcgcat tacggtaaag 533
Lys Leu Arg Gln Ile Val Asn Val Lys Gly Thr
165 170

tgc 536

<210> 1696

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1696

Gly Thr Glu Leu Gly Ala Leu Leu Leu Arg Val Leu Asn Arg Glu Glu
1 5 10 15

Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln
20 25 30

Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln
35 40 45

Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val
50 55 60

Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr
65 70 75 80

Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser
85 90 95

Ala Pro His Gly Ala Gly Arg Arg Met Tyr Arg Asn Gln Ala Lys Lys
100 105 110

Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr
115 120 125

Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp
130 135 140

Ile Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His
145 150 155 160

Lys Leu Arg Gln Ile Val Asn Val Lys Gly Thr
165 170

<210> 1697

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXA00286

<400> 1697

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ccataaattg cgccagatcg tcaacgtgaa aggcacctaa agcgcattac ggtaaagtgc 60

gagaggtatt ttgacggggtt tagattgagg gatgtggata gtg ctg aaa atc cca 115
                                   Val Leu Lys Ile Pro
                                   1 5

cgg ctg ctt cta cgc cgt gtg ctt ccg gta ctc atc acc ttg gcg ctc 163
Arg Leu Leu Leu Arg Arg Val Leu Pro Val Leu Ile Thr Leu Ala Leu
      10 15 20

ctg tgc gga ctg gtg ctt gcg tgg ttt atc tat cct gcg aag gct gag 211
Leu Cys Gly Leu Val Leu Ala Trp Phe Ile Tyr Pro Ala Lys Ala Glu
      25 30 35

ccc aaa aaa gat gat gta gtt ctg gtg ctg gcc ggt tcc agc gat ggt 259
Pro Lys Lys Asp Asp Val Val Leu Val Leu Ala Gly Ser Ser Asp Gly
      40 45 50

cga cac gaa tat ggt gcc gag ctt gtt gaa gaa ggc tac gcc agc aat 307
Arg His Glu Tyr Gly Ala Glu Leu Val Glu Glu Gly Tyr Ala Ser Asn
      55 60 65

tac gtc gtc tcc aac ccg agt ggc tcc aaa gac aaa gtg gga tat gcc 355
Tyr Val Val Ser Asn Pro Ser Gly Ser Lys Asp Lys Val Gly Tyr Ala
      70 75 80 85

cac tgc gca gga aag tca ccg cca aaa aat gcg gaa agt ttc tgc atg 403
His Cys Ala Gly Lys Ser Arg Pro Lys Asn Ala Glu Ser Phe Cys Met
      90 95 100

gat cct tac ccc gtg atc acc tcc ggc gaa gcc cgc acg ttt aac gag 451
Asp Pro Tyr Pro Val Ile Thr Ser Gly Glu Ala Arg Thr Phe Asn Glu
      105 110 115

ctt gcc aaa aag gaa ggc tgg gaa agc gta ttg gta gtg acc agc cgc 499
Leu Ala Lys Lys Glu Gly Trp Glu Ser Val Leu Val Val Thr Ser Arg
      120 125 130

acg cac acc caa cgc gtt cgc acc atg ttt gac cag tgc tat acc ggt 547
Thr His Thr Gln Arg Val Arg Thr Met Phe Asp Gln Cys Tyr Thr Gly
      135 140 145

gat tcc aca gtg ctc aac gtc aac agc cta gga cgt acc ggg ctt cac 595
Asp Ser Thr Val Leu Asn Val Asn Ser Leu Gly Arg Thr Gly Leu His
      150 155 160 165

aat gca gta ctc cac gag att ggc ggc ttc att aaa ttt tgg att acc 643
Asn Ala Val Leu His Glu Ile Gly Gly Phe Ile Lys Phe Trp Ile Thr
      170 175 180

gct ccg tgc gcg gac aca aac taaggacgtt ccagctccaa cag 687
Ala Pro Cys Ala Asp Thr Asn
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<210> 1698

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 1698

Val Leu Lys Ile Pro Arg Leu Leu Leu Arg Arg Val Leu Pro Val Leu
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 Ile Thr Leu Ala Leu Leu Cys Gly Leu Val Leu Ala Trp Phe Ile Tyr
 20 25 30
 Pro Ala Lys Ala Glu Pro Lys Lys Asp Asp Val Val Leu Val Leu Ala
 35 40 45
 Gly Ser Ser Asp Gly Arg His Glu Tyr Gly Ala Glu Leu Val Glu Glu
 50 55 60
 Gly Tyr Ala Ser Asn Tyr Val Val Ser Asn Pro Ser Gly Ser Lys Asp
 65 70 75 80
 Lys Val Gly Tyr Ala His Cys Ala Gly Lys Ser Arg Pro Lys Asn Ala
 85 90 95
 Glu Ser Phe Cys Met Asp Pro Tyr Pro Val Ile Thr Ser Gly Glu Ala
 100 105 110
 Arg Thr Phe Asn Glu Leu Ala Lys Lys Glu Gly Trp Glu Ser Val Leu
 115 120 125
 Val Val Thr Ser Arg Thr His Thr Gln Arg Val Arg Thr Met Phe Asp
 130 135 140
 Gln Cys Tyr Thr Gly Asp Ser Thr Val Leu Asn Val Asn Ser Leu Gly
 145 150 155 160
 Arg Thr Gly Leu His Asn Ala Val Leu His Glu Ile Gly Gly Phe Ile
 165 170 175
 Lys Phe Trp Ile Thr Ala Pro Cys Ala Asp Thr Asn
 180 185

<210> 1699

<211> 552

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(529)

<223> RXA00294

<400> 1699

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 agttggtgcc gaatcaacaa tctcttttgg aggaacttta atg agc att tcc aac 115
 Met Ser Ile Ser Asn
 1 5
 gca atc ctg cgt ggt gtg tct ggc gct tat att ctg cag tcc ggc tac 163
 Ala Ile Leu Arg Gly Val Ser Gly Ala Tyr Ile Leu Gln Ser Gly Tyr
 10 15 20
 gga aaa ctt gga ttg cct aat gag gcc gct gct ggc att cag ggt cta 211

Gly Lys Leu Gly Leu Pro Asn Glu Ala Ala Ala Gly Ile Gln Gly Leu
 25 30 35
 gct gca acg ggt atc cca gcg gtg gct gat atg gat tca gat act ttc 259
 Ala Ala Thr Gly Ile Pro Ala Val Ala Asp Met Asp Ser Asp Thr Phe
 40 45 50
 ggt aag ttt gtt gcc tac tcg gag ttg ggt atc ggt gga gct ttg ctt 307
 Gly Lys Phe Val Ala Tyr Ser Glu Leu Gly Ile Gly Gly Ala Leu Leu
 55 60 65
 gct cca ttt atc cct agc cgt ctt gca ggt ttg ggt ctt ggt gct ttc 355
 Ala Pro Phe Ile Pro Ser Arg Leu Ala Gly Leu Gly Leu Gly Ala Phe
 70 75 80 85
 tct aca ggt ttg ttg gcc att tac ttc cgt aac cca gcg atg act caa 403
 Ser Thr Gly Leu Leu Ala Ile Tyr Phe Arg Asn Pro Ala Met Thr Gln
 90 95 100
 gac gac gga atc cgc cct tcc cag gat gga acc gga ttg tct aag gat 451
 Asp Asp Gly Ile Arg Pro Ser Gln Asp Gly Thr Gly Leu Ser Lys Asp
 105 110 115
 ctt ttc ctt gct gct att gcg ggt gct ttg gtg ttc gca cct gct aag 499
 Leu Phe Leu Ala Ala Ile Ala Gly Ala Leu Val Phe Ala Pro Ala Lys
 120 125 130
 aag cgt aag aag gcg aag aac aag tct aag taagcttgct tgaacggcgc 549
 Lys Arg Lys Lys Ala Lys Asn Lys Ser Lys
 135 140
 ttg 552

 <210> 1700
 <211> 143
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1700
 Met Ser Ile Ser Asn Ala Ile Leu Arg Gly Val Ser Gly Ala Tyr Ile
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 Leu Gln Ser Gly Tyr Gly Lys Leu Gly Leu Pro Asn Glu Ala Ala Ala
 20 25 30
 Gly Ile Gln Gly Leu Ala Ala Thr Gly Ile Pro Ala Val Ala Asp Met
 35 40 45
 Asp Ser Asp Thr Phe Gly Lys Phe Val Ala Tyr Ser Glu Leu Gly Ile
 50 55 60
 Gly Gly Ala Leu Leu Ala Pro Phe Ile Pro Ser Arg Leu Ala Gly Leu
 65 70 75 80
 Gly Leu Gly Ala Phe Ser Thr Gly Leu Leu Ala Ile Tyr Phe Arg Asn
 85 90 95
 Pro Ala Met Thr Gln Asp Asp Gly Ile Arg Pro Ser Gln Asp Gly Thr
 100 105 110

Gly Leu Ser Lys Asp Leu Phe Leu Ala Ala Ile Ala Gly Ala Leu Val
 115 120 125

Phe Ala Pro Ala Lys Lys Arg Lys Lys Ala Lys Asn Lys Ser Lys
 130 135 140

<210> 1701

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1012)

<223> RXA00297

<400> 1701

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aaaacaacat ggcacaataa cgatcatgca acaggtgctc atg ggt ttc acg gtg 115
 Met Gly Phe Thr Val
 1 5

gtg ttc atc gtc atc gga ata ggt tgg att ctg ggt aga aga gac acc 163
 Val Phe Ile Val Ile Gly Ile Gly Trp Ile Leu Gly Arg Arg Asp Thr
 10 15 20

ttg ggc aca cat gcc cag aaa cct ttg agc ctg ttt gtc tat tac gtg 211
 Leu Gly Thr His Ala Gln Lys Pro Leu Ser Leu Phe Val Tyr Tyr Val
 25 30 35

gcc acc cca gcg ttg ttg ttt gat cgg gtc acc aag tca gat acc tcg 259
 Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr Lys Ser Asp Thr Ser
 40 45 50

acg att ttc tct ctg aac ttc gtg gtc att gca ctg tct gcg ttg atc 307
 Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala Leu Ser Ala Leu Ile
 55 60 65

gta ggt ttc ctg ttt ttc cta ctg atg cgg ttc gtg atc aaa aga act 355
 Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe Val Ile Lys Arg Thr
 70 75 80 85

gcc gca gta tcg gtg atc ggc atg cta gct gcg tcc tac gcc aac gcc 403
 Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala Ser Tyr Ala Asn Ala
 90 95 100

ggt aac ctg ggt atc cct ttg gca gcc tat att ttg gat gat ttc acc 451
 Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile Leu Asp Asp Phe Thr
 105 110 115

gtg gtg att ccc gtg att ttg ttc cag gtg gcg ttc tac gca ccg atc 499
 Val Val Ile Pro Val Ile Leu Phe Gln Val Ala Phe Tyr Ala Pro Ile
 120 125 130

acc atg acc atc atg gag atg ctg acc aac aag aaa tcc acc aac ttg 547
 Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys Lys Ser Thr Asn Leu
 135 140 145

gtg cgc aac ctg ctg gtc acg cca cta acc aac acc atg gtg ctg gca 595

Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn Thr Met Val Leu Ala
 150 155 160 165
 gcg att gcc ggt att gct gtg tct ttg act tcg atg agc gtg ccc gtg 643
 Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser Met Ser Val Pro Val
 170 175 180
 gtg att gct cag cca gtg gaa atg ttg gcg aat gct tca gtg cca ctg 691
 Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn Ala Ser Val Pro Leu
 185 190 195
 gct ttg gtg gtg ttc gga ctg tcc ttg tcc aag agc aag atc ctg gaa 739
 Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys Ser Lys Ile Leu Glu
 200 205 210
 aag ggg cag gta tcc agg cgc gat gtg ttt acg gcg gca ctg ttc aag 787
 Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr Ala Ala Leu Phe Lys
 215 220 225
 aat gtt ctg cac cca att gtt gcg gga ctt tta gcc tta gcc ttt ggt 835
 Asn Val Leu His Pro Ile Val Ala Gly Leu Leu Ala Leu Ala Phe Gly
 230 235 240 245
 atg gaa ggt act gcc ttg ttg tcg gcg gtg att ctc ggt gca ctg cca 883
 Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile Leu Gly Ala Leu Pro
 250 255 260
 aca gcg cag aat gtc tac acc tac gcg ttg cga ttt aga aca gct gaa 931
 Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg Phe Arg Thr Ala Glu
 265 270 275
 tcg atg gcg aga gac aca ggg gtg gtc acc aca ctc att tcc ttc ccc 979
 Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr Leu Ile Ser Phe Pro
 280 285 290
 gta ttg gtg gcg gtc tcc att atc ttt gga tct taggggttagc attagtggtc 1032
 Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser
 295 300
 atg 1035
 <210> 1702
 <211> 304
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1702
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 20 25 30
 Phe Val Tyr Tyr Val Ala Thr Pro Ala Leu Leu Phe Asp Arg Val Thr
 35 40 45
 Lys Ser Asp Thr Ser Thr Ile Phe Ser Leu Asn Phe Val Val Ile Ala
 50 55 60
 Leu Ser Ala Leu Ile Val Gly Phe Leu Phe Phe Leu Leu Met Arg Phe

65	70	75	80
Val Ile Lys Arg Thr Ala Ala Val Ser Val Ile Gly Met Leu Ala Ala	85	90	95
Ser Tyr Ala Asn Ala Gly Asn Leu Gly Ile Pro Leu Ala Ala Tyr Ile	100	105	110
Leu Asp Asp Phe Thr Val Val Ile Pro Val Ile Leu Phe Gln Val Ala	115	120	125
Phe Tyr Ala Pro Ile Thr Met Thr Ile Met Glu Met Leu Thr Asn Lys	130	135	140
Lys Ser Thr Asn Leu Val Arg Asn Leu Leu Val Thr Pro Leu Thr Asn	145	150	155
Thr Met Val Leu Ala Ala Ile Ala Gly Ile Ala Val Ser Leu Thr Ser	165	170	175
Met Ser Val Pro Val Val Ile Ala Gln Pro Val Glu Met Leu Ala Asn	180	185	190
Ala Ser Val Pro Leu Ala Leu Val Val Phe Gly Leu Ser Leu Ser Lys	195	200	205
Ser Lys Ile Leu Glu Lys Gly Gln Val Ser Arg Arg Asp Val Phe Thr	210	215	220
Ala Ala Leu Phe Lys Asn Val Leu His Pro Ile Val Ala Gly Leu Leu	225	230	235
Ala Leu Ala Phe Gly Met Glu Gly Thr Ala Leu Leu Ser Ala Val Ile	245	250	255
Leu Gly Ala Leu Pro Thr Ala Gln Asn Val Tyr Thr Tyr Ala Leu Arg	260	265	270
Phe Arg Thr Ala Glu Ser Met Ala Arg Asp Thr Gly Val Val Thr Thr	275	280	285
Leu Ile Ser Phe Pro Val Leu Val Ala Val Ser Ile Ile Phe Gly Ser	290	295	300

<210> 1703

<211> 303

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(280)

<223> RXA00320

<400> 1703

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tacaaaccgt gatttgtttc gtgattggag ctgagcccac atg gct aaa gaa gat 115

Met Ala Lys Glu Asp

1

5

ttg aag tgg ttc tac gat ctg gca acc ggc aag gtt ttt caa ggc aag 163
 Leu Lys Trp Phe Tyr Asp Leu Ala Thr Gly Lys Val Phe Gln Gly Lys
 10 15 20

gtt tcc ggc ttt gaa acc cgc atg ggc cca tat gac act gaa gag gaa 211
 Val Ser Gly Phe Glu Thr Arg Met Gly Pro Tyr Asp Thr Glu Glu Glu
 25 30 35

gcc cat cac gcc atc tcc att gcg gca gcc cga acc aag gca gcc gaa 259
 Ala His His Ala Ile Ser Ile Ala Ala Ala Arg Thr Lys Ala Ala Glu
 40 45 50

att tgg gac gac aag gaa gac taaaaaaaaac tggggtcaca ctt 303
 Ile Trp Asp Asp Lys Glu Asp
 55 60

<210> 1704

<211> 60

<212> PRT

<213> Corynebacterium glutamicum

<400> 1704

Met Ala Lys Glu Asp Leu Lys Trp Phe Tyr Asp Leu Ala Thr Gly Lys
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Val Phe Gln Gly Lys Val Ser Gly Phe Glu Thr Arg Met Gly Pro Tyr
 20 25 30

Asp Thr Glu Glu Ala His His Ala Ile Ser Ile Ala Ala Ala Arg
 35 40 45

Thr Lys Ala Ala Glu Ile Trp Asp Asp Lys Glu Asp
 50 55 60

<210> 1705

<211> 1938

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1915)

<223> RXA00321

<400> 1705

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gcttcacaat cacataagtc tttaaaggat ggatacaaca atg ggc cag cat cta 115
 Met Gly Gln His Leu
 1 5

gaa gtg gaa act aag ttt tcc gtc agt gaa tca act cag att cca caa 163
 Glu Val Glu Thr Lys Phe Ser Val Ser Glu Ser Thr Gln Ile Pro Gln
 10 15 20

ctt gag gct atc gca gaa gtc gac cac att gat cgc acc gaa atc cac 211
 Leu Glu Ala Ile Ala Glu Val Asp His Ile Asp Arg Thr Glu Ile His
 25 30 35

caa cta agc gct gtt tac ttt gac acc gta gat ttg cgc ctc acc cgc	259
Gln Leu Ser Ala Val Tyr Phe Asp Thr Val Asp Leu Arg Leu Thr Arg	
40 45 50	
gca aaa att acc ctc cgt cgc cgc acc ggt gga aac gat gcc ggc tgg	307
Ala Lys Ile Thr Leu Arg Arg Arg Thr Gly Gly Asn Asp Ala Gly Trp	
55 60 65	
cac att aag ttc ccc gga acc atc ggt cgc cgt gaa gtc caa gcc cca	355
His Ile Lys Phe Pro Gly Thr Ile Gly Arg Arg Glu Val Gln Ala Pro	
70 75 80 85	
ctt gat ggc gaa ggc gca aca gaa acc ctc cct cca cgt gag ctc ttg	403
Leu Asp Gly Glu Gly Ala Thr Glu Thr Leu Pro Pro Arg Glu Leu Leu	
90 95 100	
gga cac atc cga gcg ctg atc caa ggc cgt gag ctg acc cct atc gcc	451
Gly His Ile Arg Ala Leu Ile Gln Gly Arg Glu Leu Thr Pro Ile Ala	
105 110 115	
cag gtg gat aat gaa cgc cac atg tct tac ctc gcg gat gag gac ggc	499
Gln Val Asp Asn Glu Arg His Met Ser Tyr Leu Ala Asp Glu Asp Gly	
120 125 130	
gca gtc atc gca gaa ttc tgc gac gat cat gta tcc acc gtg tcc cac	547
Ala Val Ile Ala Glu Phe Cys Asp Asp His Val Ser Thr Val Ser His	
135 140 145	
ctt cca ggt ggc gtg cgc aag cag tgg cgt gag tgg gaa ttc gaa ctc	595
Leu Pro Gly Gly Val Arg Lys Gln Trp Arg Glu Trp Glu Phe Glu Leu	
150 155 160 165	
gct gat ggc acc ctc gcc gaa gaa gcc atc tca gta ctg ctg caa tct	643
Ala Asp Gly Thr Leu Ala Glu Glu Ala Ile Ser Val Leu Leu Gln Ser	
170 175 180	
gca cag tca gtc ctg acc gca gct gga gct ttt gtc tcc aac agc cca	691
Ala Gln Ser Val Leu Thr Ala Ala Gly Ala Phe Val Ser Asn Ser Pro	
185 190 195	
tcc aaa ctt gtt tcg gcg ctg gac gaa tca gtc aac cac gcg cca aag	739
Ser Lys Leu Val Ser Ala Leu Asp Glu Ser Val Asn His Ala Pro Lys	
200 205 210	
cct cca cag atg gcg cag ctg gac aag aat gac cca gca cgt ggt gtt	787
Pro Pro Gln Met Ala Gln Leu Asp Lys Asn Asp Pro Ala Arg Gly Val	
215 220 225	
ctt gca gca atc gca gcc aac gcc tca aag atc gcc gaa tac gat cct	835
Leu Ala Ala Ile Ala Ala Asn Ala Ser Lys Ile Ala Glu Tyr Asp Pro	
230 235 240 245	
cga gta cgc gcc gat gaa tat gat tca gtc cac cag atg cgc gta gct	883
Arg Val Arg Ala Asp Glu Tyr Asp Ser Val His Gln Met Arg Val Ala	
250 255 260	
acc cga gaa cta cgc agc cac ctc caa acc ttt gag ggc atc ctc ggc	931
Thr Arg Glu Leu Arg Ser His Leu Gln Thr Phe Glu Gly Ile Leu Gly	
265 270 275	

ggc gaa gac tac ctc aac ctg gaa aag gaa ctg aag gtt ctc gcc aac	979
Gly Glu Asp Tyr Leu Asn Leu Glu Lys Glu Leu Lys Val Leu Ala Asn	
280 285 290	
atc ttg ggt cgc gca cgc gat gct gaa gtt gtg gaa gag cgc ctc agc	1027
Ile Leu Gly Arg Ala Arg Asp Ala Glu Val Val Glu Glu Arg Leu Ser	
295 300 305	
aac ctg att aac act gag gtt ggc gac tcc atc gag gag gag act aag	1075
Asn Leu Ile Asn Thr Glu Val Gly Asp Ser Ile Glu Glu Glu Thr Lys	
310 315 320 325	
aag gaa ctg ctt gaa gat ctt ggt gca gaa tac cgt cgt gag cat gag	1123
Lys Glu Leu Leu Glu Asp Leu Gly Ala Glu Tyr Arg Arg Glu His Glu	
330 335 340	
cga gta gtt cgt gcg ctg gat aat gat cgc tac act gat ctt ctt cag	1171
Arg Val Val Arg Ala Leu Asp Asn Asp Arg Tyr Thr Asp Leu Leu Gln	
345 350 355	
gca ctg gaa aac ctc ctt gtt gat cca ccg ctg atc aca gaa gtc gaa	1219
Ala Leu Glu Asn Leu Leu Val Asp Pro Pro Leu Ile Thr Glu Val Glu	
360 365 370	
gaa ccc gaa gct acc gaa gcc cct gag tcc gct gag act acc gag tcc	1267
Glu Pro Glu Ala Thr Glu Ala Pro Glu Ser Ala Glu Thr Thr Glu Ser	
375 380 385	
act gac gtc tct gaa gca acc gaa gaa gca gac gca gaa gct gag tct	1315
Thr Asp Val Ser Glu Ala Thr Glu Glu Ala Asp Ala Glu Ala Glu Ser	
390 395 400 405	
gtc gaa gaa gct act gag cag gaa gaa tca gca gac gcg cct gaa tct	1363
Val Glu Glu Ala Thr Glu Gln Glu Glu Ser Ala Asp Ala Pro Glu Ser	
410 415 420	
gca gat ctg gac gct ctc gat gag gag tac tcc cct ggt tcc caa gcg	1411
Ala Asp Leu Asp Ala Leu Asp Glu Glu Tyr Ser Pro Gly Ser Gln Ala	
425 430 435	
ccg gtg gag gag ccg aag gaa ccg aag aag gtt gat gct gct ctc gta	1459
Pro Val Glu Glu Pro Lys Glu Pro Lys Lys Val Asp Ala Ala Leu Val	
440 445 450	
ctt cta gag cac ctt gat aag gcg cac gtg aag ctc gtc aag ctg gaa	1507
Leu Leu Glu His Leu Asp Lys Ala His Val Lys Leu Val Lys Leu Glu	
455 460 465	
aag aag gct cgc tca cag tgg gat gat ctc agc att ccg atg ctg gag	1555
Lys Lys Ala Arg Ser Gln Trp Asp Asp Leu Ser Ile Pro Met Leu Glu	
470 475 480 485	
cgg gaa gaa aac ttc cac aac ctg cgc aag gct gcc aag aag ctt cgc	1603
Arg Glu Glu Asn Phe His Asn Leu Arg Lys Ala Ala Lys Lys Leu Arg	
490 495 500	
tac agt gca gag gca gtg ggc aaa gca acc acc gtt gag acg aag aaa	1651
Tyr Ser Ala Glu Ala Val Gly Lys Ala Thr Thr Val Glu Thr Lys Lys	
505 510 515	
ctg tac aag gcg tgc agt ggt ttg cag tca gtt ctt ggc gat tac caa	1699

Leu Tyr Lys Ala Cys Ser Gly Leu Gln Ser Val Leu Gly Asp Tyr Gln
 520 525 530
 gat gcc att act tcc cgt aat gag ctg ttg cgc cga gct cag gtt gcc 1747
 Asp Ala Ile Thr Ser Arg Asn Glu Leu Leu Arg Arg Ala Gln Val Ala
 535 540 545
 cgc cgc caa ggc cgg gat acc ttc gca tac gga atc ctc tac cag cac 1795
 Arg Arg Gln Gly Arg Asp Thr Phe Ala Tyr Gly Ile Leu Tyr Gln His
 550 555 560 565
 gaa caa acc ctg tcg agg gaa tac ctg act ggt tat tcc gat gcg ttc 1843
 Glu Gln Thr Leu Ser Arg Glu Tyr Leu Thr Gly Tyr Ser Asp Ala Phe
 570 575 580
 aag agc gta gaa aaa gcc tat gca aag ctg gct gaa gat acc gcc aag 1891
 Lys Ser Val Glu Lys Ala Tyr Ala Lys Leu Ala Glu Asp Thr Ala Lys
 585 590 595
 cgt tca aag aag aac aag cgt aag taaacgcagg caataaaaaa ctg 1938
 Arg Ser Lys Lys Asn Lys Arg Lys
 600 605

 <210> 1706
 <211> 605
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 1706
 Met Gly Gln His Leu Glu Val Glu Thr Lys Phe Ser Val Ser Glu Ser
 1 5 10 15
 Thr Gln Ile Pro Gln Leu Glu Ala Ile Ala Glu Val Asp His Ile Asp
 20 25 30
 Arg Thr Glu Ile His Gln Leu Ser Ala Val Tyr Phe Asp Thr Val Asp
 35 40 45
 Leu Arg Leu Thr Arg Ala Lys Ile Thr Leu Arg Arg Arg Thr Gly Gly
 50 55 60
 Asn Asp Ala Gly Trp His Ile Lys Phe Pro Gly Thr Ile Gly Arg Arg
 65 70 75 80
 Glu Val Gln Ala Pro Leu Asp Gly Glu Gly Ala Thr Glu Thr Leu Pro
 85 90 95
 Pro Arg Glu Leu Leu Gly His Ile Arg Ala Leu Ile Gln Gly Arg Glu
 100 105 110
 Leu Thr Pro Ile Ala Gln Val Asp Asn Glu Arg His Met Ser Tyr Leu
 115 120 125
 Ala Asp Glu Asp Gly Ala Val Ile Ala Glu Phe Cys Asp Asp His Val
 130 135 140
 Ser Thr Val Ser His Leu Pro Gly Gly Val Arg Lys Gln Trp Arg Glu
 145 150 155 160
 Trp Glu Phe Glu Leu Ala Asp Gly Thr Leu Ala Glu Glu Ala Ile Ser

165	170	175
Val Leu Leu Gln Ser Ala Gln Ser Val Leu Thr Ala Ala Gly Ala Phe 180 185 190		
Val Ser Asn Ser Pro Ser Lys Leu Val Ser Ala Leu Asp Glu Ser Val 195 200 205		
Asn His Ala Pro Lys Pro Pro Gln Met Ala Gln Leu Asp Lys Asn Asp 210 215 220		
Pro Ala Arg Gly Val Leu Ala Ala Ile Ala Ala Asn Ala Ser Lys Ile 225 230 235 240		
Ala Glu Tyr Asp Pro Arg Val Arg Ala Asp Glu Tyr Asp Ser Val His 245 250 255		
Gln Met Arg Val Ala Thr Arg Glu Leu Arg Ser His Leu Gln Thr Phe 260 265 270		
Glu Gly Ile Leu Gly Gly Glu Asp Tyr Leu Asn Leu Glu Lys Glu Leu 275 280 285		
Lys Val Leu Ala Asn Ile Leu Gly Arg Ala Arg Asp Ala Glu Val Val 290 295 300		
Glu Glu Arg Leu Ser Asn Leu Ile Asn Thr Glu Val Gly Asp Ser Ile 305 310 315 320		
Glu Glu Glu Thr Lys Lys Glu Leu Leu Glu Asp Leu Gly Ala Glu Tyr 325 330 335		
Arg Arg Glu His Glu Arg Val Val Arg Ala Leu Asp Asn Asp Arg Tyr 340 345 350		
Thr Asp Leu Leu Gln Ala Leu Glu Asn Leu Leu Val Asp Pro Pro Leu 355 360 365		
Ile Thr Glu Val Glu Glu Pro Glu Ala Thr Glu Ala Pro Glu Ser Ala 370 375 380		
Glu Thr Thr Glu Ser Thr Asp Val Ser Glu Ala Thr Glu Glu Ala Asp 385 390 395 400		
Ala Glu Ala Glu Ser Val Glu Glu Ala Thr Glu Gln Glu Glu Ser Ala 405 410 415		
Asp Ala Pro Glu Ser Ala Asp Leu Asp Ala Leu Asp Glu Glu Tyr Ser 420 425 430		
Pro Gly Ser Gln Ala Pro Val Glu Glu Pro Lys Glu Pro Lys Lys Val 435 440 445		
Asp Ala Ala Leu Val Leu Leu Glu His Leu Asp Lys Ala His Val Lys 450 455 460		
Leu Val Lys Leu Glu Lys Lys Ala Arg Ser Gln Trp Asp Asp Leu Ser 465 470 475 480		
Ile Pro Met Leu Glu Arg Glu Glu Asn Phe His Asn Leu Arg Lys Ala 485 490 495		

Ala Lys Lys Leu Arg Tyr Ser Ala Glu Ala Val Gly Lys Ala Thr Thr
 500 505 510

Val Glu Thr Lys Lys Leu Tyr Lys Ala Cys Ser Gly Leu Gln Ser Val
 515 520 525

Leu Gly Asp Tyr Gln Asp Ala Ile Thr Ser Arg Asn Glu Leu Leu Arg
 530 535 540

Arg Ala Gln Val Ala Arg Arg Gln Gly Arg Asp Thr Phe Ala Tyr Gly
 545 550 555 560

Ile Leu Tyr Gln His Glu Gln Thr Leu Ser Arg Glu Tyr Leu Thr Gly
 565 570 575

Tyr Ser Asp Ala Phe Lys Ser Val Glu Lys Ala Tyr Ala Lys Leu Ala
 580 585 590

Glu Asp Thr Ala Lys Arg Ser Lys Lys Asn Lys Arg Lys
 595 600 605

<210> 1707

<211> 1227

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1204)

<223> RXA00322

<400> 1707

cgcggttttt tgatgacacg ggggtgggag gtgtccagct tgggtgggttc actgagaacc 60

gcaccgaaat tagaactctc ctacgaataa ggaaaccgca atg act ctc tcc cac 115
 Met Thr Leu Ser His
 1 5

ttc tcc gac aac gtc acc gac gca caa gac tct tac cgt cag att tta 163
 Phe Ser Asp Asn Val Thr Asp Ala Gln Asp Ser Tyr Arg Gln Ile Leu
 10 15 20

gaa gaa agc atc atc agc cac cta ggt ttc tgt gcg ctt cgt ggg tgg 211
 Glu Glu Ser Ile Ile Ser His Leu Gly Phe Cys Ala Leu Arg Gly Trp
 25 30 35

act ccc gcc gat ctc cgc cat gag ttt tcc gcc gat att gat cca ctc 259
 Thr Pro Ala Asp Leu Arg His Glu Phe Ser Ala Asp Ile Asp Pro Leu
 40 45 50

ctg ttt cac gcg cta cct gag att gct tac tcc tgc tcc gat gag atg 307
 Leu Phe His Ala Leu Pro Glu Ile Ala Tyr Ser Cys Ser Asp Glu Met
 55 60 65

tac aca ctg tgg gtg aac gga acg cgt gcc gcc gaa act agc cac ttg 355
 Tyr Thr Leu Trp Val Asn Gly Thr Arg Ala Ala Glu Thr Ser His Leu
 70 75 80 85

ccg gtg atg acc ctg gag aag att ctc acc gag cta ccg aag cta agt 403

Pro Val Met Thr Leu Glu Lys Ile Leu Thr Glu Leu Pro Lys Leu Ser	
90 95 100	
acc ttg cct gac tgg gca atg ctc gca gag ctc cac gcc tta gac aat	451
Thr Leu Pro Asp Trp Ala Met Leu Ala Glu Leu His Ala Leu Asp Asn	
105 110 115	
caa gac acc agc cca atg acc ccg gca cag gcc aaa gcg cat cat cgt	499
Gln Asp Thr Ser Pro Met Thr Pro Ala Gln Ala Lys Ala His His Arg	
120 125 130	
atc acc gca ctt ttg aaa aag gca gag tcc acc aac ttc gaa gaa gaa	547
Ile Thr Ala Leu Leu Lys Lys Ala Glu Ser Thr Asn Phe Glu Glu Glu	
135 140 145	
gcc gaa gca ttg atc ctt aaa gca gag aca ctt cga cag cag tac cgg	595
Ala Glu Ala Leu Ile Leu Lys Ala Glu Thr Leu Arg Gln Gln Tyr Arg	
150 155 160 165	
att gaa tca ctg ctg att aat tcc tat gac caa gat gtc caa gct cga	643
Ile Glu Ser Leu Leu Ile Asn Ser Tyr Asp Gln Asp Val Gln Ala Arg	
170 175 180	
tct tct acg att cgt gca tct cgg gtg tat ctg gaa gct cca tgg atc	691
Ser Ser Thr Ile Arg Ala Ser Arg Val Tyr Leu Glu Ala Pro Trp Ile	
185 190 195	
cga cac caa tac aaa ctg ctc aat gcc att gct cgg gtg cat tcc agc	739
Arg His Gln Tyr Lys Leu Leu Asn Ala Ile Ala Arg Val His Ser Ser	
200 205 210	
gaa gcg ctg ctg atc acc aaa tct ggc atc tgc acc ctc ttc ggc gag	787
Glu Ala Leu Leu Ile Thr Lys Ser Gly Ile Cys Thr Leu Phe Gly Glu	
215 220 225	
caa gat gac gta gcc cac att att gat ctg ttc aac agt ctt aat cga	835
Gln Asp Asp Val Ala His Ile Ile Asp Leu Phe Asn Ser Leu Asn Arg	
230 235 240 245	
caa cgt gcc cac ttc atg aaa acg tca gca ggt gcc cga att gcc caa	883
Gln Arg Ala His Phe Met Lys Thr Ser Ala Gly Ala Arg Ile Ala Gln	
250 255 260	
tta aat ggc gaa aca agc tca tat cgc cgt agt ttt atg atc tcc tac	931
Leu Asn Gly Glu Thr Ser Ser Tyr Arg Arg Ser Phe Met Ile Ser Tyr	
265 270 275	
gcc agc caa atc tct aga ctt ctc atc tca gca aaa gag gat gca ttc	979
Ala Ser Gln Ile Ser Arg Leu Leu Ile Ser Ala Lys Glu Asp Ala Phe	
280 285 290	
aac gaa cta gct ggt cag gca cca cta gct cac agc gcc atc gtt cct	1027
Asn Glu Leu Ala Gly Gln Ala Pro Leu Ala His Ser Ala Ile Val Pro	
295 300 305	
gtc cta gag aac aga agt gtg agg tca aag gaa gca ctg aag gaa acc	1075
Val Leu Glu Asn Arg Ser Val Arg Ser Lys Glu Ala Leu Lys Glu Thr	
310 315 320 325	
ttc ccg aat atg cgg aca atg acc ttc aaa tcg acc aac cga cga ggc	1123
Phe Pro Asn Met Arg Thr Met Thr Phe Lys Ser Thr Asn Arg Arg Gly	

330

335

340

att att gac gga ttt aat gct gcc aat gaa tcc cac ctt ggc ggg gaa 1171
Ile Ile Asp Gly Phe Asn Ala Ala Asn Glu Ser His Leu Gly Gly Glu
345 350 355

tct gcc agc ttg gaa gac tca aca ttc atg ttc tagagcgggt gaaagcccca 1224
Ser Ala Ser Leu Glu Asp Ser Thr Phe Met Phe
360 365

ttt 1227

<210> 1708

<211> 368

<212> PRT

<213> Corynebacterium glutamicum

<400> 1708

Met Thr Leu Ser His Phe Ser Asp Asn Val Thr Asp Ala Gln Asp Ser
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Tyr Arg Gln Ile Leu Glu Glu Ser Ile Ile Ser His Leu Gly Phe Cys
20 25 30

Ala Leu Arg Gly Trp Thr Pro Ala Asp Leu Arg His Glu Phe Ser Ala
35 40 45

Asp Ile Asp Pro Leu Leu Phe His Ala Leu Pro Glu Ile Ala Tyr Ser
50 55 60

Cys Ser Asp Glu Met Tyr Thr Leu Trp Val Asn Gly Thr Arg Ala Ala
65 70 75 80

Glu Thr Ser His Leu Pro Val Met Thr Leu Glu Lys Ile Leu Thr Glu
85 90 95

Leu Pro Lys Leu Ser Thr Leu Pro Asp Trp Ala Met Leu Ala Glu Leu
100 105 110

His Ala Leu Asp Asn Gln Asp Thr Ser Pro Met Thr Pro Ala Gln Ala
115 120 125

Lys Ala His His Arg Ile Thr Ala Leu Leu Lys Lys Ala Glu Ser Thr
130 135 140

Asn Phe Glu Glu Glu Ala Glu Ala Leu Ile Leu Lys Ala Glu Thr Leu
145 150 155 160

Arg Gln Gln Tyr Arg Ile Glu Ser Leu Leu Ile Asn Ser Tyr Asp Gln
165 170 175

Asp Val Gln Ala Arg Ser Ser Thr Ile Arg Ala Ser Arg Val Tyr Leu
180 185 190

Glu Ala Pro Trp Ile Arg His Gln Tyr Lys Leu Leu Asn Ala Ile Ala
195 200 205

Arg Val His Ser Ser Glu Ala Leu Leu Ile Thr Lys Ser Gly Ile Cys
210 215 220

Thr Leu Phe Gly Glu Gln Asp Asp Val Ala His Ile Ile Asp Leu Phe
 225 230 235 240
 Asn Ser Leu Asn Arg Gln Arg Ala His Phe Met Lys Thr Ser Ala Gly
 245 250 255
 Ala Arg Ile Ala Gln Leu Asn Gly Glu Thr Ser Ser Tyr Arg Arg Ser
 260 265 270
 Phe Met Ile Ser Tyr Ala Ser Gln Ile Ser Arg Leu Leu Ile Ser Ala
 275 280 285
 Lys Glu Asp Ala Phe Asn Glu Leu Ala Gly Gln Ala Pro Leu Ala His
 290 295 300
 Ser Ala Ile Val Pro Val Leu Glu Asn Arg Ser Val Arg Ser Lys Glu
 305 310 315 320
 Ala Leu Lys Glu Thr Phe Pro Asn Met Arg Thr Met Thr Phe Lys Ser
 325 330 335
 Thr Asn Arg Arg Gly Ile Ile Asp Gly Phe Asn Ala Ala Asn Glu Ser
 340 345 350
 His Leu Gly Gly Glu Ser Ala Ser Leu Glu Asp Ser Thr Phe Met Phe
 355 360 365

<210> 1709

<211> 768

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(745)

<223> RXA00325

<400> 1709

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 accgcggttg cggccacgca ggctcacaaa ggacaccact atg aca agc att att 115
 Met Thr Ser Ile Ile
 1 5
 gca agc aac agc gac cta tcg gag gcg ctg cgc acc cac act gcg cag 163
 Ala Ser Asn Ser Asp Leu Ser Glu Ala Leu Arg Thr His Thr Ala Gln
 10 15 20
 gcc cat gaa gag gcc gag cac tca acg ttt atg aat gat ctg ctc acc 211
 Ala His Glu Glu Ala Glu His Ser Thr Phe Met Asn Asp Leu Leu Thr
 25 30 35
 ggg aag ctc gat gcg cag gca ttt atc aag ttg cag gag caa tca tgg 259
 Gly Lys Leu Asp Ala Gln Ala Phe Ile Lys Leu Gln Glu Gln Ser Trp
 40 45 50
 ttg ttc tac acc gct ttg gaa gct gca gct cgt gca tgt gca gag gat 307
 Leu Phe Tyr Thr Ala Leu Glu Ala Ala Ala Arg Ala Cys Ala Glu Asp
 55 60 65

tcc cgt gcg gct ggt ctg ctg gac cca cgc ctc gag cgc aag gaa acg 355
 Ser Arg Ala Ala Gly Leu Leu Asp Pro Arg Leu Glu Arg Lys Glu Thr
 70 75 80 85

ttg gaa gct gat ctg gat aag ctg cac gaa aac acc acc tgg cgt gac 403
 Leu Glu Ala Asp Leu Asp Lys Leu His Glu Asn Thr Thr Trp Arg Asp
 90 95 100

aac gtc acg gcc act gca gcg aca gcg tct tat gtg gaa cgt ctt gaa 451
 Asn Val Thr Ala Thr Ala Ala Thr Ala Ser Tyr Val Glu Arg Leu Glu
 105 110 115

agc atc gaa gcg gcc aag gat ttc cct cgt ttg gtt gct cat cac tat 499
 Ser Ile Glu Ala Ala Lys Asp Phe Pro Arg Leu Val Ala His His Tyr
 120 125 130

gtc cgc tac ctg ggt gat ttg tcc ggt ggg cag gtt att gca cgt ctg 547
 Val Arg Tyr Leu Gly Asp Leu Ser Gly Gly Gln Val Ile Ala Arg Leu
 135 140 145

gtg aac agg gaa tat gga gtt tcg gaa gag gcg ttg agc ttc tac tgc 595
 Val Asn Arg Glu Tyr Gly Val Ser Glu Glu Ala Leu Ser Phe Tyr Cys
 150 155 160 165

ttt gaa gat ctt ggc aag ctc aaa ccg tac aag gat aat tac cgt gca 643
 Phe Glu Asp Leu Gly Lys Leu Lys Pro Tyr Lys Asp Asn Tyr Arg Ala
 170 175 180

gag ctt gat gct ttg gaa tta aca gca gag gag cgt gct gcg ttg ctg 691
 Glu Leu Asp Ala Leu Glu Leu Thr Ala Glu Glu Arg Ala Ala Leu Leu
 185 190 195

gat gaa gca tct gat gcg ttc agg ttt aat cag caa gtt ttt cag gct 739
 Asp Glu Ala Ser Asp Ala Phe Arg Phe Asn Gln Gln Val Phe Gln Ala
 200 205 210

ctt gct taaccgaagg tgaagtcttg gcg 768
 Leu Ala
 215

<210> 1710
 <211> 215
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1710
 Met Thr Ser Ile Ile Ala Ser Asn Ser Asp Leu Ser Glu Ala Leu Arg
 1 5 10 15

Thr His Thr Ala Gln Ala His Glu Glu Ala Glu His Ser Thr Phe Met
 20 25 30

Asn Asp Leu Leu Thr Gly Lys Leu Asp Ala Gln Ala Phe Ile Lys Leu
 35 40 45

Gln Glu Gln Ser Trp Leu Phe Tyr Thr Ala Leu Glu Ala Ala Ala Arg
 50 55 60

Ala Cys Ala Glu Asp Ser Arg Ala Ala Gly Leu Leu Asp Pro Arg Leu
 65 70 75 80

cgc gaa gac ggc ccc atc tac gca gat gat ctg atc gat gag gat gag 355
 Arg Glu Asp Gly Pro Ile Tyr Ala Asp Asp Leu Ile Asp Glu Asp Glu
 70 75 80 85
 gac tac cgc gca cag acc aag agc cag atc aac gac gag gtt atc aac 403
 Asp Tyr Arg Ala Gln Thr Lys Ser Gln Ile Asn Asp Glu Val Ile Asn
 90 95 100
 gag atc cgc gat ggt att tca agc ttc gtt gat ggc atc gta aat ggc 451
 Glu Ile Arg Asp Gly Ile Ser Ser Phe Val Asp Gly Ile Val Asn Gly
 105 110 115
 ctt ggc cag ggt cgc cgc ggt gga cgt tac ggt gat ttc ggt ggg cca 499
 Leu Gly Gln Gly Arg Arg Gly Gly Arg Tyr Gly Asp Phe Gly Gly Pro
 120 125 130
 cgc ggc cct cgc ggt cca cgc aat gac ggt cca ttc ggc cca ttt gga 547
 Arg Gly Pro Arg Gly Pro Arg Asn Asp Gly Pro Phe Gly Pro Phe Gly
 135 140 145
 cca ttc ggt ccg gga tac cgc ggt ccg cgt ttc tagcgggttac ggtaggggttt 600
 Pro Phe Gly Pro Gly Tyr Arg Gly Pro Arg Phe
 150 155 160
 tag 603

<210> 1712

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1712

Met Ala Ile Lys Leu Ser Ile Asp Leu Ser Asp Ala Thr Phe Ala Glu
 1 5 10 15
 Leu Ser Ala Val Ile Gly Tyr Ala His Gln Leu Gly Val Asp Ala Asp
 20 25 30
 Glu Lys Leu Thr Phe Glu Gly Thr Val Leu Asn Ile Glu Phe Asp Gly
 35 40 45
 Asp Leu Gln Phe Asp Asp Val Phe Asp Ala Phe Asp Glu Ala Glu Ile
 50 55 60
 Glu Leu Asp Asn Pro Arg Glu Asp Gly Pro Ile Tyr Ala Asp Asp Leu
 65 70 75 80
 Ile Asp Glu Asp Glu Asp Tyr Arg Ala Gln Thr Lys Ser Gln Ile Asn
 85 90 95
 Asp Glu Val Ile Asn Glu Ile Arg Asp Gly Ile Ser Ser Phe Val Asp
 100 105 110
 Gly Ile Val Asn Gly Leu Gly Gln Gly Arg Arg Gly Gly Arg Tyr Gly
 115 120 125
 Asp Phe Gly Gly Pro Arg Gly Pro Arg Gly Pro Arg Asn Asp Gly Pro
 130 135 140

Phe Gly Pro Phe Gly Pro Phe Gly Pro Gly Tyr Arg Gly Pro Arg Phe
 145 150 155 160

<210> 1713

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXA00336

<400> 1713

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gcagtatccg ccctctacat gtttggattt gattgtaaca atg gca aag ccg aag 115
                                         Met Ala Lys Pro Lys
                                         1 5

aga agt tgg ctt gac gga ccc gaa att cca gct gat ttt gac gat cct 163
Arg Ser Trp Leu Asp Gly Pro Glu Ile Pro Ala Asp Phe Asp Asp Pro
          10          15          20

gat gca ccc ggc agg tgg cct ggc gaa aag ttg ggg ctt cct caa gaa 211
Asp Ala Pro Gly Arg Trp Pro Gly Glu Lys Leu Gly Leu Pro Gln Glu
          25          30          35

ggg gcc ggc tct ctg tcc tca gtg gct cgt cgt atc ggc ggg gtc tgc 259
Gly Ala Gly Ser Leu Ser Ser Val Ala Arg Arg Ile Gly Gly Val Cys
          40          45          50

gtg gac tgg ggt gtt tcc tgg gtt att gct att gtg ctg tcc aat ttc 307
Val Asp Trp Gly Val Ser Trp Val Ile Ala Ile Val Leu Ser Asn Phe
          55          60          65

acg gat gtg ctg ggc gat gta gcg aca tcc acg ctc att att ttc gtg 355
Thr Asp Val Leu Gly Asp Val Ala Thr Ser Thr Leu Ile Ile Phe Val
          70          75          80          85

atc ctg ggt tgg ctt acc ggt tgg atc ttt gct cgc acc cca ggt cat 403
Ile Leu Gly Trp Leu Thr Gly Trp Ile Phe Ala Arg Thr Pro Gly His
          90          95          100

gcc gtg ttt ggc atg ggc ctt gcg cgt gtg gat gca gag gaa cgt gtg 451
Ala Val Phe Gly Met Gly Leu Ala Arg Val Asp Ala Glu Glu Arg Val
          105          110          115

ggc tgg tgg cgt gcg ctg gtt cgc cca ctg ctg acg atc ttg att ctg 499
Gly Trp Trp Arg Ala Leu Val Arg Pro Leu Leu Thr Ile Leu Ile Leu
          120          125          130

cct gcc gtg atg gtg gat gct gac ggc cgt ggg ctc cac gac aag gca 547
Pro Ala Val Met Val Asp Ala Asp Gly Arg Gly Leu His Asp Lys Ala
          135          140          145

acg gga act gca gtt atc cgc ggg taatttgtct tgagtgaaat tta 594
Thr Gly Thr Ala Val Ile Arg Gly
150 155

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<210> 1714

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1714

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Met Ala Lys Pro Lys Arg Ser Trp Leu Asp Gly Pro Glu Ile Pro Ala
 1              5              10              15

Asp Phe Asp Asp Pro Asp Ala Pro Gly Arg Trp Pro Gly Glu Lys Leu
          20              25              30

Gly Leu Pro Gln Glu Gly Ala Gly Ser Leu Ser Ser Val Ala Arg Arg
          35              40              45

Ile Gly Gly Val Cys Val Asp Trp Gly Val Ser Trp Val Ile Ala Ile
          50              55              60

Val Leu Ser Asn Phe Thr Asp Val Leu Gly Asp Val Ala Thr Ser Thr
          65              70              75              80

Leu Ile Ile Phe Val Ile Leu Gly Trp Leu Thr Gly Trp Ile Phe Ala
          85              90              95

Arg Thr Pro Gly His Ala Val Phe Gly Met Gly Leu Ala Arg Val Asp
          100             105             110

Ala Glu Glu Arg Val Gly Trp Trp Arg Ala Leu Val Arg Pro Leu Leu
          115             120             125

Thr Ile Leu Ile Leu Pro Ala Val Met Val Asp Ala Asp Gly Arg Gly
          130             135             140

Leu His Asp Lys Ala Thr Gly Thr Ala Val Ile Arg Gly
145              150              155

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<210> 1715

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(525)

<223> RXA00337

<400> 1715

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gat gtg gag gga ggc gtc gaa aag cat tct tta agc act gcg gac att    48
Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr Ala Asp Ile
 1              5              10              15

gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt ttg ggg cgg    96
Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val Leu Gly Arg
          20              25              30

cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc ccg ttg ggc    144
Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala Arg Leu Gly
          35              40              45

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115	120	125
Arg His Thr Glu Ala Leu	Arg Gly Glu Thr Gly His	Ile Ser Val Val
130	135	140
Asp Tyr Ala Asp Gly Ser Val	Thr Gln Ala Pro His	Pro Val Ser Arg
145	150	155 160
Ser Ala Gly Leu Ser Ala Phe	Val Ala Ala Ala Gln Thr	Glu Thr
165	170	175

<210> 1717
 <211> 840
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(817)
 <223> RXA00339

<400> 1717

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acagggttgaa gttgatgtga ttctgatccg cacagacccc tggaccatgt ctgcgcgagc 60
agtgaactaa attcttgaga actaaaaaag gagaacttca atg aag ctg gac cca 115
                               Met Lys Leu Asp Pro
                               1 5
tct ctg cac aaa acc ctg ctg cag ctc gcc acc acc ctg cgc acc caa 163
Ser Leu His Lys Thr Leu Leu Gln Leu Ala Thr Thr Leu Arg Thr Gln
                               10 15 20
aac gcc aac tcc gca ccg aag acc acc ccg gag cag gaa gct gta gac 211
Asn Ala Asn Ser Ala Pro Lys Thr Thr Pro Glu Gln Glu Ala Val Asp
                               25 30 35
aag gct gtc gct gaa ctt tcc cgc aac cgc gac gct gca tcc gct gga 259
Lys Ala Val Ala Glu Leu Ser Arg Asn Arg Asp Ala Ala Ser Ala Gly
                               40 45 50
caa atg gct gtc gat gac atg gaa aac gaa atc ctg cgc att cag tcc 307
Gln Met Ala Val Asp Asp Met Glu Asn Glu Ile Leu Arg Ile Gln Ser
                               55 60 65
gac gaa cgc aaa ctg cgc cgc cgc aag aaa gac ggc cag gac gca ctc 355
Asp Glu Arg Lys Leu Arg Arg Arg Lys Lys Asp Gly Gln Asp Ala Leu
                               70 75 80 85
ggt gca gaa act gac gaa gag cgt cgc cgc gac ctc aac cac gac gtc 403
Gly Ala Glu Thr Asp Glu Glu Arg Arg Arg Asp Leu Asn His Asp Val
                               90 95 100
tac act gcg aag tcc cgc atc gct gac ctc atg agc gaa ctg caa gaa 451
Tyr Thr Ala Lys Ser Arg Ile Ala Asp Leu Met Ser Glu Leu Gln Glu
                               105 110 115
gct cac aat gaa atc cat gcg ctg cgc aac aac cgc gac ctc gca cag 499
Ala His Asn Glu Ile His Ala Leu Arg Asn Asn Arg Asp Leu Ala Gln
                               120 125 130

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tct cgc gtc aaa gac acc gaa cgc aaa gtt gcc gac gcc cgc gca gcc 547
 Ser Arg Val Lys Asp Thr Glu Arg Lys Val Ala Asp Ala Arg Ala Ala
 135 140 145

gca gaa gcc gcc gca gca gca acc cca gaa ggt gaa gac cca gca gta 595
 Ala Glu Ala Ala Ala Ala Ala Thr Pro Glu Gly Glu Asp Pro Ala Val
 150 155 160 165

gtc atc gca cac ctg gaa gag aaa ctt ccc tcc gaa gca ctg gca gaa 643
 Val Ile Ala His Leu Glu Glu Lys Leu Pro Ser Glu Ala Leu Ala Glu
 170 175 180

ttc cat gca caa cgc ctc gaa aac ggc gta ggc gca gca ctc ttc aac 691
 Phe His Ala Gln Arg Leu Glu Asn Gly Val Gly Ala Ala Leu Phe Asn
 185 190 195

ggc cgc tcc tgc agc gga tgc gcc atg gtt ctc cct gca acc ggt atc 739
 Gly Arg Ser Cys Ser Gly Cys Ala Met Val Leu Pro Ala Thr Gly Ile
 200 205 210

tcc gac atc cgc aac acc ccc aaa gat gag gtt cca cag tgc cca gaa 787
 Ser Asp Ile Arg Asn Thr Pro Lys Asp Glu Val Pro Gln Cys Pro Glu
 215 220 225

tgt ggc tct tac ctc atc act gac atc tct tagaaagacc acccagtgaa 837
 Cys Gly Ser Tyr Leu Ile Thr Asp Ile Ser
 230 235

att 840

<210> 1718

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 1718

Met Lys Leu Asp Pro Ser Leu His Lys Thr Leu Leu Gln Leu Ala Thr
 1 5 10 15

Thr Leu Arg Thr Gln Asn Ala Asn Ser Ala Pro Lys Thr Thr Pro Glu
 20 25 30

Gln Glu Ala Val Asp Lys Ala Val Ala Glu Leu Ser Arg Asn Arg Asp
 35 40 45

Ala Ala Ser Ala Gly Gln Met Ala Val Asp Asp Met Glu Asn Glu Ile
 50 55 60

Leu Arg Ile Gln Ser Asp Glu Arg Lys Leu Arg Arg Arg Lys Lys Asp
 65 70 75 80

Gly Gln Asp Ala Leu Gly Ala Glu Thr Asp Glu Glu Arg Arg Arg Asp
 85 90 95

Leu Asn His Asp Val Tyr Thr Ala Lys Ser Arg Ile Ala Asp Leu Met
 100 105 110

Ser Glu Leu Gln Glu Ala His Asn Glu Ile His Ala Leu Arg Asn Asn
 115 120 125

Arg Asp Leu Ala Gln Ser Arg Val Lys Asp Thr Glu Arg Lys Val Ala
 130 135 140
 Asp Ala Arg Ala Ala Ala Glu Ala Ala Ala Ala Thr Pro Glu Gly
 145 150 155 160
 Glu Asp Pro Ala Val Val Ile Ala His Leu Glu Glu Lys Leu Pro Ser
 165 170 175
 Glu Ala Leu Ala Glu Phe His Ala Gln Arg Leu Glu Asn Gly Val Gly
 180 185 190
 Ala Ala Leu Phe Asn Gly Arg Ser Cys Ser Gly Cys Ala Met Val Leu
 195 200 205
 Pro Ala Thr Gly Ile Ser Asp Ile Arg Asn Thr Pro Lys Asp Glu Val
 210 215 220
 Pro Gln Cys Pro Glu Cys Gly Ser Tyr Leu Ile Thr Asp Ile Ser
 225 230 235

<210> 1719

<211> 1082

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1059)

<223> RXA00349

<400> 1719

gag aaa atc ctg gac gag ttg gag caa tcc cct gcg tct tat ggt ttc 48
 Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr Gly Phe
 1 5 10 15
 cct gtt gcg ttg ctt ggc tgg cca atg atg ggt ggt gct gtt gct gtg 96
 Pro Val Ala Leu Leu Gly Trp Pro Met Met Gly Gly Ala Val Ala Val
 20 25 30
 ctg ttg ggt ggt gga tgc cag gtt tcc cta att gct ttt att acc gcg 144
 Leu Leu Gly Gly Gly Cys Gln Val Ser Leu Ile Ala Phe Ile Thr Ala
 35 40 45
 ttc acg atc att gcc acg acg tca ttt ttg gga aag aag ggt ttg cct 192
 Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly Leu Pro
 50 55 60
 act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg ctg cct gca 240
 Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu Pro Ala
 65 70 75 80
 tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag atc aaa ccg 288
 Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile Lys Pro
 85 90 95
 agc cag atc atc gca tct gga att gtt gtg ctg ttg gca ggt ttg aca 336
 Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala Gly Leu Thr
 100 105 110

ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg gtg aca gca Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val Thr Ala 115 120 125	384
agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc att gtt gct Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile Val Ala 130 135 140	432
ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat gtc atg ttg Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val Met Leu 145 150 155 160	480
cct gcc atg gag tcc gct gca gca cct aat tat tcg tct aca ttc gcc Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr Phe Ala 165 170 175	528
cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca gtg ggt tgt Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val Gly Cys 180 185 190	576
tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act gcg ctg atg Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala Leu Met 195 200 205	624
ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc ccc gtc tct Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro Val Ser 210 215 220	672
gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt ggt ttg ctt Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly Leu Leu 225 230 235 240	720
gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att gcc ggc atc Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala Gly Ile 245 250 255	768
aca cca atg ctt cca ggt cta gca att tac cgc gga atg tac gcc acc Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr Ala Thr 260 265 270	816
ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg gtt gct tta Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val Ala Leu 275 280 285	864
gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt gag tgg att Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu Trp Ile 290 295 300	912
gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac cgt gca ttt Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg Ala Phe 305 310 315 320	960
acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag cag aat cag Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln Asn Gln 325 330 335	1008
cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc ggt aat aaa Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly Asn Lys 340 345 350	1056
agg taaaaatcaa cctgcttagg cgt	1082

Arg

<210> 1720

<211> 353

<212> PRT

<213> Corynebacterium glutamicum

<400> 1720

Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr Gly Phe
 1 5 10 15

Pro Val Ala Leu Leu Gly Trp Pro Met Met Gly Gly Ala Val Ala Val
 20 25 30

Leu Leu Gly Gly Gly Cys Gln Val Ser Leu Ile Ala Phe Ile Thr Ala
 35 40 45

Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly Leu Pro
 50 55 60

Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu Pro Ala
 65 70 75 80

Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile Lys Pro
 85 90 95

Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala Gly Leu Thr
 100 105 110

Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val Thr Ala
 115 120 125

Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile Val Ala
 130 135 140

Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val Met Leu
 145 150 155 160

Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr Phe Ala
 165 170 175

Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val Gly Cys
 180 185 190

Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala Leu Met
 195 200 205

Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro Val Ser
 210 215 220

Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly Leu Leu
 225 230 235 240

Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala Gly Ile
 245 250 255

Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr Ala Thr
 260 265 270

Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val Ala Leu
 275 280 285

Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu Trp Ile
 290 295 300

Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg Ala Phe
 305 310 315 320

Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln Asn Gln
 325 330 335

Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly Asn Lys
 340 345 350

Arg

<210> 1721

<211> 149

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(126)

<223> RXA00355

<400> 1721

atc gct ttc ggt cgc gca gct cac cgc atg aag cag cag ggc caa agc 48
 Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys Gln Gln Gly Gln Ser
 1 5 10 15

gga gct ttc acc gtc ctc gaa gtt gct cca tac ctg ctc tcc cca gag 96
 Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu
 20 25 30

aac ttg gac gat ctg atc gca cgc gac gtc taatttagct cgaggggcaa 146
 Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
 35 40

gga 149

<210> 1722

<211> 42

<212> PRT

<213> Corynebacterium glutamicum

<400> 1722

Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys Gln Gln Gly Gln Ser
 1 5 10 15

Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu
 20 25 30

Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
 35 40

<210> 1724
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1724
 Met Phe Pro Ser Pro Ala Thr Gly Gly Asp Asp Ile Asn Arg Arg Pro
 1 5 10 15
 Leu Asn Glu Pro Asn Ala Asp Ala Thr Thr Ile Pro Thr Ala Leu Lys
 20 25 30
 Val Val Phe Trp Met Leu Phe Ala Thr Ala Ala Phe Met Ile Phe Thr
 35 40 45
 Gly Leu Val Met Tyr Thr Ala Gly Tyr Thr Gly Pro Asp Asp Val Asp
 50 55 60
 Glu Ser Tyr Lys Ala Val Val Val Asn Asn Gln Glu Phe Ile Gly Gly
 65 70 75 80
 Ile Asn Ala Phe Ala Gly Val Val Ile Ala Ala Leu Thr Ser Gln Leu
 85 90 95
 Pro Lys Gly Gly Lys Asn Pro Arg Arg Leu Leu Leu Ala Ile Met Leu
 100 105 110
 Leu Val Leu Leu Thr Asp Leu Leu Ser Phe Ala Thr Arg Ala Gly Gly
 115 120 125
 Phe Ala Leu Ala Ile Ile Ala Val Leu Leu Ala Leu Glu Ala Leu Leu
 130 135 140
 Met Phe Arg Pro Ala Val Asn Asp His Ile Asp Arg Asn His Met Ala
 145 150 155 160
 Arg Val Met Asn Arg Glu Lys
 165

<210> 1725
 <211> 744
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(721)
 <223> RXA00380

<400> 1725
 caggcaatgc gacctgcct cagtgacatc cttggtgttc caagacgatc aaattgtcgg 60
 cgtgcattac aacgaaccag ctcaggagat ttgatcactc gtg cgt ttg acc aaa 115
 Val Arg Leu Thr Lys
 1 5
 cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta 163
 Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val
 10 15 20

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gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc 211
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly
      25                      30                      35

gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac 259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr
      40                      45                      50

gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc 307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu
      55                      60                      65

atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt 355
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val
      70                      75                      80                      85

gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa 403
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu
      90                      95                      100

tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac 451
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn
      105                      110                      115

ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac 499
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr
      120                      125                      130

tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac 547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr
      135                      140                      145

cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt 595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly
      150                      155                      160                      165

gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac 643
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His
      170                      175                      180

cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg 691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu
      185                      190                      195

gat gtt gcg ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt 741
Asp Val Ala Leu Pro Leu Val Asp Glu Ala
      200                      205

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agc

744

<210> 1726

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 1726

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Val Arg Leu Thr Lys Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser
  1                      5                      10                      15

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Gly Leu Ala Leu Val Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp
 20 25 30
 Ala Val Ala Val Gly Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys
 35 40 45
 Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
 50 55 60
 Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
 65 70 75 80
 Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
 85 90 95
 Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
 100 105 110
 Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
 115 120 125
 Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
 130 135 140
 Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
 145 150 155 160
 Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
 165 170 175
 Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
 180 185 190
 Ser Lys Asp Val Leu Asp Val Ala Leu Pro Leu Val Asp Glu Ala
 195 200 205

<210> 1727

<211> 836

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(813)

<223> RXA00387

<400> 1727

caa aac gac cca gaa acc tgg gaa gac tac gaa ctt cgc gtc aac cac 48
 Gln Asn Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His
 1 5 10 15
 cca ctg cgc atc gaa ggc gac cgc gtc tac ctt cag ggc cac ggc ttc 96
 Pro Leu Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe
 20 25 30
 gcc cca aca ttc acc gtg acc tgg cca aat ggc gag acc cgc acc cag 144
 Ala Pro Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln
 35 40 45
 acc gtg cag tgg cgc cca gac gac ccg acc ttc ttc ctg tcc tca ggc 192

Thr	Val	Gln	Trp	Arg	Pro	Asp	Asp	Pro	Thr	Phe	Phe	Leu	Ser	Ser	Gly		
50						55					60						
gtg	gtc	cgt	ttc	gat	cca	ccc	gcc	ggc	atg	tac	cca	gac	ctt	tac	gag	240	
Val	Val	Arg	Phe	Asp	Pro	Pro	Ala	Gly	Met	Tyr	Pro	Asp	Leu	Tyr	Glu		
65					70				75						80		
cgc	cgc	caa	aac	cag	ttg	gcc	atc	cag	gga	ctt	ttc	gca	ccg	acc	gcg	288	
Arg	Arg	Gln	Asn	Gln	Leu	Ala	Ile	Gln	Gly	Leu	Phe	Ala	Pro	Thr	Ala		
				85				90						95			
gaa	tgg	gaa	ggc	gac	aac	aac	gaa	ctg	ctg	acc	tcc	tcc	tac	ccg	gcg	336	
Glu	Trp	Glu	Gly	Asp	Asn	Asn	Glu	Leu	Leu	Thr	Ser	Ser	Tyr	Pro	Ala		
			100				105						110				
atg	cgt	gac	cca	gcc	gtg	gcg	atc	gat	att	tac	cgc	ggc	gac	aat	ggc	384	
Met	Arg	Asp	Pro	Ala	Val	Ala	Ile	Asp	Ile	Tyr	Arg	Gly	Asp	Asn	Gly		
		115				120						125					
ctc	gat	acc	ggc	atc	gga	cag	tca	ttg	ttc	agc	ctg	gac	tct	agt	ctc	432	
Leu	Asp	Thr	Gly	Ile	Gly	Gln	Ser	Leu	Phe	Ser	Leu	Asp	Ser	Ser	Leu		
	130				135						140						
atg	cac	agc	ggc	gtg	ctg	caa	aaa	att	gag	cgc	gtc	aac	ctc	caa	atc	480	
Met	His	Ser	Gly	Val	Leu	Gln	Lys	Ile	Glu	Arg	Val	Asn	Leu	Gln	Ile		
145					150				155						160		
ggc	gac	acc	gtc	acc	ctg	gat	gat	ggc	acc	acc	gtc	tcc	ttc	gac	ggc	528	
Gly	Asp	Thr	Val	Thr	Leu	Asp	Asp	Gly	Thr	Thr	Val	Ser	Phe	Asp	Gly		
				165				170						175			
gcg	tca	gaa	ttt	gcc	aac	tac	cag	atc	agc	cgc	gac	ccc	aca	caa	aac	576	
Ala	Ser	Glu	Phe	Ala	Asn	Tyr	Gln	Ile	Ser	Arg	Asp	Pro	Thr	Gln	Asn		
			180				185						190				
tgg	gtg	ctg	gtc	acc	acc	gtg	att	tcg	ctg	gtc	tcc	ctg	gtt	gga	tcc	624	
Trp	Val	Leu	Val	Thr	Thr	Val	Ile	Ser	Leu	Val	Ser	Leu	Val	Gly	Ser		
		195				200						205					
ctg	atg	atc	cga	cgc	cgc	cgc	att	tgg	gtg	cgt	ttc	tat	cca	caa	gaa	672	
Leu	Met	Ile	Arg	Arg	Arg	Arg	Ile	Trp	Val	Arg	Phe	Tyr	Pro	Gln	Glu		
	210				215						220						
aac	gga	acc	acc	cgc	gtg	gaa	acc	ggc	gga	ctt	gcc	cgc	acc	gac	cgc	720	
Asn	Gly	Thr	Thr	Arg	Val	Glu	Thr	Gly	Gly	Leu	Ala	Arg	Thr	Asp	Arg		
225					230				235						240		
gca	ggc	tgg	ggt	ggc	gaa	tac	gag	aaa	ttc	cac	cgc	gaa	ctg	ctg	ggt	768	
Ala	Gly	Trp	Gly	Gly	Glu	Tyr	Glu	Lys	Phe	His	Arg	Glu	Leu	Leu	Gly		
			245				250						255				
ctg	aag	gag	gaa	gat	gaa	gac	gaa	gag	tac	ttc	gac	cac	gac	gac		813	
Leu	Lys	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Tyr	Phe	Asp	His	Asp	Asp			
			260				265						270				
taacaccgca	attttaaaggc	ttt														836	

<210> 1728

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 1728

Gln Asn Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His
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Pro Leu Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe
20 25 30
Ala Pro Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln
35 40 45
Thr Val Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly
50 55 60
Val Val Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu
65 70 75 80
Arg Arg Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala
85 90 95
Glu Trp Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala
100 105 110
Met Arg Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly
115 120 125
Leu Asp Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu
130 135 140
Met His Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile
145 150 155 160
Gly Asp Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly
165 170 175
Ala Ser Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn
180 185 190
Trp Val Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser
195 200 205
Leu Met Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu
210 215 220
Asn Gly Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg
225 230 235 240
Ala Gly Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly
245 250 255
Leu Lys Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
260 265 270

<210> 1729

<211> 987

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> RXA00392

<400> 1729

tgcttgaaat acgttcggca ggctatgggg gagtgtgaaa cgctattgtg aaatgaatag 60

ataggttcca tagtcgatcg aggaggagtc gcagaagttt atg tgg gtt ggt tat 115
 Met Trp Val Gly Tyr
 1 5

gcg gtt cga cag atc gcc agt gtt ttt ctt act ctt ttg cgc atg ctg 163
 Ala Val Arg Gln Ile Ala Ser Val Phe Leu Thr Leu Leu Arg Met Leu
 10 15 20

cca cta gca gcg cga aat cga gtt gcc agg gga cgc atc ccg gaa acc 211
 Pro Leu Ala Ala Arg Asn Arg Val Ala Arg Gly Arg Ile Pro Glu Thr
 25 30 35

ggc gat gtg gtg atc tca ttg acc acc cat ggg aag cga att aac tac 259
 Gly Asp Val Val Ile Ser Leu Thr Thr His Gly Lys Arg Ile Asn Tyr
 40 45 50

gtt cac ttc acc atc gaa tcg atc gca cgc ggc cat gtg aaa gca cca 307
 Val His Phe Thr Ile Glu Ser Ile Ala Arg Gly His Val Lys Ala Pro
 55 60 65

att gtg ctg tgg ttg gac aaa cca gac ttt gat gcg ccg tgg cct gcc 355
 Ile Val Leu Trp Leu Asp Lys Pro Asp Phe Asp Ala Pro Trp Pro Ala
 70 75 80 85

acc att aag cga ctt gtc gcc cgc ggt ctg caa gta cgg tgc agc gac 403
 Thr Ile Lys Arg Leu Val Ala Arg Gly Leu Gln Val Arg Cys Ser Asp
 90 95 100

ggc ttc tac ggc ccc cac acc aaa tac tgg aac caa ttc cga gaa atc 451
 Gly Phe Tyr Gly Pro His Thr Lys Tyr Trp Asn Gln Phe Arg Glu Ile
 105 110 115

cac ggc acc ggc gtg cgt gtc gcc acc gtc gac gat gac atg atc tac 499
 His Gly Thr Gly Val Arg Val Ala Thr Val Asp Asp Asp Met Ile Tyr
 120 125 130

ccc gag tgg ttc ctg cag cgc ttg ctt ttt att ggc gac ctg cgc atg 547
 Pro Glu Trp Phe Leu Gln Arg Leu Leu Phe Ile Gly Asp Leu Arg Met
 135 140 145

gat gcg gtt gtc gcc tac cgg gcg cac aga att gag ctt cgc gac gac 595
 Asp Ala Val Val Ala Tyr Arg Ala His Arg Ile Glu Leu Arg Asp Asp
 150 155 160 165

cga atg ctc ccg tac gtt aaa tgg agt gcc gca gac acc tca aaa gcg 643
 Arg Met Leu Pro Tyr Val Lys Trp Ser Ala Ala Asp Thr Ser Lys Ala
 170 175 180

tca ttc ctg cac ttt gcc acg gga gtg tca ggc gtt ttg tac ccc gtg 691
 Ser Phe Leu His Phe Ala Thr Gly Val Ser Gly Val Leu Tyr Pro Val
 185 190 195

acc ttc att gat tat gtg gtc tcc cag ggc gat gta ttc ctt gag aac 739
 Thr Phe Ile Asp Tyr Val Val Ser Gln Gly Asp Val Phe Leu Glu Asn

200	205	210	
tgc aag cgc gcc gat gac gta tgg ctg cat gcc tgc gca ctg cgc tct			787
Cys Lys Arg Ala Asp Asp Val Trp Leu His Ala Cys Ala Leu Arg Ser			
215	220	225	
gat cac cct att cgc cag gtc tac gct cag ccc cga cac ttc gct gtc			835
Asp His Pro Ile Arg Gln Val Tyr Ala Gln Pro Arg His Phe Ala Val			
230	235	240	245
gtg ccc acc acc caa gtg gga gca cta gtt gtt ggc aac acc ctc atg			883
Val Pro Thr Thr Gln Val Gly Ala Leu Val Val Gly Asn Thr Leu Met			
250	255	260	
ggt gga aat gat gag cag atc gcc aaa gtg tac acc gat gaa gat gtg			931
Gly Gly Asn Asp Glu Gln Ile Ala Lys Val Tyr Thr Asp Glu Asp Val			
265	270	275	
gca aaa cta gtt gca gcc agc aag aat gaa gac taaaacagct tcgcgatagc			984
Ala Lys Leu Val Ala Ala Ser Lys Asn Glu Asp			
280	285		
acg			987

<210> 1730

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 1730

Met Trp Val Gly Tyr Ala Val Arg Gln Ile Ala Ser Val Phe Leu Thr
1 5 10 15

Leu Leu Arg Met Leu Pro Leu Ala Ala Arg Asn Arg Val Ala Arg Gly
20 25 30

Arg Ile Pro Glu Thr Gly Asp Val Val Ile Ser Leu Thr Thr His Gly
35 40 45

Lys Arg Ile Asn Tyr Val His Phe Thr Ile Glu Ser Ile Ala Arg Gly
50 55 60

His Val Lys Ala Pro Ile Val Leu Trp Leu Asp Lys Pro Asp Phe Asp
65 70 75 80

Ala Pro Trp Pro Ala Thr Ile Lys Arg Leu Val Ala Arg Gly Leu Gln
85 90 95

Val Arg Cys Ser Asp Gly Phe Tyr Gly Pro His Thr Lys Tyr Trp Asn
100 105 110

Gln Phe Arg Glu Ile His Gly Thr Gly Val Arg Val Ala Thr Val Asp
115 120 125

Asp Asp Met Ile Tyr Pro Glu Trp Phe Leu Gln Arg Leu Leu Phe Ile
130 135 140

Gly Asp Leu Arg Met Asp Ala Val Val Ala Tyr Arg Ala His Arg Ile
145 150 155 160

Glu Leu Arg Asp Asp Arg Met Leu Pro Tyr Val Lys Trp Ser Ala Ala
 165 170 175
 Asp Thr Ser Lys Ala Ser Phe Leu His Phe Ala Thr Gly Val Ser Gly
 180 185 190
 Val Leu Tyr Pro Val Thr Phe Ile Asp Tyr Val Val Ser Gln Gly Asp
 195 200 205
 Val Phe Leu Glu Asn Cys Lys Arg Ala Asp Asp Val Trp Leu His Ala
 210 215 220
 Cys Ala Leu Arg Ser Asp His Pro Ile Arg Gln Val Tyr Ala Gln Pro
 225 230 235 240
 Arg His Phe Ala Val Val Pro Thr Thr Gln Val Gly Ala Leu Val Val
 245 250 255
 Gly Asn Thr Leu Met Gly Gly Asn Asp Glu Gln Ile Ala Lys Val Tyr
 260 265 270
 Thr Asp Glu Asp Val Ala Lys Leu Val Ala Ala Ser Lys Asn Glu Asp
 275 280 285

<210> 1731

<211> 456

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(433)

<223> RXA00394

<400> 1731

acccacttga acctctcctt aaatatttgc ttcaacctcc cacaatacgg aactttgagg 60
 cattcttggg tatcggtatg tattgagtag gtttgaatat gtg agt gag tcc aat 115
 Val Ser Glu Ser Asn 5
 1

acc ccc aat ctc cag aca cac caa gcg ccg gaa tta aac ccg gaa cta 163
 Thr Pro Asn Leu Gln Thr His Gln Ala Pro Glu Leu Asn Pro Glu Leu 20
 10 15

caa aaa gct gcc cgg aaa aac gtg ctg att tac ggt ctg gca cgt ttg 211
 Gln Lys Ala Ala Arg Lys Asn Val Leu Ile Tyr Gly Leu Ala Arg Leu 35
 25 30

ctt ctg ttc gtc gtg ctg acc ttg att att cat agc ctg gct ctg ctg 259
 Leu Leu Phe Val Val Leu Thr Leu Ile Ile His Ser Leu Ala Leu Leu 50
 40 45

att agt gcg cct gtg cca ctc gtt atg tct gcg atg ctg gct ctg att 307
 Ile Ser Ala Pro Val Pro Leu Val Met Ser Ala Met Leu Ala Leu Ile 65
 55 60

gtg gcg ttc cca ttg tcc atg ctg gtg ttc agc aaa ctg cgc atg aat 355
 Val Ala Phe Pro Leu Ser Met Leu Val Phe Ser Lys Leu Arg Met Asn 85
 70 75 80

gaa tgg gtt cga agc gag ctg gcg gac cgc taaaaaatcc cccctcgttct 453
Glu Trp Val Arg Ser Glu Leu Ala Asp Arg
105 110

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<210> 1732
<211> 111
<212> PRT
<213> Corynebacterium glutamicum
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Arg Lys Ala His Lys Glu Trp Val Arg Ser Glu Leu Ala Asp Arg
100 105 110

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<220>  
<221> CDS  
<222> (101)..(400)  
<223> RXA00395
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ctg att att ttg gtt atc gtc gca atc gtc ttg ctg tgg aag gcc ttc 163
Leu Ile Ile Leu Val Ile Val Ala Ile Val Leu Leu Trp Lys Ala Phe
10 15 20

aag cca tct aca tgg aag cgt aac gcg gag atc aat cag ggc cag gca 211
Lys Pro Ser Thr Trp Lys Arg Asn Ala Glu Ile Asn Gln Gly Gln Ala
25 30 35
cct cgt gca gtg aaa ggc ccc gac gat gat gaa gaa ttc ttg tgg aat 259
Pro Arg Ala Val Lys Gly Pro Asp Asp Asp Glu Glu Phe Leu Trp Asn
40 45 50
att gaa aag aat cgc ttc aaa cag cgt cgc gcc gac gag gct gcc caa 307
Ile Glu Lys Asn Arg Phe Lys Gln Arg Arg Ala Asp Glu Ala Ala Gln
55 60 65
tta gaa gag gaa gaa cgt ctc aaa cgg gcc agg gaa cgc tac gca aag 355
Leu Glu Glu Glu Glu Arg Leu Lys Arg Ala Arg Glu Arg Tyr Ala Lys
70 75 80 85
cct gaa agc tca gaa gaa ggt cca gag aag ccc act gag gat tct 400
Pro Glu Ser Ser Glu Glu Gly Pro Glu Lys Pro Thr Glu Asp Ser
90 95 100
taaaagggct tctttaaaaa gat 423

<210> 1734

<211> 100

<212> PRT

<213> Corynebacterium glutamicum

<400> 1734

Val Gly Arg Leu Leu Leu Ile Ile Leu Val Ile Val Ala Ile Val Leu
1 5 10 15
Leu Trp Lys Ala Phe Lys Pro Ser Thr Trp Lys Arg Asn Ala Glu Ile
20 25 30
Asn Gln Gly Gln Ala Pro Arg Ala Val Lys Gly Pro Asp Asp Asp Glu
35 40 45
Glu Phe Leu Trp Asn Ile Glu Lys Asn Arg Phe Lys Gln Arg Arg Ala
50 55 60
Asp Glu Ala Ala Gln Leu Glu Glu Glu Glu Arg Leu Lys Arg Ala Arg
65 70 75 80
Glu Arg Tyr Ala Lys Pro Glu Ser Ser Glu Glu Gly Pro Glu Lys Pro
85 90 95
Thr Glu Asp Ser
100

<210> 1735

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXA00396

<400> 1735

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gacaagacct acattttgag ccagcgctaa ggagaaccca gtg aca gaa att gca 115
Val Thr Glu Ile Ala
1 5

gaa aac ctt cag cgc ttg ggt att gaa tta cct gat cta cca gca ccg 163
Glu Asn Leu Gln Arg Leu Gly Ile Glu Leu Pro Asp Leu Pro Ala Pro
10 15 20

cag tat tcc tac gta ccg ttc aac cgc caa gga aac acc ctc tat gta 211
Gln Tyr Ser Tyr Val Pro Phe Asn Arg Gln Gly Asn Thr Leu Tyr Val
25 30 35

tcg ggg cag att tca cga acc gca gcg gga gac atc ctc gcc gga cga 259
Ser Gly Gln Ile Ser Arg Thr Ala Ala Gly Asp Ile Leu Ala Gly Arg
40 45 50

gtt ggc gaa gac gca aca tta gaa gaa gga atc cac gcc gca gag gta 307
Val Gly Glu Asp Ala Thr Leu Glu Glu Gly Ile His Ala Ala Glu Val
55 60 65

gcc acc atc aat ctg ctg gcc aga atc cac caa tcc atc ggt tta gac 355
Ala Thr Ile Asn Leu Leu Ala Arg Ile His Gln Ser Ile Gly Leu Asp
70 75 80 85

aat gtg gcc caa att ctg aaa ctg aat gtg tgg gtc aat agc tcc gat 403
Asn Val Ala Gln Ile Leu Lys Leu Asn Val Trp Val Asn Ser Ser Asp
90 95 100

gac ttt att cag cag cct caa gtg gcc gac ggt gca tcc cag ctc ctt 451
Asp Phe Ile Gln Gln Pro Gln Val Ala Asp Gly Ala Ser Gln Leu Leu
105 110 115

gag gca gtg ttg ggt gag gcc gga aaa cat gca cgc aca gca cta ccc 499
Glu Ala Val Leu Gly Glu Ala Gly Lys His Ala Arg Thr Ala Leu Pro
120 125 130

aca aat act ctc ccc cag gga gca cta gtg gaa ttg gat gct gtc gtt 547
Thr Asn Thr Leu Pro Gln Gly Ala Leu Val Glu Leu Asp Ala Val Val
135 140 145

gcg gtc acc gag gcc gcc gaa gtt taggacgcgt gggcgaaaat ttc 594
Ala Val Thr Glu Ala Ala Glu Val
150 155

<210> 1736

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1736

Val Thr Glu Ile Ala Glu Asn Leu Gln Arg Leu Gly Ile Glu Leu Pro
1 5 10 15

Asp Leu Pro Ala Pro Gln Tyr Ser Tyr Val Pro Phe Asn Arg Gln Gly
20 25 30

Asn Thr Leu Tyr Val Ser Gly Gln Ile Ser Arg Thr Ala Ala Gly Asp

35	40	45
Ile Leu Ala Gly Arg Val Gly Glu Asp Ala Thr Leu Glu Glu Gly Ile 50 55 60		
His Ala Ala Glu Val Ala Thr Ile Asn Leu Leu Ala Arg Ile His Gln 65 70 75 80		
Ser Ile Gly Leu Asp Asn Val Ala Gln Ile Leu Lys Leu Asn Val Trp 85 90 95		
Val Asn Ser Ser Asp Asp Phe Ile Gln Gln Pro Gln Val Ala Asp Gly 100 105 110		
Ala Ser Gln Leu Leu Glu Ala Val Leu Gly Glu Ala Gly Lys His Ala 115 120 125		
Arg Thr Ala Leu Pro Thr Asn Thr Leu Pro Gln Gly Ala Leu Val Glu 130 135 140		
Leu Asp Ala Val Val Ala Val Thr Glu Ala Ala Glu Val 145 150 155		

<210> 1737

<211> 563

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(540)

<223> RXA00397

<400> 1737

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ttc ccg atc aac gca gaa acc cga tgc att cag ctc gac gcc ggt gtt Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala Gly Val 20 25 30	96
gca gta aag aag gac ggc gtg gtg ctg ggt acc tca gat atg gcg agg Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met Ala Arg 35 40 45	144
tcc ctg cct cga acc gcc gct ggc caa gaa gcc tat gag tac ttc ttc Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr Phe Phe 50 55 60	192
aag gtg gtt cgt gaa ggc atc atc ggg cag ctg cgc ccg ggc gtg atc Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly Val Ile 65 70 75 80	240
tgc gct gac gtg cac gaa gca acc ctt gat tac cta agc ccg cag cta Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro Gln Leu 85 90 95	288
cct cgc atg att gac atc gga atg ctg ggt gcc gac acc gat ttc aac Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp Phe Asn	336

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      . 100                      105                      110
acc atc tac cgc aag cgc aat gtt ggc cac ctc atg ggc aag cag gaa 384
Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys Gln Glu
      115                      120                      125

tcc ttt gcc aat gag ctt cgc cct gga tac aag cac att ctt cac cac 432
Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu His His
      130                      135                      140

ggc tcc tat ggt gcc gcg gag atc cct tgg cgc tac aac ggt gta gcc 480
Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly Val Ala
      145                      150                      155

att ggt acc gag gat ctg tgg tac atc ggc gca gac aag acc tac att 528
Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr Tyr Ile
      165                      170                      175

ttg agc cag cgc taaggagaac ccagtgcag aaa 563
Leu Ser Gln Arg
      180

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<210> 1738
 <211> 180
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 1738
Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro Val Asp
  1                      5                      10                      15

Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala Gly Val
      20                      25                      30

Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met Ala Arg
      35                      40                      45

Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr Phe Phe
      50                      55                      60

Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly Val Ile
      65                      70                      75                      80

Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro Gln Leu
      85                      90                      95

Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp Phe Asn
      100                      105                      110

Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys Gln Glu
      115                      120                      125

Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu His His
      130                      135                      140

Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly Val Ala
      145                      150                      155                      160

Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr Tyr Ile
      165                      170                      175

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Leu Ser Gln Arg
180

<210> 1739

<211> 704

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(681)

<223> RXA00398

<400> 1739

tac	ctc	ccc	gag	cct	ttc	acc	gtg	gag	gat	tac	act	gcg	cgt	gtt	gaa	48
Tyr	Leu	Pro	Glu	Pro	Phe	Thr	Val	Glu	Asp	Tyr	Thr	Ala	Arg	Val	Glu	
1				5					10					15		

ggc	ctc	gaa	gtt	gct	ggc	gga	gcg	att	gtt	tcc	ggg	tct	ttc	cag	gct	96
Gly	Leu	Glu	Val	Ala	Gly	Gly	Ala	Ile	Val	Ser	Gly	Ser	Phe	Gln	Ala	
			20					25						30		

ttc	gac	cag	ggc	tac	ctc	aaa	gat	gct	ctc	gca	gtg	ctt	ggc	cca	ggc	144
Phe	Asp	Gln	Gly	Tyr	Leu	Lys	Asp	Ala	Leu	Ala	Val	Leu	Gly	Pro	Gly	
		35					40					45				

tat	gtc	ggg	gtc	act	cag	atc	ccc	gca	gat	acc	tct	gat	cag	gag	att	192
Tyr	Val	Gly	Val	Thr	Gln	Ile	Pro	Ala	Asp	Thr	Ser	Asp	Gln	Glu	Ile	
	50					55						60				

ctt	gat	ctg	gac	aaa	gct	ggc	gtg	aag	gct	gtg	cgt	tta	aac	ttg	aag	240
Leu	Asp	Leu	Asp	Lys	Ala	Gly	Val	Lys	Ala	Val	Arg	Leu	Asn	Leu	Lys	
65					70					75					80	

cgc	ggg	ggg	tgc	gca	ggg	ctt	gac	gat	ctc	gag	acc	ttg	gca	cgc	cga	288
Arg	Gly	Gly	Ser	Ala	Gly	Leu	Asp	Asp	Leu	Glu	Thr	Leu	Ala	Arg	Arg	
			85						90					95		

gtc	cac	gac	cta	gcc	ggg	tgg	cac	acc	gaa	ctc	tat	gtg	gat	gct	cgc	336
Val	His	Asp	Leu	Ala	Gly	Trp	His	Thr	Glu	Leu	Tyr	Val	Asp	Ala	Arg	
			100					105					110			

gaa	cta	gac	gag	ttg	gaa	tca	acc	ttg	gcc	tcc	ctc	cct	gct	gtc	agc	384
Glu	Leu	Asp	Glu	Leu	Glu	Ser	Thr	Leu	Ala	Ser	Leu	Pro	Ala	Val	Ser	
		115					120					125				

att	gat	cac	tta	ggg	ctc	cac	cgc	gat	gga	ctt	ccc	gca	ctt	ctt	cgc	432
Ile	Asp	His	Leu	Gly	Leu	His	Arg	Asp	Gly	Leu	Pro	Ala	Leu	Leu	Arg	
	130					135					140					

ttg	gta	gaa	aat	ggc	att	aaa	gtc	aaa	gca	acc	gga	ttc	gga	cgg	gta	480
Leu	Val	Glu	Asn	Gly	Ile	Lys	Val	Lys	Ala	Thr	Gly	Phe	Gly	Arg	Val	
145					150					155					160	

gaa	cta	gat	cca	act	gaa	gtc	atc	cag	gca	atc	atg	gct	gtc	gat	ccc	528
Glu	Leu	Asp	Pro	Thr	Glu	Val	Ile	Gln	Ala	Ile	Met	Ala	Val	Asp	Pro	
				165					170					175		

act	gct	ttg	atg	atc	gga	act	gat	ctt	cca	tcc	acc	cgc	act	aag	cga	576
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr Lys Arg
 180 185 190
 cct ttc gaa gac gct gac cta gat ttg atc gct gaa acg gtt ggc gaa 624
 Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val Gly Glu
 195 200 205
 gat cat gtc gac aac gtc ttc tgg aac aac gct gca gcg ttc tac ctc 672
 Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Phe Tyr Leu
 210 215 220
 gga gac cag tagttttaag acccgaaatg tct 704
 Gly Asp Gln
 225

<210> 1740

<211> 227

<212> PRT

<213> Corynebacterium glutamicum

<400> 1740

Tyr Leu Pro Glu Pro Phe Thr Val Glu Asp Tyr Thr Ala Arg Val Glu
 1 5 10 15
 Gly Leu Glu Val Ala Gly Gly Ala Ile Val Ser Gly Ser Phe Gln Ala
 20 25 30
 Phe Asp Gln Gly Tyr Leu Lys Asp Ala Leu Ala Val Leu Gly Pro Gly
 35 40 45
 Tyr Val Gly Val Thr Gln Ile Pro Ala Asp Thr Ser Asp Gln Glu Ile
 50 55 60
 Leu Asp Leu Asp Lys Ala Gly Val Lys Ala Val Arg Leu Asn Leu Lys
 65 70 75 80
 Arg Gly Gly Ser Ala Gly Leu Asp Asp Leu Glu Thr Leu Ala Arg Arg
 85 90 95
 Val His Asp Leu Ala Gly Trp His Thr Glu Leu Tyr Val Asp Ala Arg
 100 105 110
 Glu Leu Asp Glu Leu Glu Ser Thr Leu Ala Ser Leu Pro Ala Val Ser
 115 120 125
 Ile Asp His Leu Gly Leu His Arg Asp Gly Leu Pro Ala Leu Leu Arg
 130 135 140
 Leu Val Glu Asn Gly Ile Lys Val Lys Ala Thr Gly Phe Gly Arg Val
 145 150 155 160
 Glu Leu Asp Pro Thr Glu Val Ile Gln Ala Ile Met Ala Val Asp Pro
 165 170 175
 Thr Ala Leu Met Ile Gly Thr Asp Leu Pro Ser Thr Arg Thr Lys Arg
 180 185 190
 Pro Phe Glu Asp Ala Asp Leu Asp Leu Ile Ala Glu Thr Val Gly Glu
 195 200 205

Asp His Val Asp Asn Val Phe Trp Asn Asn Ala Ala Ala Phe Tyr Leu
 210 215 220

Gly Asp Gln
 225

<210> 1741
 <211> 570
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(547)
 <223> RXA00408

<400> 1741
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 gacaaatacg cacaggcgaa cccagaacc acatgagggc atg aat cca gtg tca 115
 Met Asn Pro Val Ser
 1 5
 cca aaa ctg acc acg gcc agg tac ctc acc cgc att cca tgg ctg ctg 163
 Pro Lys Leu Thr Thr Ala Arg Tyr Leu Thr Arg Ile Pro Trp Leu Leu
 10 15 20
 atc agc gcg att gtg ttt ggg gtg ctt gga gtt ttt gtg tct tcg tgg 211
 Ile Ser Ala Ile Val Phe Gly Val Leu Gly Val Phe Val Ser Ser Trp
 25 30 35
 ttt tac gcc ggt gtg atc gta gtt gcc gtc att ctt atc tgg cag ctg 259
 Phe Tyr Ala Gly Val Ile Val Val Ala Val Ile Leu Ile Trp Gln Leu
 40 45 50
 tgg ctg atc ccg cag cag gtc aag cga ctg gga tgg ctg gaa acc tcc 307
 Trp Leu Ile Pro Gln Gln Val Lys Arg Leu Gly Trp Leu Glu Thr Ser
 55 60 65
 gat gag ctg ctg atc acc aag gga aaa ctg tgg cac acc ttc acg gtt 355
 Asp Glu Leu Leu Ile Thr Lys Gly Lys Leu Trp His Thr Phe Thr Val
 70 75 80 85
 gtt ccc tat ggc cgc atc cag ttt gtt gat gtc acc gca ggt ccc ctc 403
 Val Pro Tyr Gly Arg Ile Gln Phe Val Asp Val Thr Ala Gly Pro Leu
 90 95 100
 gag cgc gcg ttt ggc atg aaa caa gtg caa ttg cat acc gcg tcg gcg 451
 Glu Arg Ala Phe Gly Met Lys Gln Val Gln Leu His Thr Ala Ser Ala
 105 110 115
 tcc tct gac tcc acc att caa ggc ctg cct gtc gcg gaa gcc gat gcc 499
 Ser Ser Asp Ser Thr Ile Gln Gly Leu Pro Val Ala Glu Ala Asp Ala
 120 125 130
 tta cgt gag cga ctg gct att aag gcc cgg gag agg atg agc gga cta 547
 Leu Arg Glu Arg Leu Ala Ile Lys Ala Arg Glu Arg Met Ser Gly Leu
 135 140 145
 tgagcagcct tgaagggttt cga 570

<210> 1742
 <211> 149
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1742
 Met Asn Pro Val Ser Pro Lys Leu Thr Thr Ala Arg Tyr Leu Thr Arg
 1 5 10 15
 Ile Pro Trp Leu Leu Ile Ser Ala Ile Val Phe Gly Val Leu Gly Val
 20 25 30
 Phe Val Ser Ser Trp Phe Tyr Ala Gly Val Ile Val Val Ala Val Ile
 35 40 45
 Leu Ile Trp Gln Leu Trp Leu Ile Pro Gln Gln Val Lys Arg Leu Gly
 50 55 60
 Trp Leu Glu Thr Ser Asp Glu Leu Leu Ile Thr Lys Gly Lys Leu Trp
 65 70 75 80
 His Thr Phe Thr Val Val Pro Tyr Gly Arg Ile Gln Phe Val Asp Val
 85 90 95
 Thr Ala Gly Pro Leu Glu Arg Ala Phe Gly Met Lys Gln Val Gln Leu
 100 105 110
 His Thr Ala Ser Ala Ser Ser Asp Ser Thr Ile Gln Gly Leu Pro Val
 115 120 125
 Ala Glu Ala Asp Ala Leu Arg Glu Arg Leu Ala Ile Lys Ala Arg Glu
 130 135 140
 Arg Met Ser Gly Leu
 145

<210> 1743
 <211> 1536
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1513)
 <223> RXA00409

<400> 1743
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 agcgactggc tattaaggcc cgggagagga tgagcggact atg agc agc ctt gaa 115
 Met Ser Ser Leu Glu
 1 5
 ggg ttt cga aaa gtc cac cgc gcc acc cca ttc ctt cgc atc tgg acc 163
 Gly Phe Arg Lys Val His Arg Ala Thr Pro Phe Leu Arg Ile Trp Thr
 10 15 20
 atc atc gtc gca gtt ctc gcg gca ttc gca ttc aat tcc ggc gca tcc 211

Ile Ile Val Ala Val Leu Ala Ala Phe Ala Phe Asn Ser Gly Ala Ser	
25 30 35	
gtt tta agt ttc atc tgg ggt gtc gtc acc ggc gaa tac gga ttc gca	259
Val Leu Ser Phe Ile Trp Gly Val Val Thr Gly Glu Tyr Gly Phe Ala	
40 45 50	
gtg ctg ccg att cta ttg acc gtc ggt ggc gcc gtc att gtg gtg gca	307
Val Leu Pro Ile Leu Leu Thr Val Gly Gly Ala Val Ile Val Val Ala	
55 60 65	
ctg gcc tgg att atc acc gga att tgg tgg aaa gcc gtc gga ttc cgc	355
Leu Ala Trp Ile Ile Thr Gly Ile Trp Trp Lys Ala Val Gly Phe Arg	
70 75 80 85	
atc acc aat gaa gag gtg cag ctg caa cgc gga gtg atc agc aaa gac	403
Ile Thr Asn Glu Glu Val Gln Leu Gln Arg Gly Val Ile Ser Lys Asp	
90 95 100	
ctc cgc acc gcc cga ttt gac cgt atc caa gcc gtt gac ctg gtg gaa	451
Leu Arg Thr Ala Arg Phe Asp Arg Ile Gln Ala Val Asp Leu Val Glu	
105 110 115	
tca ttc atc gcc cgt atc ttc cga ctg gca gaa gtc cgc atc gaa acc	499
Ser Phe Ile Ala Arg Ile Phe Arg Leu Ala Glu Val Arg Ile Glu Thr	
120 125 130	
gcc ggc ggc agc gac tcc gcc atc agc att ggc ttt tta aga aaa agc	547
Ala Gly Gly Ser Asp Ser Ala Ile Ser Ile Gly Phe Leu Arg Lys Ser	
135 140 145	
gag gcc gag gcc cta aaa agg gag ctt ctc gac gcc tcc cag cac tca	595
Glu Ala Glu Ala Leu Lys Arg Glu Leu Leu Asp Ala Ser Gln His Ser	
150 155 160 165	
gtc gcc acc acc cca gcc gga gtt ccg gct gag cct ggg gta ggg gag	643
Val Ala Thr Thr Pro Ala Gly Val Pro Ala Glu Pro Gly Val Gly Glu	
170 175 180	
acc gtt gta gtt gag agc gcg ggc gat gtt ctg gtt cca caa atc ccc	691
Thr Val Val Val Glu Ser Ala Gly Asp Val Leu Val Pro Gln Ile Pro	
185 190 195	
gtg caa cgc acc ctc gcc agc acc gcc tta tca cta gca acc atc atc	739
Val Gln Arg Thr Leu Ala Ser Thr Ala Leu Ser Leu Ala Thr Ile Ile	
200 205 210	
acc gcg atc ggt att gtg att ttg ctc ttc gtt cct ttc gga gtg agc	787
Thr Ala Ile Gly Ile Val Ile Leu Leu Phe Val Pro Phe Gly Val Ser	
215 220 225	
att gcc gtg ccg ttc ttt gta ggc atg gtg cca gcg gtc tgg aac ttg	835
Ile Ala Val Pro Phe Phe Val Gly Met Val Pro Ala Val Trp Asn Leu	
230 235 240 245	
atc gat aag tcg tgg caa ttc acc gca aca cag cgc aac gat gtc ctg	883
Ile Asp Lys Ser Trp Gln Phe Thr Ala Thr Gln Arg Asn Asp Val Leu	
250 255 260	
cat gtc agc tat gga ctt gcc aac cgc cgc aaa caa tca atc cca ctg	931
His Val Ser Tyr Gly Leu Ala Asn Arg Arg Lys Gln Ser Ile Pro Leu	

265	270	275	
gga cgc atc cac gca gtg aaa cta	aaa cag cca ttg ctg tgg cga ctg		979
Gly Arg Ile His Ala Val Lys Leu	Lys Gln Pro Leu Leu Trp Arg Leu		
280	285	290	
ggt ggc tgg tgg acc gtg acc gtg cct gta gtt ggc tac ggc gac acc			1027
Val Gly Trp Trp Thr Val Thr Val Pro Val Val Gly Tyr Gly Asp Thr			
295	300	305	
acc caa ggc gga acc tcc aaà atc ttg ccc gtg ggt tcc aaa gaa ctc			1075
Thr Gln Gly Gly Thr Ser Lys Ile Leu Pro Val Gly Ser Lys Glu Leu			
310	315	320	325
gca cta aaa gtc ctt gaa gcg gtg ggg cca cta aac agc gcc gac atc			1123
Ala Leu Lys Val Leu Glu Ala Val Gly Pro Leu Asn Ser Ala Asp Ile			
330	335	340	
gcc gaa tct gca gac cca tca cat atg agc aga ccc cag tac aca cca			1171
Ala Glu Ser Ala Asp Pro Ser His Met Ser Arg Pro Gln Tyr Thr Pro			
345	350	355	
cca gtt gct gca cgc ctg ctc aca cca gtc gat cgg acc cgc caa ggc			1219
Pro Val Ala Ala Arg Leu Leu Thr Pro Val Asp Arg Thr Arg Gln Gly			
360	365	370	
gtc acg ttg att ggt gtg gct ggt gcc cct ggt gcg gtg gtc gtg cat			1267
Val Thr Leu Ile Gly Val Ala Gly Ala Pro Gly Ala Val Val Val His			
375	380	385	
gaa ggc aga ttc atg cca cgt atg tct gtg att gat acc tcc cac atc			1315
Glu Gly Arg Phe Met Pro Arg Met Ser Val Ile Asp Thr Ser His Ile			
390	395	400	405
caa gaa ctc acc ctt aaa cac ggg ccg atc caa aga ata ctg gga ctc			1363
Gln Glu Leu Thr Leu Lys His Gly Pro Ile Gln Arg Ile Leu Gly Leu			
410	415	420	
tcc acc gtt gtg ttt aac ctg gtc caa ggg cca gtg gga atg gcc gca			1411
Ser Thr Val Val Phe Asn Leu Val Gln Gly Pro Val Gly Met Ala Ala			
425	430	435	
tcg gat ctc agt gca gct gat gga aaa gaa ctt ctc aac att ctc cgc			1459
Ser Asp Leu Ser Ala Ala Asp Gly Lys Glu Leu Leu Asn Ile Leu Arg			
440	445	450	
aac aga aaa cta ccc gca ctg gaa tca gct ccg ctg gga caa aac agc			1507
Asn Arg Lys Leu Pro Ala Leu Glu Ser Ala Pro Leu Gly Gln Asn Ser			
455	460	465	
ctg gac taaggtgtaa tcatgcacat ctc			1536
Leu Asp			
470			

<210> 1744

<211> 471

<212> PRT

<213> Corynebacterium glutamicum

<400> 1744

Met Ser Ser Leu Glu Gly Phe Arg Lys Val His Arg Ala Thr Pro Phe
 1 5 10 15
 Leu Arg Ile Trp Thr Ile Ile Val Ala Val Leu Ala Ala Phe Ala Phe
 20 25 30
 Asn Ser Gly Ala Ser Val Leu Ser Phe Ile Trp Gly Val Val Thr Gly
 35 40 45
 Glu Tyr Gly Phe Ala Val Leu Pro Ile Leu Leu Thr Val Gly Gly Ala
 50 55 60
 Val Ile Val Val Ala Leu Ala Trp Ile Ile Thr Gly Ile Trp Trp Lys
 65 70 75 80
 Ala Val Gly Phe Arg Ile Thr Asn Glu Glu Val Gln Leu Gln Arg Gly
 85 90 95
 Val Ile Ser Lys Asp Leu Arg Thr Ala Arg Phe Asp Arg Ile Gln Ala
 100 105 110
 Val Asp Leu Val Glu Ser Phe Ile Ala Arg Ile Phe Arg Leu Ala Glu
 115 120 125
 Val Arg Ile Glu Thr Ala Gly Gly Ser Asp Ser Ala Ile Ser Ile Gly
 130 135 140
 Phe Leu Arg Lys Ser Glu Ala Glu Ala Leu Lys Arg Glu Leu Leu Asp
 145 150 155 160
 Ala Ser Gln His Ser Val Ala Thr Thr Pro Ala Gly Val Pro Ala Glu
 165 170 175
 Pro Gly Val Gly Glu Thr Val Val Val Glu Ser Ala Gly Asp Val Leu
 180 185 190
 Val Pro Gln Ile Pro Val Gln Arg Thr Leu Ala Ser Thr Ala Leu Ser
 195 200 205
 Leu Ala Thr Ile Ile Thr Ala Ile Gly Ile Val Ile Leu Leu Phe Val
 210 215 220
 Pro Phe Gly Val Ser Ile Ala Val Pro Phe Phe Val Gly Met Val Pro
 225 230 235 240
 Ala Val Trp Asn Leu Ile Asp Lys Ser Trp Gln Phe Thr Ala Thr Gln
 245 250 255
 Arg Asn Asp Val Leu His Val Ser Tyr Gly Leu Ala Asn Arg Arg Lys
 260 265 270
 Gln Ser Ile Pro Leu Gly Arg Ile His Ala Val Lys Leu Lys Gln Pro
 275 280 285
 Leu Leu Trp Arg Leu Val Gly Trp Trp Thr Val Thr Val Pro Val Val
 290 295 300
 Gly Tyr Gly Asp Thr Thr Gln Gly Gly Thr Ser Lys Ile Leu Pro Val
 305 310 315 320
 Gly Ser Lys Glu Leu Ala Leu Lys Val Leu Glu Ala Val Gly Pro Leu

325										330					335				
Asn	Ser	Ala	Asp	Ile	Ala	Glu	Ser	Ala	Asp	Pro	Ser	His	Met	Ser	Arg				
			340						345				350						
Pro	Gln	Tyr	Thr	Pro	Pro	Val	Ala	Ala	Arg	Leu	Leu	Thr	Pro	Val	Asp				
		355					360					365							
Arg	Thr	Arg	Gln	Gly	Val	Thr	Leu	Ile	Gly	Val	Ala	Gly	Ala	Pro	Gly				
		370				375					380								
Ala	Val	Val	Val	His	Glu	Gly	Arg	Phe	Met	Pro	Arg	Met	Ser	Val	Ile				
					390					395					400				
Asp	Thr	Ser	His	Ile	Gln	Glu	Leu	Thr	Leu	Lys	His	Gly	Pro	Ile	Gln				
				405					410					415					
Arg	Ile	Leu	Gly	Leu	Ser	Thr	Val	Val	Phe	Asn	Leu	Val	Gln	Gly	Pro				
			420					425					430						
Val	Gly	Met	Ala	Ala	Ser	Asp	Leu	Ser	Ala	Ala	Asp	Gly	Lys	Glu	Leu				
		435					440					445							
Leu	Asn	Ile	Leu	Arg	Asn	Arg	Lys	Leu	Pro	Ala	Leu	Glu	Ser	Ala	Pro				
		450				455				460									
Leu	Gly	Gln	Asn	Ser	Leu	Asp													
		465			470														

<210> 1745

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXA00411

<400> 1745

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aaaccttgac	caagaccacg	accatcaagg	agatcacccg	atg	aac	gag	atg	atc	115
				Met	Asn	Glu	Met	Ile	
				1				5	

ctc	gca	gct	gac	tgg	aac	cgg	cta	gga	ccc	acc	ttc	caa	aca	gcc	atc	163
Leu	Ala	Ala	Asp	Trp	Asn	Arg	Leu	Gly	Pro	Thr	Phe	Gln	Thr	Ala	Ile	
			10					15						20		

att	gac	acc	ctg	ttg	atg	gtc	atc	atc	acc	atg	gtg	gtg	gct	ggc	tta	211
Ile	Asp	Thr	Leu	Met	Val	Ile	Ile	Thr	Met	Val	Val	Ala	Gly	Leu		
			25				30					35				

ctg	ggt	ctt	gtc	gtc	ggc	ctg	ctg	ctt	tac	acc	acc	cgc	gct	ggt	gga	259
Leu	Gly	Leu	Val	Val	Gly	Leu	Leu	Leu	Tyr	Thr	Thr	Arg	Ala	Gly	Gly	
			40				45					50				

atc	ttg	aag	aac	aag	gtc	atc	tac	acc	att	ttg	aat	gtg	ctg	gtg	aac	307
Ile	Leu	Lys	Asn	Lys	Val	Ile	Tyr	Thr	Ile	Leu	Asn	Val	Leu	Val	Asn	

55	60	65	
ttt gtt cga ccc atc cca ttc att att ttg atc gcc gcc atc aag cca			355
Phe Val Arg Pro Ile Pro Phe Ile Ile Leu Ile Ala Ala Ile Lys Pro			
70	75	80	85
cta acg gtc gcc gtc atg ggc acc tcc atc ggc cga gat gcc ggc atc			403
Leu Thr Val Ala Val Met Gly Thr Ser Ile Gly Arg Asp Ala Gly Ile			
	90	95	100
ttc gtc atg gtt gtc gca gcg att ttc tct gtg gct cga atc gtg gag			451
Phe Val Met Val Val Ala Ala Ile Phe Ser Val Ala Arg Ile Val Glu			
	105	110	115
caa aac ttg gtc tcc att gat cct ggt gtc atc gag gca gct cgc tcc			499
Gln Asn Leu Val Ser Ile Asp Pro Gly Val Ile Glu Ala Ala Arg Ser			
	120	125	130
atg ggt gcg tcc ccg atg cgc atc atc gcc acc gtg atc att cca gaa			547
Met Gly Ala Ser Pro Met Arg Ile Ile Ala Thr Val Ile Ile Pro Glu			
	135	140	145
gca ctt gga cca ttg gtt ctg ggt tac acc ttc ctg ttc atc gcg atc			595
Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe Leu Phe Ile Ala Ile			
	150	155	160
gtc gat atg tcc gca atg gtc ggc tac atc ggt ggc ggt ggt ctt ggt			643
Val Asp Met Ser Ala Met Val Gly Tyr Ile Gly Gly Gly Gly Leu Gly			
	170	175	180
gac ttc gcc att gtt tac ggc tac cgc gcc ttc gac aac gaa gtt atg			691
Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Phe Asp Asn Glu Val Met			
	185	190	195
tac gtt gcc gtc ctg gtt atc gtc atc atc gtg cag gca gcc cag ctt			739
Tyr Val Ala Val Leu Val Ile Val Ile Ile Val Gln Ala Ala Gln Leu			
	200	205	210
ctg ggc aat tgg ctg tcc aag aag atc atg cgc cgc taaacctctt			785
Leu Gly Asn Trp Leu Ser Lys Lys Ile Met Arg Arg			
	215	220	225
gcatagaaaa acc			798

<210> 1746

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 1746

Met Asn Glu Met Ile Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
1 5 10 15

Phe Gln Thr Ala Ile Ile Asp Thr Leu Leu Met Val Ile Ile Thr Met
20 25 30

Val Val Ala Gly Leu Leu Gly Leu Val Val Gly Leu Leu Leu Tyr Thr
35 40 45

Thr Arg Ala Gly Gly Ile Leu Lys Asn Lys Val Ile Tyr Thr Ile Leu

caa caa ctg act gac ctg ctg aaa gac aca gta gtg ttc ctt acc cct 259
 Gln Gln Leu Thr Asp Leu Leu Lys Asp Thr Val Val Phe Leu Thr Pro
 40 45 50

ggg agc acc gct ccg gaa aat gcc ccc gtg gcg acg ata gaa ggg gtg 307
 Gly Ser Thr Ala Pro Glu Asn Ala Pro Val Ala Thr Ile Glu Gly Val
 55 60 65

cgg gtt gac gtc gat aag cag gtg gca gag tac aac aaa cat ggg atc 355
 Arg Val Asp Val Asp Lys Gln Val Ala Glu Tyr Asn Lys His Gly Ile
 70 75 80 85

cgc ctg ccc agc ttg ggc gcg cgc act gtg gag gcg cag tac cgc ggc 403
 Arg Leu Pro Ser Leu Gly Ala Arg Thr Val Glu Ala Gln Tyr Arg Gly
 90 95 100

gag ccg gag gca gag gct gcg tgg cgc acg gcg atg gag ctc gta gag 451
 Glu Pro Glu Ala Glu Ala Ala Trp Arg Thr Ala Met Glu Leu Val Glu
 105 110 115

atc gca ggc ggc tgg cta gaa att gaa gcc aag cgc cgg gcg cgg aag 499
 Ile Ala Gly Gly Trp Leu Glu Ile Glu Ala Lys Arg Arg Ala Arg Lys
 120 125 130

gcg ctg gct gag gcc ttc ggc gcg gag gtc cag cca ctg ccg ctt gac 547
 Ala Leu Ala Glu Ala Phe Gly Ala Glu Val Gln Pro Leu Pro Leu Asp
 135 140 145

acc gaa taggacaaat ggggtctatcc tgg 576
 Thr Glu
 150

<210> 1748

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 1748

Met Thr Tyr Pro Val Leu Ser Val Leu Asp Asn Ser Gly Asp His Asn
 1 5 10 15

Ile Ile Trp His Val Gln Thr Tyr Pro Ala Ala Leu Pro Thr Gly Ala
 20 25 30

Trp Ile Ala Asp Glu Gln Gln Leu Thr Asp Leu Leu Lys Asp Thr Val
 35 40 45

Val Phe Leu Thr Pro Gly Ser Thr Ala Pro Glu Asn Ala Pro Val Ala
 50 55 60

Thr Ile Glu Gly Val Arg Val Asp Val Asp Lys Gln Val Ala Glu Tyr
 65 70 75 80

Asn Lys His Gly Ile Arg Leu Pro Ser Leu Gly Ala Arg Thr Val Glu
 85 90 95

Ala Gln Tyr Arg Gly Glu Pro Glu Ala Glu Ala Ala Trp Arg Thr Ala
 100 105 110

Met Glu Leu Val Glu Ile Ala Gly Gly Trp Leu Glu Ile Glu Ala Lys

115	120	125
Arg Arg Ala Arg Lys Ala Leu Ala Glu Ala Phe Gly Ala Glu Val Gln		
130	135	140
Pro Leu Pro Leu Asp Thr Glu		
145	150	

<210> 1749
 <211> 594
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(571)
 <223> RXA00424

<400> 1749
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 atcagtgagt agtcttggca acatggatac caggatgaga ttg cag gta gca gca 115
 Leu Gln Val Ala Ala
 1 5
 ggt tcc gcg ctg att ggt gct ggg gtt gcg gtt aat gat tac gta caa 163
 Gly Ser Ala Leu Ile Gly Ala Gly Val Ala Val Asn Asp Tyr Val Gln
 10 15 20
 agc cca gtc cgc cgg gcc atc agt tat ggt gcg ttg gcg ctt tct ggg 211
 Ser Pro Val Arg Arg Ala Ile Ser Tyr Gly Ala Leu Ala Leu Ser Gly
 25 30 35
 gcg acg gtg att gcg atg ggt cag gac ccg act ggg gag cgg tcc atc 259
 Ala Thr Val Ile Ala Met Gly Gln Asp Pro Thr Gly Glu Arg Ser Ile
 40 45 50
 att gcg aaa gat tcc gcg acg atg gtt gat caa atc cgc cag gag atc 307
 Ile Ala Lys Asp Ser Ala Thr Met Val Asp Gln Ile Arg Gln Glu Ile
 55 60 65
 ggc gat ttg ggt gtc acg cct ggt cca gaa tct gat gtg gat gcc atc 355
 Gly Asp Leu Gly Val Thr Pro Gly Pro Glu Ser Asp Val Asp Ala Ile
 70 75 80 85
 acg gag cga ggt ccg ctg gtg acg tgg ctg ttg ctt gct gtt ttt gtc 403
 Thr Glu Arg Gly Pro Leu Val Thr Trp Leu Leu Leu Ala Val Phe Val
 90 95 100
 gtg gca ttt ttc acc ttg gcg tat ttc tcc atg cgc atg gat gtg gcg 451
 Val Ala Phe Phe Thr Leu Ala Tyr Phe Ser Met Arg Met Asp Val Ala
 105 110 115
 gtg atg aga agg atc gct aag ttc ttt gaa aaa cgt ggc gct tcc agg 499
 Val Met Arg Arg Ile Ala Lys Phe Phe Glu Lys Arg Gly Ala Ser Arg
 120 125 130
 cca ttc acc tgc act ggc atg gtg tac gcc gct ttt att tac gca atc 547
 Pro Phe Thr Cys Thr Gly Met Val Tyr Ala Ala Phe Ile Tyr Ala Ile
 135 140 145

tgt gag ctg gag gcc cgc aca aaa tgacctatcc cgtgttgagt gtt
 Cys Glu Leu Glu Ala Arg Thr Lys
 150 155

594

<210> 1750

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1750

Leu Gln Val Ala Ala Gly Ser Ala Leu Ile Gly Ala Gly Val Ala Val
 1 5 10 15

Asn Asp Tyr Val Gln Ser Pro Val Arg Arg Ala Ile Ser Tyr Gly Ala
 20 25 30

Leu Ala Leu Ser Gly Ala Thr Val Ile Ala Met Gly Gln Asp Pro Thr
 35 40 45

Gly Glu Arg Ser Ile Ile Ala Lys Asp Ser Ala Thr Met Val Asp Gln
 50 55 60

Ile Arg Gln Glu Ile Gly Asp Leu Gly Val Thr Pro Gly Pro Glu Ser
 65 70 75 80

Asp Val Asp Ala Ile Thr Glu Arg Gly Pro Leu Val Thr Trp Leu Leu
 85 90 95

Leu Ala Val Phe Val Val Ala Phe Phe Thr Leu Ala Tyr Phe Ser Met
 100 105 110

Arg Met Asp Val Ala Val Met Arg Arg Ile Ala Lys Phe Phe Glu Lys
 115 120 125

Arg Gly Ala Ser Arg Pro Phe Thr Cys Thr Gly Met Val Tyr Ala Ala
 130 135 140

Phe Ile Tyr Ala Ile Cys Glu Leu Glu Ala Arg Thr Lys
 145 150 155

<210> 1751

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA00425

<400> 1751

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tccatgttgc caagactact cactgattaa ggtgggtgggc atg ttt gaa aga ttc 115
 Met Phe Glu Arg Phe
 1 5

aaa aaa gcc aag gct ccc gag gtc cac atc gcg gcg gaa cgc acc aac 163

Lys Lys Ala Lys Ala Pro Glu Val His Ile Ala Ala Glu Arg Thr Asn
 10 15 20
 ctt ccg ctt aac gat ttc atg acc cgc ctc ttc gcc cag gaa ctc ccc 211
 Leu Pro Leu Asn Asp Phe Met Thr Arg Leu Phe Ala Gln Glu Leu Pro
 25 30 35
 ctg ctc gat agc acc tca cgt tca gag gtc tac cgc ctg ctt cgg gaa 259
 Leu Leu Asp Ser Thr Ser Arg Ser Glu Val Tyr Arg Leu Leu Arg Glu
 40 45 50
 tac gac ggc cca aca att agc tcc cag gaa gaa atc ccc gca gag att 307
 Tyr Asp Gly Pro Thr Ile Ser Ser Gln Glu Glu Ile Pro Ala Glu Ile
 55 60 65
 cgt gaa ctc atg gat ctt taggcaataa atgtgagatt gga 348
 Arg Glu Leu Met Asp Leu
 70 75

<210> 1752

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 1752

Met Phe Glu Arg Phe Lys Lys Ala Lys Ala Pro Glu Val His Ile Ala
 1 5 10 15
 Ala Glu Arg Thr Asn Leu Pro Leu Asn Asp Phe Met Thr Arg Leu Phe
 20 25 30
 Ala Gln Glu Leu Pro Leu Leu Asp Ser Thr Ser Arg Ser Glu Val Tyr
 35 40 45
 Arg Leu Leu Arg Glu Tyr Asp Gly Pro Thr Ile Ser Ser Gln Glu Glu
 50 55 60
 Ile Pro Ala Glu Ile Arg Glu Leu Met Asp Leu
 65 70 75

<210> 1753

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA00428

<400> 1753

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 gccggattca accgctacta cgcagccctt aagggtctaaa atg ccc ggt cta gtt 115
 Met Pro Gly Leu Val
 1 5
 ctc tcc aca aac gtc gcc cat atc caa caa gac cca ggt ggc gat gac 163
 Leu Ser Thr Asn Val Ala His Ile Gln Gln Asp Pro Gly Gly Asp Asp

10	15	20	
cgc atc agc ggc atc aac aaa ctc ccc gtc gcc acc ggc atc gat gta			211
Arg Ile Ser Gly Ile Asn Lys Leu Pro Val Ala Thr Gly Ile Asp Val			
25	30	35	
ttc atc ccc gga ccc aac tac ggc gac ggc tcc ggc gta gtc ggc gac			259
Phe Ile Pro Gly Pro Asn Tyr Gly Asp Gly Ser Gly Val Val Gly Asp			
40	45	50	
gcc atc ggc gat tcc ctc cac cac ggc ggc gcc cac aaa gcc atc tac			307
Ala Ile Gly Asp Ser Leu His His Gly Gly Ala His Lys Ala Ile Tyr			
55	60	65	
gcc tac agc cgc gaa gaa ctc gac ttc ttt gac ccc acc tac cgc aac			355
Ala Tyr Ser Arg Glu Glu Leu Asp Phe Phe Asp Pro Thr Tyr Arg Asn			
70	75	80	85
gga tac ttc ggc gaa aac ctc acc acc agc gga atc gtg ttg gaa gac			403
Gly Tyr Phe Gly Glu Asn Leu Thr Thr Ser Gly Ile Val Leu Glu Asp			
90	95	100	
ctc ctg atc aac caa caa gtg cgc atc ggc acc acg ctg ctc gaa gtc			451
Leu Leu Ile Asn Gln Gln Val Arg Ile Gly Thr Thr Leu Leu Glu Val			
105	110	115	
tcc att ccc cgc cga ccc tgc cgc acg ttc gcc cac tgg ctc gac atc			499
Ser Ile Pro Arg Arg Pro Cys Arg Thr Phe Ala His Trp Leu Asp Ile			
120	125	130	
aaa ggc tgg cta aaa acc ttc acc caa cgc ggc ctc ccc ggc agc tac			547
Lys Gly Trp Leu Lys Thr Phe Thr Gln Arg Gly Leu Pro Gly Ser Tyr			
135	140	145	
ttc cga gtc atc gaa gaa ggc cac atc aac ccc ggc gac ccc att gaa			595
Phe Arg Val Ile Glu Glu Gly His Ile Asn Pro Gly Asp Pro Ile Glu			
150	155	160	165
gtt ctg cag gcc ccc gac cac gac atc acc atg tcc atg gcc ttc cgt			643
Val Leu Gln Ala Pro Asp His Asp Ile Thr Met Ser Met Ala Phe Arg			
170	175	180	
gca aaa atg gga aac aaa gac ctc gcg cgc cgg gtt gtt gca gcc aac			691
Ala Lys Met Gly Asn Lys Asp Leu Ala Arg Arg Val Val Ala Ala Asn			
185	190	195	
tgt ctc cca gcg cgc tac cac gag gaa cta cta aaa ctg atc			733
Cys Leu Pro Ala Arg Tyr His Glu Glu Leu Leu Lys Leu Ile			
200	205	210	
tagggcctat tgaatttctc gtc			756

<210> 1754

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 1754

Met	Pro	Gly	Leu	Val	Leu	Ser	Thr	Asn	Val	Ala	His	Ile	Gln	Gln	Asp
1					5				10						15

Pro Gly Gly Asp Asp Arg Ile Ser Gly Ile Asn Lys Leu Pro Val Ala
 20 25 30
 Thr Gly Ile Asp Val Phe Ile Pro Gly Pro Asn Tyr Gly Asp Gly Ser
 35 40 45
 Gly Val Val Gly Asp Ala Ile Gly Asp Ser Leu His His Gly Gly Ala
 50 55 60
 His Lys Ala Ile Tyr Ala Tyr Ser Arg Glu Glu Leu Asp Phe Phe Asp
 65 70 75 80
 Pro Thr Tyr Arg Asn Gly Tyr Phe Gly Glu Asn Leu Thr Thr Ser Gly
 85 90 95
 Ile Val Leu Glu Asp Leu Leu Ile Asn Gln Gln Val Arg Ile Gly Thr
 100 105 110
 Thr Leu Leu Glu Val Ser Ile Pro Arg Arg Pro Cys Arg Thr Phe Ala
 115 120 125
 His Trp Leu Asp Ile Lys Gly Trp Leu Lys Thr Phe Thr Gln Arg Gly
 130 135 140
 Leu Pro Gly Ser Tyr Phe Arg Val Ile Glu Glu Gly His Ile Asn Pro
 145 150 155 160
 Gly Asp Pro Ile Glu Val Leu Gln Ala Pro Asp His Asp Ile Thr Met
 165 170 175
 Ser Met Ala Phe Arg Ala Lys Met Gly Asn Lys Asp Leu Ala Arg Arg
 180 185 190
 Val Val Ala Ala Asn Cys Leu Pro Ala Arg Tyr His Glu Glu Leu Leu
 195 200 205
 Lys Leu Ile
 210

<210> 1755

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA00429

<400> 1755

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caaagaacca tcattttccg agtgaagtaa ggtacccttc atg aag acc ttc aat 115
 Met Lys Thr Phe Asn
 1 5

ccc acc atg att gcc gga ctc atc ggc gta ctc tac ttc gtg ctg ctc 163
 Pro Thr Met Ile Ala Gly Leu Ile Gly Val Leu Tyr Phe Val Leu Leu
 10 15 20

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acc ctg att ttc tcc atc caa gac atg gaa cta gca gca gaa atc gcc 211
Thr Leu Ile Phe Ser Ile Gln Asp Met Glu Leu Ala Ala Glu Ile Ala
      25                      30                      35

ttc gga atc gtc acc atc gtc ggc ctg atc gcg gtg tgg gac aac ttc 259
Phe Gly Ile Val Thr Ile Val Gly Leu Ile Ala Val Trp Asp Asn Phe
      40                      45                      50

cgc gac cgc aac aac tcc acc tgg aaa acc tgg acc ggc ctc gtc ggc 307
Arg Asp Arg Asn Asn Ser Thr Trp Lys Thr Trp Thr Gly Leu Val Gly
      55                      60                      65

gga ctg cta atc gcc gtc ccc gga atc tgc ctt ctt gtg gga aac ctc 355
Gly Leu Leu Ile Ala Val Pro Gly Ile Cys Leu Leu Val Gly Asn Leu
      70                      75                      80                      85

gtg ctc ctc gca gtc gac ggc aac ccc tca acc atg gtg aac acc ctg 403
Val Leu Leu Ala Val Asp Gly Asn Pro Ser Thr Met Val Asn Thr Leu
      90                      95                      100

ctc agc gtc gca ggg atc ggc gcg atc ttc ctc ctt ccg atc ggc atc 451
Leu Ser Val Ala Gly Ile Gly Ala Ile Phe Leu Leu Pro Ile Gly Ile
      105                      110                      115

atc atg tgc ctc atc gcc gga ttc aac cgc tac tac gca gcc ctt aag 499
Ile Met Cys Leu Ile Ala Gly Phe Asn Arg Tyr Tyr Ala Ala Leu Lys
      120                      125                      130

gtc taaaatgccc ggtctagttc tct 525
Val

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<210> 1756

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 1756

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Met Lys Thr Phe Asn Pro Thr Met Ile Ala Gly Leu Ile Gly Val Leu
  1                      5                      10                      15

Tyr Phe Val Leu Leu Thr Leu Ile Phe Ser Ile Gln Asp Met Glu Leu
      20                      25                      30

Ala Ala Glu Ile Ala Phe Gly Ile Val Thr Ile Val Gly Leu Ile Ala
      35                      40                      45

Val Trp Asp Asn Phe Arg Asp Arg Asn Asn Ser Thr Trp Lys Thr Trp
      50                      55                      60

Thr Gly Leu Val Gly Gly Leu Leu Ile Ala Val Pro Gly Ile Cys Leu
      65                      70                      75                      80

Leu Val Gly Asn Leu Val Leu Leu Ala Val Asp Gly Asn Pro Ser Thr
      85                      90                      95

Met Val Asn Thr Leu Leu Ser Val Ala Gly Ile Gly Ala Ile Phe Leu
      100                      105                      110

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Leu Pro Ile Gly Ile Ile Met Cys Leu Ile Ala Gly Phe Asn Arg Tyr
 115 120 125

Tyr Ala Ala Leu Lys Val
 130

<210> 1757

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> RXA00430

<400> 1757

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cctcgtgtcc gaaaatcttg atgttacgat cgtccgacca atg agc ctg aaa acc 115
 Met Ser Leu Lys Thr
 1 5

caa gct ttc cgg ttc atc ctc acc ggt ggc ctc tca gcc atc gtg gac 163
 Gln Ala Phe Arg Phe Ile Leu Thr Gly Gly Leu Ser Ala Ile Val Asp
 10 15 20

ctc ggc ctg ctg tca ctt ttg cag cta gtg ttc ggc ctt ccc gta cct 211
 Leu Gly Leu Leu Ser Leu Leu Gln Leu Val Phe Gly Leu Pro Val Pro
 25 30 35

gtt gcc cgc acg atc tcc ttc atc gcc ggc acc acc acc gcc tac atg 259
 Val Ala Arg Thr Ile Ser Phe Ile Ala Gly Thr Thr Thr Ala Tyr Met
 40 45 50

atc aac cgc cgg tgg acc ttc caa gca gaa agc tcc acc tcc agg ttc 307
 Ile Asn Arg Arg Trp Thr Phe Gln Ala Glu Ser Ser Thr Ser Arg Phe
 55 60 65

ctt gct gtg gtg gcc ctc tac ggc gtg acc ttc ctg atc aac att gga 355
 Leu Ala Val Val Ala Leu Tyr Gly Val Thr Phe Leu Ile Asn Ile Gly
 70 75 80 85

ctg caa acc ctc tgc tcc gca ttg ttt gag aat tgg ggc tgg aac gaa 403
 Leu Gln Thr Leu Cys Ser Ala Leu Phe Glu Asn Trp Gly Trp Asn Glu
 90 95 100

gcc gtc gcg atg gtg gtc gcc ttc gtg atc gcc caa ggc acc cgg aac 451
 Ala Val Ala Met Val Val Ala Phe Val Ile Ala Gln Gly Thr Arg Asn
 105 110 115

ggt cat caa ctt cat cgt cca aag aac cat cat ttt ccg agt gaa gta 499
 Gly His Gln Leu His Arg Pro Lys Asn His His Phe Pro Ser Glu Val
 120 125 130

agg tac ccc tca tgaagacctt caatcccacc atg 534
 Arg Tyr Pro Ser
 135

<210> 1758

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 1758

Met Ser Leu Lys Thr Gln Ala Phe Arg Phe Ile Leu Thr Gly Gly Leu
 1 5 10 15

Ser Ala Ile Val Asp Leu Gly Leu Leu Ser Leu Leu Gln Leu Val Phe
 20 25 30

Gly Leu Pro Val Pro Val Ala Arg Thr Ile Ser Phe Ile Ala Gly Thr
 35 40 45

Thr Thr Ala Tyr Met Ile Asn Arg Arg Trp Thr Phe Gln Ala Glu Ser
 50 55 60

Ser Thr Ser Arg Phe Leu Ala Val Val Ala Leu Tyr Gly Val Thr Phe
 65 70 75 80

Leu Ile Asn Ile Gly Leu Gln Thr Leu Cys Ser Ala Leu Phe Glu Asn
 85 90 95

Trp Gly Trp Asn Glu Ala Val Ala Met Val Val Ala Phe Val Ile Ala
 100 105 110

Gln Gly Thr Arg Asn Gly His Gln Leu His Arg Pro Lys Asn His His
 115 120 125

Phe Pro Ser Glu Val Arg Tyr Pro Ser
 130 135

<210> 1759

<211> 648

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(625)

<223> RXA00433

<400> 1759

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agtctcgaac atactaaatc acctaatacag ggggaattac atg gat gtg tta aag 115
 Met Asp Val Leu Lys
 1 5

atc gcc atc atc gct gca gcc atg att ggt gtg ccg gtt ctg gtg gtt 163
 Ile Ala Ile Ile Ala Ala Met Ile Gly Val Pro Val Leu Val Val
 10 15 20

ttc ctc att gtg ttt gcg gtg cac aag ttg gct aag gaa gtg ccg cgg 211
 Phe Leu Ile Val Phe Ala Val His Lys Leu Ala Lys Glu Val Pro Arg
 25 30 35

tct ggt cgt cgt ccg ggt att ggg ttg ggg ttg ttg ctt ggt ttt gtt 259
 Ser Gly Arg Arg Pro Gly Ile Gly Leu Gly Leu Leu Leu Gly Phe Val

40	45	50	
gcg ggg ctc atc gtg tgg ttt gtg tgg ttg agt tgg ggt ggt tat tac			307
Ala Gly Leu Ile Val Trp Phe Val Trp Leu Ser Trp Gly Gly Tyr Tyr			
55	60	65	
gag aat gag ttt ggg cag atg caa ggt ccg tat cgt ccg tgg cag gtt			355
Glu Asn Glu Phe Gly Gln Met Gln Gly Pro Tyr Arg Pro Trp Gln Val			
70	75	80	85
gtt gct tgt ggt gtc acg atg gtc gcg gtc act gtg att ctt ggt ctg			403
Val Ala Cys Gly Val Thr Met Val Ala Val Thr Val Ile Leu Gly Leu			
90	95	100	
tgg act agg tgg act gcg tct ggt ccg ttt tat tcg gcg ttg ggt ggt			451
Trp Thr Arg Trp Thr Ala Ser Gly Pro Phe Tyr Ser Ala Leu Gly Gly			
105	110	115	
gcg tcg ggg ttt agt ttc gcg tgg gcc atg gat gcc att cct cag gat			499
Ala Ser Gly Phe Ser Phe Ala Trp Ala Met Asp Ala Ile Pro Gln Asp			
120	125	130	
gaa acc gga ttg tcg gcg ttt ggc tta gtg atg gtc att gtt ggt gtt			547
Glu Thr Gly Leu Ser Ala Phe Gly Leu Val Met Val Ile Val Gly Val			
135	140	145	
ggg gcg ggg cta aat gtg gtg gca act ctg acg tca atc ggc gca acg			595
Gly Ala Gly Leu Asn Val Val Ala Thr Leu Thr Ser Ile Gly Ala Thr			
150	155	160	165
atc tgg aat aac cgg cta ccc tcg aat gca tgactaaaac cacgcgccaa			645
Ile Trp Asn Asn Arg Leu Pro Ser Asn Ala			
170	175		
acc			648

<210> 1760

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 1760

Met Asp Val Leu Lys Ile Ala Ile Ile Ala Ala Ala Met Ile Gly Val
1 5 10 15

Pro Val Leu Val Val Phe Leu Ile Val Phe Ala Val His Lys Leu Ala
20 25 30

Lys Glu Val Pro Arg Ser Gly Arg Arg Pro Gly Ile Gly Leu Gly Leu
35 40 45

Leu Leu Gly Phe Val Ala Gly Leu Ile Val Trp Phe Val Trp Leu Ser
50 55 60

Trp Gly Gly Tyr Tyr Glu Asn Glu Phe Gly Gln Met Gln Gly Pro Tyr
65 70 75 80

Arg Pro Trp Gln Val Val Ala Cys Gly Val Thr Met Val Ala Val Thr
85 90 95

Val Ile Leu Gly Leu Trp Thr Arg Trp Thr Ala Ser Gly Pro Phe Tyr
 100 105 110

Ser Ala Leu Gly Gly Ala Ser Gly Phe Ser Phe Ala Trp Ala Met Asp
 115 120 125

Ala Ile Pro Gln Asp Glu Thr Gly Leu Ser Ala Phe Gly Leu Val Met
 130 135 140

Val Ile Val Gly Val Gly Ala Gly Leu Asn Val Val Ala Thr Leu Thr
 145 150 155 160

Ser Ile Gly Ala Thr Ile Trp Asn Asn Arg Leu Pro Ser Asn Ala
 165 170 175

<210> 1761

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00451

<400> 1761

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cacctgacaa gtgtggcaca tacctactac ggttatctct atg aac act gaa gag 115
 Met Asn Thr Glu Glu
 1 5

gat ggc ctg agc ttt gca gtt acg gct acc tta gtt gaa ggt aaa tgg 163
 Asp Gly Leu Ser Phe Ala Val Thr Ala Thr Leu Val Glu Gly Lys Trp
 10 15 20

cag gta cgc gag ttt gag gat cac ttc tcc aag ctc tct acc tct att 211
 Gln Val Arg Glu Phe Glu Asp His Phe Ser Lys Leu Ser Thr Ser Ile
 25 30 35

aat gcg gtt cgc tcg ctg cgt agc gag ggg ccg gcg ttt gcg ctg ttg 259
 Asn Ala Val Arg Ser Leu Arg Ser Glu Gly Pro Ala Phe Ala Leu Leu
 40 45 50

tgc gtt gat gat gaa tat ttt gtg atg gtg cgt ccc acc cca agt agg 307
 Cys Val Asp Asp Glu Tyr Phe Val Met Val Arg Pro Thr Pro Ser Arg
 55 60 65

gta ttc ctt ttc ctt tcg gat gcg ccg atg gct gtc gac gat gat ttc 355
 Val Phe Leu Phe Leu Ser Asp Ala Pro Met Ala Val Asp Asp Asp Phe
 70 75 80 85

gcc gcc gcg gtg atg gat gaa ctc gat gcg gat ctt cca gat atc aac 403
 Ala Ala Ala Val Met Asp Glu Leu Asp Ala Asp Leu Pro Asp Ile Asn
 90 95 100

cct gat gat ttg gac gac atc gat cca tgg cca gaa ggt gat ttc gat 451
 Pro Asp Asp Leu Asp Asp Ile Asp Pro Trp Pro Glu Gly Asp Phe Asp
 105 110 115

att ttg gcg gat ttg ggg ctg tct gag gag gtt ctt tcc gtg att tgc 499
 Ile Leu Ala Asp Leu Gly Leu Ser Glu Glu Val Leu Ser Val Ile Cys
 120 125 130

gat gac atg gat ttg gat cct tcc gaa caa ttg ctg cgc atc gcg gaa 547
 Asp Asp Met Asp Leu Asp Pro Ser Glu Gln Leu Leu Arg Ile Ala Glu
 135 140 145

gaa ctc ggt ttt gat aat gat ctg gct cgg gtg gtg gga ttc gac 592
 Glu Leu Gly Phe Asp Asn Asp Leu Ala Arg Val Val Gly Phe Asp
 150 155 160

tagtgggcgt tttacctgtg cag 615

<210> 1762

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1762

Met Asn Thr Glu Glu Asp Gly Leu Ser Phe Ala Val Thr Ala Thr Leu
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Val Glu Gly Lys Trp Gln Val Arg Glu Phe Glu Asp His Phe Ser Lys
 20 25 30

Leu Ser Thr Ser Ile Asn Ala Val Arg Ser Leu Arg Ser Glu Gly Pro
 35 40 45

Ala Phe Ala Leu Leu Cys Val Asp Asp Glu Tyr Phe Val Met Val Arg
 50 55 60

Pro Thr Pro Ser Arg Val Phe Leu Phe Leu Ser Asp Ala Pro Met Ala
 65 70 75 80

Val Asp Asp Asp Phe Ala Ala Ala Val Met Asp Glu Leu Asp Ala Asp
 85 90 95

Leu Pro Asp Ile Asn Pro Asp Asp Leu Asp Asp Ile Asp Pro Trp Pro
 100 105 110

Glu Gly Asp Phe Asp Ile Leu Ala Asp Leu Gly Leu Ser Glu Glu Val
 115 120 125

Leu Ser Val Ile Cys Asp Asp Met Asp Leu Asp Pro Ser Glu Gln Leu
 130 135 140

Leu Arg Ile Ala Glu Glu Leu Gly Phe Asp Asn Asp Leu Ala Arg Val
 145 150 155 160

Val Gly Phe Asp

<210> 1763

<211> 1203

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(1180)
 <223> RXA00457

<400> 1763

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ccaatcgggc agacacttcc tcctagaaag gtcctcctc atg acc att gct ctt 115
                                     Met Thr Ile Ala Leu
                                     1 5

gaa cac cca gta ctg cac tcc acg gcg atc gcg ttg cct gct cgt ttt 163
Glu His Pro Val Leu His Ser Thr Ala Ile Ala Leu Pro Ala Arg Phe
                                     10 15 20

cag gcg agc tat acg acg cgt ttg gtg gcg gtg ggc gtc gat aag cgt 211
Gln Ala Ser Tyr Thr Thr Arg Leu Val Ala Val Gly Val Asp Lys Arg
                                     25 30 35

cct tct gat ttt tgg ttg gaa aca gcc ggc acg ccg cag gcg ggc gat 259
Pro Ser Asp Phe Trp Leu Glu Thr Ala Gly Thr Pro Gln Ala Gly Asp
                                     40 45 50

gtg gtg att gcg cgg gtg acg gcg att aat aat cac aag cgg gtg gag 307
Val Val Ile Ala Arg Val Thr Ala Ile Asn Asn His Lys Arg Val Glu
                                     55 60 65

acg ccg gag tcg cgc aag gcc att ttg ttt gag ggg gtg ttg gtg atg 355
Thr Pro Glu Ser Arg Lys Ala Ile Leu Phe Glu Gly Val Leu Val Met
                                     70 75 80 85

ttg gcg tat ggg cac cgg tat gcg gcg gat cag ttt tta gcg cat gta 403
Leu Ala Tyr Gly His Arg Tyr Ala Ala Asp Gln Phe Leu Ala His Val
                                     90 95 100

ccg gag gat ttg ggg cca tgc cat ttg gtg gcg gct ggt ggc atc gcg 451
Pro Glu Asp Leu Gly Pro Cys His Leu Val Ala Ala Gly Gly Ile Ala
                                     105 110 115

gga acg gtg acg gcg ctg cac gat cgg gtg gat gaa ccc aca gag att 499
Gly Thr Val Thr Ala Leu His Asp Arg Val Asp Glu Pro Thr Glu Ile
                                     120 125 130

gaa ccg ttg gga ttg ctc acc aat gcg cgc gga act gtg aat gta cgg 547
Glu Pro Leu Gly Leu Leu Thr Asn Ala Arg Gly Thr Val Asn Val Arg
                                     135 140 145

gac ttt gcg gct ttt gat aat cct ttg aaa gtg gag gct ccc aac aag 595
Asp Phe Ala Ala Phe Asp Asn Pro Leu Lys Val Glu Ala Pro Asn Lys
                                     150 155 160 165

cgt gcg cag gtg atc gcg gtg ctg gga acg tcg atg aac tct gga aaa 643
Arg Ala Gln Val Ile Ala Val Leu Gly Thr Ser Met Asn Ser Gly Lys
                                     170 175 180

tcc acc acg ctt gcc tgc ttg gtc aat ggt ttg gct gcg gcg ggg cag 691
Ser Thr Thr Leu Ala Cys Leu Val Asn Gly Leu Ala Ala Ala Gly Gln
                                     185 190 195

aag gtg gcg gct gga aag atc acg ggc act ggt gct gga aat gac cgc 739
Lys Val Ala Ala Gly Lys Ile Thr Gly Thr Gly Ala Gly Asn Asp Arg

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200	205	210	
atg att tat cac gat gct ggt gct cac agc gtt att gat ttc acc gac Met Ile Tyr His Asp Ala Gly Ala His Ser Val Ile Asp Phe Thr Asp 215 220 225			787
ttt ggc tac cca act acg ttc aag ctg aat ttc gcg gag att cgt gcg Phe Gly Tyr Pro Thr Thr Phe Lys Leu Asn Phe Ala Glu Ile Arg Ala 230 235 240 245			835
ctg agc gtc aac atg att aat gtg ctg gct gat tct ggt gcg gat acc Leu Ser Val Asn Met Ile Asn Val Leu Ala Asp Ser Gly Ala Asp Thr 250 255 260			883
gtg atc gtg gaa atc gcg gac gga att tat cag ggc gaa acc tcg cgg Val Ile Val Glu Ile Ala Asp Gly Ile Tyr Gln Gly Glu Thr Ser Arg 265 270 275			931
ctg ttg cgc gat caa gtg ttc cag gaa gcc gtg gat cat gtg gtg ttc Leu Leu Arg Asp Gln Val Phe Gln Glu Ala Val Asp His Val Val Phe 280 285 290			979
tcc gct gtt gat gcc ttg ggc gcg aag gcc ggt gtg cag gaa ctg cag Ser Ala Val Asp Ala Leu Gly Ala Lys Ala Gly Val Gln Glu Leu Gln 295 300 305			1027
gcg gcg ggg ctt cat gtg gct gcg gcc tcc gga gtg atg acg gct tcg Ala Ala Gly Leu His Val Ala Ala Ala Ser Gly Val Met Thr Ala Ser 310 315 320 325			1075
ccg ctg gcc acc gcg gaa gct gcc gct gtg ctt gaa gtt cca gtg gtg Pro Leu Ala Thr Ala Glu Ala Ala Ala Val Leu Glu Val Pro Val Val 330 335 340			1123
ccc act ttt gat ctc acc aac ccg gag atc gtc aca gcg gtg cta acg Pro Thr Phe Asp Leu Thr Asn Pro Glu Ile Val Thr Ala Val Leu Thr 345 350 355			1171
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<210> 1764

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 1764

Met Thr Ile Ala Leu Glu His Pro Val Leu His Ser Thr Ala Ile Ala
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Leu Pro Ala Arg Phe Gln Ala Ser Tyr Thr Thr Arg Leu Val Ala Val
20 25 30

Gly Val Asp Lys Arg Pro Ser Asp Phe Trp Leu Glu Thr Ala Gly Thr
35 40 45

Pro Gln Ala Gly Asp Val Val Ile Ala Arg Val Thr Ala Ile Asn Asn
50 55 60

His Lys Arg Val Glu Thr Pro Glu Ser Arg Lys Ala Ile Leu Phe Glu
 65 70 75 80
 Gly Val Leu Val Met Leu Ala Tyr Gly His Arg Tyr Ala Ala Asp Gln
 85 90 95
 Phe Leu Ala His Val Pro Glu Asp Leu Gly Pro Cys His Leu Val Ala
 100 105 110
 Ala Gly Gly Ile Ala Gly Thr Val Thr Ala Leu His Asp Arg Val Asp
 115 120 125
 Glu Pro Thr Glu Ile Glu Pro Leu Gly Leu Leu Thr Asn Ala Arg Gly
 130 135 140
 Thr Val Asn Val Arg Asp Phe Ala Ala Phe Asp Asn Pro Leu Lys Val
 145 150 155 160
 Glu Ala Pro Asn Lys Arg Ala Gln Val Ile Ala Val Leu Gly Thr Ser
 165 170 175
 Met Asn Ser Gly Lys Ser Thr Thr Leu Ala Cys Leu Val Asn Gly Leu
 180 185 190
 Ala Ala Ala Gly Gln Lys Val Ala Ala Gly Lys Ile Thr Gly Thr Gly
 195 200 205
 Ala Gly Asn Asp Arg Met Ile Tyr His Asp Ala Gly Ala His Ser Val
 210 215 220
 Ile Asp Phe Thr Asp Phe Gly Tyr Pro Thr Thr Phe Lys Leu Asn Phe
 225 230 235 240
 Ala Glu Ile Arg Ala Leu Ser Val Asn Met Ile Asn Val Leu Ala Asp
 245 250 255
 Ser Gly Ala Asp Thr Val Ile Val Glu Ile Ala Asp Gly Ile Tyr Gln
 260 265 270
 Gly Glu Thr Ser Arg Leu Leu Arg Asp Gln Val Phe Gln Glu Ala Val
 275 280 285
 Asp His Val Val Phe Ser Ala Val Asp Ala Leu Gly Ala Lys Ala Gly
 290 295 300
 Val Gln Glu Leu Gln Ala Ala Gly Leu His Val Ala Ala Ala Ser Gly
 305 310 315 320
 Val Met Thr Ala Ser Pro Leu Ala Thr Ala Glu Ala Ala Ala Val Leu
 325 330 335
 Glu Val Pro Val Val Pro Thr Phe Asp Leu Thr Asn Pro Glu Ile Val
 340 345 350
 Thr Ala Val Leu Thr Asp His Ala
 355 360

<210> 1765

<211> 1503

<212> DNA

acc gat gat gtg gga tac atc aaa tcc ctc ggc gca ccg gaa att cag 691
Thr Asp Asp Val Gly Tyr Ile Lys Ser Leu Gly Ala Pro Glu Ile Gln
185 190 195

gca aag aag cag gct gcg gaa att gca gaa act gaa gct gct cgt gcg Ala Lys Lys Gln Ala Ala Glu Ile Ala Glu Thr Glu Ala Ala Arg Ala 200 205 210	739
atc gct aaa tca cgc att gct aac caa gag gca gat ctg gtt gaa cag Ile Ala Lys Ser Arg Ile Ala Asn Gln Glu Ala Asp Leu Val Glu Gln 215 220 225	787
acc caa ctt gat gcc aac aag gct gcc gct gat gct cag gtc ggt gaa Thr Gln Leu Asp Ala Asn Lys Ala Ala Ala Asp Ala Gln Val Gly Glu 230 235 240 245	835
gcc cgt gcc cag gct atg cag gct gaa cgc ctt gcc gat gaa aaa gct Ala Arg Ala Gln Ala Met Gln Ala Glu Arg Leu Ala Asp Glu Lys Ala 250 255 260	883
cga cta gag gtt ctt cgc caa cag gct gaa aat aag cag atc gag ctg Arg Leu Glu Val Leu Arg Gln Gln Ala Glu Asn Lys Gln Ile Glu Leu 265 270 275	931
gaa gcc gaa gtg aac aag gtg gcc gac gct gaa cgc tac cgc cgc aag Glu Ala Glu Val Asn Lys Val Ala Asp Ala Glu Arg Tyr Arg Arg Lys 280 285 290	979
cag gaa gtc gaa gcc gat act ttc gag caa acc agg cgc gca cag gct Gln Glu Val Glu Ala Asp Thr Phe Glu Gln Thr Arg Arg Ala Gln Ala 295 300 305	1027
cag gtc gaa atc gca gaa gcc gaa gct acc gct gca aag gtt cgt gca Gln Val Glu Ile Ala Glu Ala Glu Ala Thr Ala Ala Lys Val Arg Ala 310 315 320 325	1075
atg gct gaa gcc gaa gct gtt cga ttg aag gga cag gca gag gca gac Met Ala Glu Ala Glu Ala Val Arg Leu Lys Gly Gln Ala Glu Ala Asp 330 335 340	1123
gct atc aag gca aag gcc gag gcc tac cgc gaa aac caa gaa gca cta Ala Ile Lys Ala Lys Ala Glu Ala Tyr Arg Glu Asn Gln Glu Ala Leu 345 350 355	1171
ctc gcc cag caa gcc atg gaa atc ctg ccg gaa ctc atg agc aac ttc Leu Ala Gln Gln Ala Met Glu Ile Leu Pro Glu Leu Met Ser Asn Phe 360 365 370	1219
gcc tct gga tac gca aac att gga tcc atg aca gtg ctc tcc ggt gga Ala Ser Gly Tyr Ala Asn Ile Gly Ser Met Thr Val Leu Ser Gly Gly 375 380 385	1267
gaa gga tcc gag aat tcc gtg ggt tca cgt ttt gcc ggt gaa caa gca Glu Gly Ser Glu Asn Ser Val Gly Ser Arg Phe Ala Gly Glu Gln Ala 390 395 400 405	1315
ctt gga ctg aaa tcc att att gaa tca gtc aag caa acc acc ggc att Leu Gly Leu Lys Ser Ile Ile Glu Ser Val Lys Gln Thr Thr Gly Ile 410 415 420	1363
gat cta gct gag atc atc caa ggc cgt gct gct gga cat gca cag ggc Asp Leu Ala Glu Ile Ile Gln Gly Arg Ala Ala Gly His Ala Gln Gly 425 430 435	1411

tcc gct cag ggt gca gcg att gct gaa gcg ctt tca cgc gat gaa act 1459
Ser Ala Gln Gly Ala Ala Ile Ala Glu Ala Leu Ser Arg Asp Glu Thr
440 445 450

gtg gaa gat cgc tct gaa aaa taatctagct gccagcgca tcg 1503
Val Glu Asp Arg Ser Glu Lys
455 460

<210> 1766

<211> 460

<212> PRT

<213> Corynebacterium glutamicum

<400> 1766

Met Glu Ala Ile Ala Ile Leu Phe Val Ile Gly Ala Ile Leu Val Val
1 5 10 15

Ala Val Ile Val Leu Gly Ile Phe Phe Leu Thr Ser Arg Thr Trp Ile
20 25 30

Lys Val Ala Ala Asp Glu Ala Leu Ile Val Ser Ala Lys Lys Lys
35 40 45

Gly Glu Ser Gln Val Ile Val His Gly Lys Ala Val Val Met Pro Ile
50 55 60

Thr Gln Thr His Gln Lys Ile Ser Leu Arg Ser Arg Gln Val Asn Met
65 70 75 80

Gln Val Thr Ala Gln Ser Asp Asp Asn Val Thr Leu Asn Val Glu Ala
85 90 95

Val Ala Leu Val Lys Ile Gly Ser Glu Ala Glu Phe Ile Arg Arg Ala
100 105 110

Ala Gln Arg Phe Ala Ser Ser Asp Lys Glu Ile Val Arg Phe Thr Gln
115 120 125

Asp Gln Leu Glu Gly Val Leu Arg Gly Val Val Ala Gln Gln Thr Val
130 135 140

Thr Ser Leu Met Arg Glu Arg Lys Lys Phe Ser Glu Gln Ile Ala Glu
145 150 155 160

Thr Val Ile Pro Glu Leu Glu Lys Gln Gly Leu Ile Leu Asp Ser Phe
165 170 175

Gln Ile Arg Gly Ile Thr Asp Asp Val Gly Tyr Ile Lys Ser Leu Gly
180 185 190

Ala Pro Glu Ile Gln Ala Lys Lys Gln Ala Ala Glu Ile Ala Glu Thr
195 200 205

Glu Ala Ala Arg Ala Ile Ala Lys Ser Arg Ile Ala Asn Gln Glu Ala
210 215 220

Asp Leu Val Glu Gln Thr Gln Leu Asp Ala Asn Lys Ala Ala Ala Asp
225 230 235 240

Ala Gln Val Gly Glu Ala Arg Ala Gln Ala Met Gln Ala Glu Arg Leu

245										250					255				
Ala	Asp	Glu	Lys	Ala	Arg	Leu	Glu	Val	Leu	Arg	Gln	Gln	Ala	Glu	Asn				
			260					265					270						
Lys	Gln	Ile	Glu	Leu	Glu	Ala	Glu	Val	Asn	Lys	Val	Ala	Asp	Ala	Glu				
		275					280					285							
Arg	Tyr	Arg	Arg	Lys	Gln	Glu	Val	Glu	Ala	Asp	Thr	Phe	Glu	Gln	Thr				
	290					295					300								
Arg	Arg	Ala	Gln	Ala	Gln	Val	Glu	Ile	Ala	Glu	Ala	Glu	Ala	Thr	Ala				
305					310				315						320				
Ala	Lys	Val	Arg	Ala	Met	Ala	Glu	Ala	Glu	Ala	Val	Arg	Leu	Lys	Gly				
				325					330					335					
Gln	Ala	Glu	Ala	Asp	Ala	Ile	Lys	Ala	Lys	Ala	Glu	Ala	Tyr	Arg	Glu				
			340					345					350						
Asn	Gln	Glu	Ala	Leu	Leu	Ala	Gln	Gln	Ala	Met	Glu	Ile	Leu	Pro	Glu				
		355					360					365							
Leu	Met	Ser	Asn	Phe	Ala	Ser	Gly	Tyr	Ala	Asn	Ile	Gly	Ser	Met	Thr				
	370					375					380								
Val	Leu	Ser	Gly	Gly	Glu	Gly	Ser	Glu	Asn	Ser	Val	Gly	Ser	Arg	Phe				
385					390					395					400				
Ala	Gly	Glu	Gln	Ala	Leu	Gly	Leu	Lys	Ser	Ile	Ile	Glu	Ser	Val	Lys				
				405					410					415					
Gln	Thr	Thr	Gly	Ile	Asp	Leu	Ala	Glu	Ile	Ile	Gln	Gly	Arg	Ala	Ala				
			420					425					430						
Gly	His	Ala	Gln	Gly	Ser	Ala	Gln	Gly	Ala	Ala	Ile	Ala	Glu	Ala	Leu				
		435					440					445							
Ser	Arg	Asp	Glu	Thr	Val	Glu	Asp	Arg	Ser	Glu	Lys								
	450					455					460								

<210> 1767

<211> 945

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(922)

<223> RXA00463

<400> 1767

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				Met	Gln	Thr	Thr	Thr	
				1				5	

ggg	gag	acg	tcg	ata	agc	aat	gaa	acc	tcg	ttt	aac	gcc	tca	cgc	gaa	163
Gly	Glu	Thr	Ser	Ile	Ser	Asn	Glu	Thr	Ser	Phe	Asn	Ala	Ser	Arg	Glu	

	10	15	20	
acc tcg ctg acg gcg ctg ggt ttc ttg gac tat ctt gac gag gag caa				211
Thr Ser Leu Thr Ala Leu Gly Phe Leu Asp Tyr Leu Asp Glu Glu Gln	25	30	35	
cgc gcc gcc ttg ctc ggt gaa ggc ctg gac atc agc acg ctg acc tgg				259
Arg Ala Ala Leu Leu Gly Glu Gly Leu Asp Ile Ser Thr Leu Thr Trp	40	45	50	
gcc aac cag gtt acc gcg ctg cgt gtg ctg gaa tcc ctc ttc aat gag				307
Ala Asn Gln Val Thr Ala Leu Arg Val Leu Glu Ser Leu Phe Asn Glu	55	60	65	
cat gca tac gag ctg gtt tct gca gtg att cag cat gta gct caa gaa				355
His Ala Tyr Glu Leu Val Ser Ala Val Ile Gln His Val Ala Gln Glu	70	75	80	85
cct ggc gat aat cca cac cac ttt ctg aag ttc tcg cct gaa cca tcc				403
Pro Gly Asp Asn Pro His His Phe Leu Lys Phe Ser Pro Glu Pro Ser	90	95	100	
acc gag aat tct tgg gaa ttg acc ctg gat gga cca act gtc gga ttg				451
Thr Glu Asn Ser Trp Glu Leu Thr Leu Asp Gly Pro Thr Val Gly Leu	105	110	115	
aaa gtc act ttc gat ccg gac ggt cag atc act ttc aag gat gct cat				499
Lys Val Thr Phe Asp Pro Asp Gly Gln Ile Thr Phe Lys Asp Ala His	120	125	130	
ttg ggc ctg agc cca gct gag gtc gtt agt gtc act gag gcg tta gat				547
Leu Gly Leu Ser Pro Ala Glu Val Val Ser Val Thr Glu Ala Leu Asp	135	140	145	
acc tcc tat tcg gaa tcg caa atc aaa aaa gct gcg gaa caa ctg gtg				595
Thr Ser Tyr Ser Glu Ser Gln Ile Lys Lys Ala Ala Glu Gln Leu Val	150	155	160	165
gga agc ctc aat cca acc cag cag gca gcg ctc caa gga tcc ggt ttg				643
Gly Ser Leu Asn Pro Thr Gln Gln Ala Ala Leu Gln Gly Ser Gly Leu	170	175	180	
cga gga gca cag ctc act gaa gag caa aag acc ctg ttc tta aag atg				691
Arg Gly Ala Gln Leu Thr Glu Glu Gln Lys Thr Leu Phe Leu Lys Met	185	190	195	
acc tcc aac tgg atc gac ctt gcc aat ggc gat tcc ggc tct gaa cag				739
Thr Ser Asn Trp Ile Asp Leu Ala Asn Gly Asp Ser Gly Ser Glu Gln	200	205	210	
caa gaa gaa atc gct gat acg ttc agt gat acc tac atc att tgg aat				787
Gln Glu Glu Ile Ala Asp Thr Phe Ser Asp Thr Tyr Ile Ile Trp Asn	215	220	225	
gag cag aaa gat ggc tca gca ttc ttc cag atg aaa ggc cct gag ctc				835
Glu Gln Lys Asp Gly Ser Ala Phe Phe Gln Met Lys Gly Pro Glu Leu	230	235	240	245
gac ttc agc tat aaa gag agc gtg cct gaa aac gct gaa ctc tct gca				883
Asp Phe Ser Tyr Lys Glu Ser Val Pro Glu Asn Ala Glu Leu Ser Ala	250	255	260	

cgg gga gtc ccc aat att cag acc tct ttt cag tca cct taactggcat 932
 Arg Gly Val Pro Asn Ile Gln Thr Ser Phe Gln Ser Pro
 265 270

tggttttagtt tgg 945

<210> 1768

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 1768

Met Gln Thr Thr Thr Gly Glu Thr Ser Ile Ser Asn Glu Thr Ser Phe
 1 5 10 15

Asn Ala Ser Arg Glu Thr Ser Leu Thr Ala Leu Gly Phe Leu Asp Tyr
 20 25 30

Leu Asp Glu Glu Gln Arg Ala Ala Leu Leu Gly Glu Gly Leu Asp Ile
 35 40 45

Ser Thr Leu Thr Trp Ala Asn Gln Val Thr Ala Leu Arg Val Leu Glu
 50 55 60

Ser Leu Phe Asn Glu His Ala Tyr Glu Leu Val Ser Ala Val Ile Gln
 65 70 75 80

His Val Ala Gln Glu Pro Gly Asp Asn Pro His His Phe Leu Lys Phe
 85 90 95

Ser Pro Glu Pro Ser Thr Glu Asn Ser Trp Glu Leu Thr Leu Asp Gly
 100 105 110

Pro Thr Val Gly Leu Lys Val Thr Phe Asp Pro Asp Gly Gln Ile Thr
 115 120 125

Phe Lys Asp Ala His Leu Gly Leu Ser Pro Ala Glu Val Val Ser Val
 130 135 140

Thr Glu Ala Leu Asp Thr Ser Tyr Ser Glu Ser Gln Ile Lys Lys Ala
 145 150 155 160

Ala Glu Gln Leu Val Gly Ser Leu Asn Pro Thr Gln Gln Ala Ala Leu
 165 170 175

Gln Gly Ser Gly Leu Arg Gly Ala Gln Leu Thr Glu Glu Gln Lys Thr
 180 185 190

Leu Phe Leu Lys Met Thr Ser Asn Trp Ile Asp Leu Ala Asn Gly Asp
 195 200 205

Ser Gly Ser Glu Gln Gln Glu Glu Ile Ala Asp Thr Phe Ser Asp Thr
 210 215 220

Tyr Ile Ile Trp Asn Glu Gln Lys Asp Gly Ser Ala Phe Phe Gln Met
 225 230 235 240

Lys Gly Pro Glu Leu Asp Phe Ser Tyr Lys Glu Ser Val Pro Glu Asn
 245 250 255

Ala Glu Leu Ser Ala Arg Gly Val Pro Asn Ile Gln Thr Ser Phe Gln
 260 265 270

Ser Pro

<210> 1769

<211> 942

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(919)

<223> RXA00468

<400> 1769

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ggcagaattt tgctcaagtt gcctaaatca agcacccggt cgaataagtg tccacccttt 60
ggttttattct tgaactcact taagttttga atttttagtt gtg aaa gta gtt gat 115
                                   Val Lys Val Val Asp
                                   1                               5

gca caa gtg gtt atg ggg cca acc cac gct atg agc ggt gca gcc gtg 163
Ala Gln Val Val Met Gly Pro Thr His Ala Met Ser Gly Ala Ala Val
                                   10                               20

ggg ctt gct gtt gct caa att ctc cca gca gaa tgg ggt ggg gtt acc 211
Gly Leu Ala Val Ala Gln Ile Leu Pro Ala Glu Trp Gly Gly Val Thr
                                   25                               35

acc gcc acg gag gct ttt att tat gcg ggt tta gcg gcg ggt gca gcg 259
Thr Ala Thr Glu Ala Phe Ile Tyr Ala Gly Leu Ala Ala Gly Ala Ala
                                   40                               50

ctg ctc ccg gac ctt gat tca ccg cag gcc acg gtg tcg cgt tct ttt 307
Leu Leu Pro Asp Leu Asp Ser Pro Gln Ala Thr Val Ser Arg Ser Phe
                                   55                               65

ggg ccg att acc caa gtg att tcg cgt ttt aca gag aat att tgc caa 355
Gly Pro Ile Thr Gln Val Ile Ser Arg Phe Thr Glu Asn Ile Cys Gln
                                   70                               75                               80                               85

act ttc gtc aat gtc acc agg ggc agg aaa gac aaa cac tgc aac aac 403
Thr Phe Val Asn Val Thr Arg Gly Arg Lys Asp Lys His Cys Asn Asn
                                   90                               95                               100

ggg cac cgc acg ttg aca cat acg gtg tgg agc gct gct gcc aca ggc 451
Gly His Arg Thr Leu Thr His Thr Val Trp Ser Ala Ala Ala Thr Gly
                                   105                               110                               115

gct ggt gcc aca gcg cta att ggc gcc tat gga aaa cct gcg gtg att 499
Ala Gly Ala Thr Ala Leu Ile Gly Ala Tyr Gly Lys Pro Ala Val Ile
                                   120                               125                               130

ggg ttg ctg ttt ttc ttc ctc ggg ctc gcc att aga ggt ctc atg cct 547
Gly Leu Leu Phe Phe Phe Leu Gly Leu Ala Ile Arg Gly Leu Met Pro
                                   135                               140                               145

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gaa tgg tca aag aac gca gat tgg ctt tta gtt act gga gct tcc gct 595
 Glu Trp Ser Lys Asn Ala Asp Trp Leu Leu Val Thr Gly Ala Ser Ala
 150 155 160 165

gca tta gca gtg gga gta tgg aat tat gct ccc gaa agt tca ttc ggc 643
 Ala Leu Ala Val Gly Val Trp Asn Tyr Ala Pro Glu Ser Ser Phe Gly
 170 175 180

att gtg tta ggc tcc gcc att aca gtt gga agc ctg acc cac ttg gct 691
 Ile Val Leu Gly Ser Ala Ile Thr Val Gly Ser Leu Thr His Leu Ala
 185 190 195

ggc gat atg gcc act aag gcc ggt atc cca gca ttt gcc ccg gtc att 739
 Gly Asp Met Ala Thr Lys Ala Gly Ile Pro Ala Phe Ala Pro Val Ile
 200 205 210

ccg ctg aag ggc aaa cgc tgg tgg aac ctc aaa ttg cct aag ttt tta 787
 Pro Leu Lys Gly Lys Arg Trp Trp Asn Leu Lys Leu Pro Lys Phe Leu
 215 220 225

agc att cgt gcc aac ggt cct gcc gat aag ttc tta ctg ttc gta ttc 835
 Ser Ile Arg Ala Asn Gly Pro Ala Asp Lys Phe Leu Leu Phe Val Phe
 230 235 240 245

tcg gtg gcg gtc atc att cag att ggt ttg gtc tca tcg gga aat atg 883
 Ser Val Ala Val Ile Ile Gln Ile Gly Leu Val Ser Ser Gly Asn Met
 250 255 260

agc acc att atg atg aat ctg ctt agt cct gca ctg taattaatgg 929
 Ser Thr Ile Met Met Asn Leu Leu Ser Pro Ala Leu
 265 270

cagttgcggtt tcg 942

<210> 1770

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 1770

Val Lys Val Val Asp Ala Gln Val Val Met Gly Pro Thr His Ala Met
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Ser Gly Ala Ala Val Gly Leu Ala Val Ala Gln Ile Leu Pro Ala Glu
 20 25 30

Trp Gly Gly Val Thr Thr Ala Thr Glu Ala Phe Ile Tyr Ala Gly Leu
 35 40 45

Ala Ala Gly Ala Ala Leu Leu Pro Asp Leu Asp Ser Pro Gln Ala Thr
 50 55 60

Val Ser Arg Ser Phe Gly Pro Ile Thr Gln Val Ile Ser Arg Phe Thr
 65 70 75 80

Glu Asn Ile Cys Gln Thr Phe Val Asn Val Thr Arg Gly Arg Lys Asp
 85 90 95

Lys His Cys Asn Asn Gly His Arg Thr Leu Thr His Thr Val Trp Ser
 100 105 110

Ala Ala Ala Thr Gly Ala Gly Ala Thr Ala Leu Ile Gly Ala Tyr Gly
 115 120 125

Lys Pro Ala Val Ile Gly Leu Leu Phe Phe Phe Leu Gly Leu Ala Ile
 130 135 140

Arg Gly Leu Met Pro Glu Trp Ser Lys Asn Ala Asp Trp Leu Leu Val
 145 150 155 160

Thr Gly Ala Ser Ala Ala Leu Ala Val Gly Val Trp Asn Tyr Ala Pro
 165 170 175

Glu Ser Ser Phe Gly Ile Val Leu Gly Ser Ala Ile Thr Val Gly Ser
 180 185 190

Leu Thr His Leu Ala Gly Asp Met Ala Thr Lys Ala Gly Ile Pro Ala
 195 200 205

Phe Ala Pro Val Ile Pro Leu Lys Gly Lys Arg Trp Trp Asn Leu Lys
 210 215 220

Leu Pro Lys Phe Leu Ser Ile Arg Ala Asn Gly Pro Ala Asp Lys Phe
 225 230 235 240

Leu Leu Phe Val Phe Ser Val Ala Val Ile Ile Gln Ile Gly Leu Val
 245 250 255

Ser Ser Gly Asn Met Ser Thr Ile Met Met Asn Leu Leu Ser Pro Ala
 260 265 270

Leu

<210> 1771
 <211> 1299
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)...(1276)
 <223> RXA00469

<400> 1771
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cccattcact tatcagcctc aacactccac aatagagtct atg agt act ttt cag 115
 Met Ser Thr Phe Gln
 1 5

gag ccc cac cac aac cag gga ttc atc cct ttt gcc caa cct ggt tat 163
 Glu Pro His His Asn Gln Gly Phe Ile Pro Phe Ala Gln Pro Gly Tyr
 10 15 20

gaa gct cca aca cca cac ctt gca act ggt act ttt cag caa atg tgg 211
 Glu Ala Pro Thr Pro His Leu Ala Thr Gly Thr Phe Gln Gln Met Trp
 25 30 35

cag acc cgc ccc gca cgc atc cct gcc aag caa ggt ggt cac gcc aaa 259

Gln Thr Arg Pro Ala Arg Ile Pro Ala Lys Gln Gly Gly His Ala Lys	
40 45 50	
gta gct ggt gtc tgt gaa ggc att ggt gtg cgt tat caa atc gac ccg	307
Val Ala Gly Val Cys Glu Gly Ile Gly Val Arg Tyr Gln Ile Asp Pro	
55 60 65	
gtg ctc att cgt cta ttt ttc gtg gtc act ggt gtc ttc ggc gcc ggt	355
Val Leu Ile Arg Leu Phe Phe Val Val Thr Gly Val Phe Gly Ala Gly	
70 75 80 85	
gtc gca gcc tat ctc att gca tgg ctg tgc atg ccc cgc tac tcc gtt	403
Val Ala Ala Tyr Leu Ile Ala Trp Leu Cys Met Pro Arg Tyr Ser Val	
90 95 100	
ccg gtc tcc ccc atc gaa gct ctc tgg acc ccg ggc cac acc aaa gac	451
Pro Val Ser Pro Ile Glu Ala Leu Trp Thr Pro Gly His Thr Lys Asp	
105 110 115	
cgc aac cac ggc tgg tgg ctg gtc atc gcg ttc ttt atg ttc tca ggt	499
Arg Asn His Gly Trp Trp Leu Val Ile Ala Phe Phe Met Phe Ser Gly	
120 125 130	
gtt tta tcc tcc ggc gct gga gga ata tcc ggc cca gca gca gcc att	547
Val Leu Ser Ser Gly Ala Gly Gly Ile Ser Gly Pro Ala Ala Ala Ile	
135 140 145	
act tac ctt tgc ctt tta gcc atg tgg tgg gcg ttg cat aag aaa caa	595
Thr Tyr Leu Cys Leu Leu Ala Met Trp Trp Ala Leu His Lys Lys Gln	
150 155 160 165	
cca ctt cca ccc cgc gga cta ctc acc act gaa ttc act gtt tct gag	643
Pro Leu Pro Pro Arg Gly Leu Leu Thr Thr Glu Phe Thr Val Ser Glu	
170 175 180	
gat gcc acc atg aaa aac gaa gat ctc tac cca cga ccc caa cca gat	691
Asp Ala Thr Met Lys Asn Glu Asp Leu Tyr Pro Arg Pro Gln Pro Asp	
185 190 195	
cta agc act atc acc ccc gtt gag ggc tac tat gca ccc ttc gcg caa	739
Leu Ser Thr Ile Thr Pro Val Glu Gly Tyr Tyr Ala Pro Phe Ala Gln	
200 205 210	
caa acc ccc gaa gcg cct cat tgg gat cca ctt gcc caa aac caa tac	787
Gln Thr Pro Glu Ala Pro His Trp Asp Pro Leu Ala Gln Asn Gln Tyr	
215 220 225	
aac acc tgg gat gta caa gtc cct cca caa aag cct cag aaa aag cgc	835
Asn Thr Trp Asp Val Gln Val Pro Pro Gln Lys Pro Gln Lys Lys Arg	
230 235 240 245	
cat gtg tgg cca tgg att gtc ggc ggt gta gtt ggt acc gga gtt gtc	883
His Val Trp Pro Trp Ile Val Gly Gly Val Val Gly Thr Gly Val Val	
250 255 260	
atg agc gcc ctc gca ggc ctg ttt att tca aat atc gat ccc atc tac	931
Met Ser Ala Leu Ala Gly Leu Phe Ile Ser Asn Ile Asp Pro Ile Tyr	
265 270 275	
ttt gaa gac gac cct gga atc ggc gat gtc aat ctc atc ccc acc aac	979
Phe Glu Asp Asp Pro Gly Ile Gly Asp Val Asn Leu Ile Pro Thr Asn	

280	285	290	
gat gaa ctc ctc agc agc tac acc tct ggt gtg ggc gaa atg aac cta			1027
Asp Glu Leu Leu Ser Ser Tyr Thr Ser Gly Val Gly Glu Met Asn Leu			
295	300	305	
gat ttc agc aac ctc acc caa ctt gat cag .gaa caa aac gtt caa atc			1075
Asp Phe Ser Asn Leu Thr Gln Leu Asp Gln Glu Gln Asn Val Gln Ile			
310	315	320	325
acc tca ggt atc ggt gaa gtc atg gtg acc ctg cct gat gac gtg cca			1123
Thr Ser Gly Ile Gly Glu Val Met Val Thr Leu Pro Asp Asp Val Pro			
	330	335	340
gta agc ttg agt tgc tcc gcc ggt gtg ggc aca gcg cgc tgt gat gtt			1171
Val Ser Leu Ser Cys Ser Ala Gly Val Gly Thr Ala Arg Cys Asp Val			
	345	350	355
gga gac ctc gcc gcc cac aat gct gat ttg gaa ggt ccg atg ttg aat			1219
Gly Asp Leu Ala Ala His Asn Ala Asp Leu Glu Gly Pro Met Leu Asn			
	360	365	370
ctg gtt gta aat tct gga atc ggc gat gtg aag gtg gag ttc gct gat			1267
Leu Val Val Asn Ser Gly Ile Gly Asp Val Lys Val Glu Phe Ala Asp			
	375	380	385
cag aat gac tagcccgacc ctatgtgagt agt			1299
Gln Asn Asp			
390			

<210> 1772

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 1772

Met Ser Thr Phe Gln Glu Pro His His Asn Gln Gly Phe Ile Pro Phe			
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Ala Gln Pro Gly Tyr Glu Ala Pro Thr Pro His Leu Ala Thr Gly Thr			
	20	25	30
Phe Gln Gln Met Trp Gln Thr Arg Pro Ala Arg Ile Pro Ala Lys Gln			
	35	40	45
Gly Gly His Ala Lys Val Ala Gly Val Cys Glu Gly Ile Gly Val Arg			
	50	55	60
Tyr Gln Ile Asp Pro Val Leu Ile Arg Leu Phe Phe Val Val Thr Gly			
	65	70	75
Val Phe Gly Ala Gly Val Ala Ala Tyr Leu Ile Ala Trp Leu Cys Met			
	85	90	95
Pro Arg Tyr Ser Val Pro Val Ser Pro Ile Glu Ala Leu Trp Thr Pro			
	100	105	110
Gly His Thr Lys Asp Arg Asn His Gly Trp Trp Leu Val Ile Ala Phe			
	115	120	125

Phe Met Phe Ser Gly Val Leu Ser Ser Gly Ala Gly Gly Ile Ser Gly
130 135 140

Pro Ala Ala Ala Ile Thr Tyr Leu Cys Leu Leu Ala Met Trp Trp Ala
145 150 155 160

Leu His Lys Lys Gln Pro Leu Pro Pro Arg Gly Leu Leu Thr Thr Glu
165 170 175

Phe Thr Val Ser Glu Asp Ala Thr Met Lys Asn Glu Asp Leu Tyr Pro
180 185 190

Arg Pro Gln Pro Asp Leu Ser Thr Ile Thr Pro Val Glu Gly Tyr Tyr
195 200 205

Ala Pro Phe Ala Gln Gln Thr Pro Glu Ala Pro His Trp Asp Pro Leu
210 215 220

Ala Gln Asn Gln Tyr Asn Thr Trp Asp Val Gln Val Pro Pro Gln Lys
225 230 235 240

Pro Gln Lys Lys Arg His Val Trp Pro Trp Ile Val Gly Gly Val Val
245 250 255

Gly Thr Gly Val Val Met Ser Ala Leu Ala Gly Leu Phe Ile Ser Asn
260 265 270

Ile Asp Pro Ile Tyr Phe Glu Asp Asp Pro Gly Ile Gly Asp Val Asn
275 280 285

Leu Ile Pro Thr Asn Asp Glu Leu Leu Ser Ser Tyr Thr Ser Gly Val
290 295 300

Gly Glu Met Asn Leu Asp Phe Ser Asn Leu Thr Gln Leu Asp Gln Glu
305 310 315 320

Gln Asn Val Gln Ile Thr Ser Gly Ile Gly Glu Val Met Val Thr Leu
325 330 335

Pro Asp Asp Val Pro Val Ser Leu Ser Cys Ser Ala Gly Val Gly Thr
340 345 350

Ala Arg Cys Asp Val Gly Asp Leu Ala Ala His Asn Ala Asp Leu Glu
355 360 365

Gly Pro Met Leu Asn Leu Val Val Asn Ser Gly Ile Gly Asp Val Lys
370 375 380

Val Glu Phe Ala Asp Gln Asn Asp
385 390

<210> 1773

<211> 984

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(961)

<223> RXA00472

<400> 1773

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ctgctctact acggaagata ccgctatatc ggagacgaca gtg tct agt gtt gca 115
                                   Val Ser Ser Val Ala
                                   1 5

acg aaa aca acc tcg act ctg cct gaa atg aac tcc gca gta tca gca 163
Thr Lys Thr Thr Ser Thr Leu Pro Glu Met Asn Ser Ala Val Ser Ala
                                   10 15 20

gac ggc gtg acg atc act atc gat tct gcc ttc acg aca gac tct gta 211
Asp Gly Val Thr Ile Thr Ile Asp Ser Ala Phe Thr Thr Asp Ser Val
                                   25 30 35

gaa atg gaa tcc cta gac aga cct tct ggc gac atc caa ccc gag atg 259
Glu Met Glu Ser Leu Asp Arg Pro Ser Gly Asp Ile Gln Pro Glu Met
                                   40 45 50

tct aga gaa gac gga atc ttt gtc gta gtc gaa acc act ata aag aac 307
Ser Arg Glu Asp Gly Ile Phe Val Val Val Glu Thr Thr Ile Lys Asn
                                   55 60 65

gag agt gga gca gat atg gac atc acc tgt gca tcc act ggt tca act 355
Glu Ser Gly Ala Asp Met Asp Ile Thr Cys Ala Ser Thr Gly Ser Thr
                                   70 75 80 85

gtc tat gca gaa atc tcc act aat caa gag gcc gta tac caa cca ata 403
Val Tyr Ala Glu Ile Ser Thr Asn Gln Glu Ala Val Tyr Gln Pro Ile
                                   90 95 100

cgc gat tta ttc ctc atc cca gga aac ccg gaa tgc aac cat aat cta 451
Arg Asp Leu Phe Leu Ile Pro Gly Asn Pro Glu Cys Asn His Asn Leu
                                   105 110 115

gga tcc ggt ttc gac gca cca atg act tgg gta ttt caa atc cct aaa 499
Gly Ser Gly Phe Asp Ala Pro Met Thr Trp Val Phe Gln Ile Pro Lys
                                   120 125 130

gat gcc act gcg gag cga ttt gga ttc aca cat agt gag ctc ggt gat 547
Asp Ala Thr Ala Glu Arg Phe Gly Phe Thr His Ser Glu Leu Gly Asp
                                   135 140 145

ggg aaa cta act tgg att gca ctc aat gat ttg agt aat tcg gag cca 595
Gly Lys Leu Thr Trp Ile Ala Leu Asn Asp Leu Ser Asn Ser Glu Pro
                                   150 155 160 165

gct act gaa tca act atg cga gac gaa gca gca atc gat ccg agc acc 643
Ala Thr Glu Ser Thr Met Arg Asp Glu Ala Ala Ile Asp Pro Ser Thr
                                   170 175 180

cct cag caa act cca gta cag gaa act gtg atc tca caa aac acc att 691
Pro Gln Gln Thr Pro Val Gln Glu Thr Val Ile Ser Gln Asn Thr Ile
                                   185 190 195

gaa act cct gta gcc cct gct cct gcg gta cct gct tat ggc gct tct 739
Glu Thr Pro Val Ala Pro Ala Pro Ala Val Pro Ala Tyr Gly Ala Ser
                                   200 205 210

tgc cct gtc tcg atg ctc cag cag cca agt caa gct gca gat ggt tca 787

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Cys Pro Val Ser Met Leu Gln Gln Pro Ser Gln Ala Ala Asp Gly Ser
 215 220 225
 gct ttg gtc tgc att tat gca gga acc ccc aac cca atc tgg gtc tac 835
 Ala Leu Val Cys Ile Tyr Ala Gly Thr Pro Asn Pro Ile Trp Val Tyr
 230 235 240 245
 ggc cca gaa cct ctc gga gtc ggg act gct aca ccg ggt ggg gca tgc 883
 Gly Pro Glu Pro Leu Gly Val Gly Thr Ala Thr Pro Gly Gly Ala Cys
 250 255 260
 gaa gga tac gag gcc ggt ggg caa gat gct tct gga aat ata atg atg 931
 Glu Gly Tyr Glu Ala Gly Gly Gln Asp Ala Ser Gly Asn Ile Met Met
 265 270 275
 tgc tca ggc gga caa tgg gtc tat ggg cca taaatctaaa atcaaagagt 981
 Cys Ser Gly Gly Gln Trp Val Tyr Gly Pro
 280 285
 gca 984

<210> 1774
 <211> 287
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1774
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 Ser Ala Val Ser Ala Asp Gly Val Thr Ile Thr Ile Asp Ser Ala Phe
 20 25 30
 Thr Thr Asp Ser Val Glu Met Glu Ser Leu Asp Arg Pro Ser Gly Asp
 35 40 45
 Ile Gln Pro Glu Met Ser Arg Glu Asp Gly Ile Phe Val Val Val Glu
 50 55 60
 Thr Thr Ile Lys Asn Glu Ser Gly Ala Asp Met Asp Ile Thr Cys Ala
 65 70 75 80
 Ser Thr Gly Ser Thr Val Tyr Ala Glu Ile Ser Thr Asn Gln Glu Ala
 85 90 95
 Val Tyr Gln Pro Ile Arg Asp Leu Phe Leu Ile Pro Gly Asn Pro Glu
 100 105 110
 Cys Asn His Asn Leu Gly Ser Gly Phe Asp Ala Pro Met Thr Trp Val
 115 120 125
 Phe Gln Ile Pro Lys Asp Ala Thr Ala Glu Arg Phe Gly Phe Thr His
 130 135 140
 Ser Glu Leu Gly Asp Gly Lys Leu Thr Trp Ile Ala Leu Asn Asp Leu
 145 150 155 160
 Ser Asn Ser Glu Pro Ala Thr Glu Ser Thr Met Arg Asp Glu Ala Ala
 165 170 175

Ile Asp Pro Ser Thr Pro Gln Gln Thr Pro Val Gln Glu Thr Val Ile
 180 185 190
 Ser Gln Asn Thr Ile Glu Thr Pro Val Ala Pro Ala Pro Ala Val Pro
 195 200 205
 Ala Tyr Gly Ala Ser Cys Pro Val Ser Met Leu Gln Gln Pro Ser Gln
 210 215 220
 Ala Ala Asp Gly Ser Ala Leu Val Cys Ile Tyr Ala Gly Thr Pro Asn
 225 230 235 240
 Pro Ile Trp Val Tyr Gly Pro Glu Pro Leu Gly Val Gly Thr Ala Thr
 245 250 255
 Pro Gly Gly Ala Cys Glu Gly Tyr Glu Ala Gly Gly Gln Asp Ala Ser
 260 265 270
 Gly Asn Ile Met Met Cys Ser Gly Gly Gln Trp Val Tyr Gly Pro
 275 280 285

<210> 1775

<211> 1701

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1678)

<223> RXA00474

<400> 1775

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 Met Ala Leu Trp Phe
 1 5
 ccg gat tgg cct gtg cag gcg gtt cat ttg gat gaa gat gct ccc gcg 163
 Pro Asp Trp Pro Val Gln Ala Val His Leu Asp Glu Asp Ala Pro Ala
 10 15 20
 cac aat aaa cct gtg gcg att gct gcg cat tac cgc atc cag gtg tgt 211
 His Asn Lys Pro Val Ala Ile Ala Ala His Tyr Arg Ile Gln Val Cys
 25 30 35
 ggc gtg gct gcg cgc aag cgt ggg gtg cgt cgt ggg atg aag gtt cgg 259
 Gly Val Ala Ala Arg Lys Arg Gly Val Arg Arg Gly Met Lys Val Arg
 40 45 50
 cag gcg cag gct gtg tgc cct gag ctg gag gtt gtt gac gcg gat gca 307
 Gln Ala Gln Ala Val Cys Pro Glu Leu Glu Val Val Asp Ala Asp Ala
 55 60 65
 gat cgt gat gcc cgg atg ttt gag ggc atc gtg gca tcg ctc ggt gag 355
 Asp Arg Asp Ala Arg Met Phe Glu Gly Ile Val Ala Ser Leu Gly Glu
 70 75 80 85
 gtt gcc tcc agc gtc gag gtg ctt cgt ccg ggt ctg gtc gcg gtc gat 403
 Val Ala Ser Ser Val Glu Val Leu Arg Pro Gly Leu Val Ala Val Asp

90	95	100	
gcg gga gct gcc gcg cgc tat tac ggt tca gag gac atc gct gct cag Ala Gly Ala Ala Ala Arg Tyr Tyr Gly Ser Glu Asp Ile Ala Ala Gln 105 110 115			451
atg ctt atc gac gcc gcc ctg cgc caa ggc atc gac gtt ttc gcc ggg Met Leu Ile Asp Ala Ala Leu Arg Gln Gly Ile Asp Val Phe Ala Gly 120 125 130			499
gtt gcg gat gag atc acg acg gcc gtc atc gcg gcg agg gcg aat ggt Val Ala Asp Glu Ile Thr Thr Ala Val Ile Ala Ala Arg Ala Asn Gly 135 140 145			547
ggg act gtg gtg aag agg gag gcg tcg aga agc ttt tta cag cag caa Gly Thr Val Val Lys Arg Glu Ala Ser Arg Ser Phe Leu Gln Gln Gln 150 155 160 165			595
ccc ctg ggc gtg ctg gcg gcc gag gaa gcg ctg ggt tgt gag gcg gag Pro Leu Gly Val Leu Ala Ala Glu Glu Ala Leu Gly Cys Glu Ala Glu 170 175 180			643
gtg gtg cgc gcg ctg gcg gat ctg ggc atg cgc acg ctt ggt gag ctg Val Val Arg Ala Leu Ala Asp Leu Gly Met Arg Thr Leu Gly Glu Leu 185 190 195			691
gcg gaa ctg ccg gta gaa gcc gtg gcg acg cgt ttc ggc aac gct ggt Ala Glu Leu Pro Val Glu Ala Val Ala Thr Arg Phe Gly Asn Ala Gly 200 205 210			739
ctg cgg tgt cac aac att gcg cgt gcc agg cac gat cgt aag gtc gcg Leu Arg Cys His Asn Ile Ala Arg Ala Arg His Asp Arg Lys Val Ala 215 220 225			787
cca ccg atc acg cat gca gat tgg gag gtt tcg cat gtg ccg gag gag Pro Pro Ile Thr His Ala Asp Trp Glu Val Ser His Val Pro Glu Glu 230 235 240 245			835
cct att ttg cgt gtc gac gcc gcc tcg ttt gtt gcg cgc aac ctt gcc Pro Ile Leu Arg Val Asp Ala Ala Ser Phe Val Ala Arg Asn Leu Ala 250 255 260			883
tcg cgc ctg cat caa ctg ctg agc aaa ggt ggc gtg gtg tgc caa ttg Ser Arg Leu His Gln Leu Leu Ser Lys Gly Gly Val Val Cys Gln Leu 265 270 275			931
ctc aag gtc aca gcc gat ttc agt act ggt gat acg gtg agc aga att Leu Lys Val Thr Ala Asp Phe Ser Thr Gly Asp Thr Val Ser Arg Ile 280 285 290			979
tgg cgt acc ggt gaa cct tta acg gaa cag gca act gcg gat cgg gtg Trp Arg Thr Gly Glu Pro Leu Thr Glu Gln Ala Thr Ala Asp Arg Val 295 300 305			1027
cgt tgg cag ttg gat ggg tgg ttg act gcg cgc ggt gtg cat tcc gat Arg Trp Gln Leu Asp Gly Trp Leu Thr Ala Arg Gly Val His Ser Asp 310 315 320 325			1075
gat ccg aat gag cac gat ggg att acg gcg ttg tgg ctt att cct ttg Asp Pro Asn Glu His Asp Gly Ile Thr Ala Leu Trp Leu Ile Pro Leu 330 335 340			1123

gaa tgt gtg cca ccg gat atg gcc agc ggc gga ttg tgg gat acc ggg 1171
 Glu Cys Val Pro Pro Asp Met Ala Ser Gly Gly Leu Trp Asp Thr Gly
 345 350 355

cgc agc cag cag cat gtg gcc aga caa gtc att gag cgt gtg caa tca 1219
 Arg Ser Gln Gln His Val Ala Arg Gln Val Ile Glu Arg Val Gln Ser
 360 365 370

agc ttg ggc gtg gat gcg gtg ctg cag cct gtt ccg gct ggt ggt cgg 1267
 Ser Leu Gly Val Asp Ala Val Leu Gln Pro Val Pro Ala Gly Gly Arg
 375 380 385

gga gta gaa gaa cgc att cat ttt gtt ccc tat ggt gaa aaa cgt gat 1315
 Gly Val Glu Glu Arg Ile His Phe Val Pro Tyr Gly Glu Lys Arg Asp
 390 395 400 405

gct atc cgc aat cca gcg ggg tcg tgg cca ggg aaa ata cca ggt ccg 1363
 Ala Ile Arg Asn Pro Ala Gly Ser Trp Pro Gly Lys Ile Pro Gly Pro
 410 415 420

ctg cct gct cgg ttg ggc ggt ggg atc aac cac ccg gcc tcg caa gtg 1411
 Leu Pro Ala Arg Leu Gly Gly Gly Ile Asn His Pro Ala Ser Gln Val
 425 430 435

acc atg att gat aca gaa ggg cag cgt att tac gtc acc gca gag gca 1459
 Thr Met Ile Asp Thr Glu Gly Gln Arg Ile Tyr Val Thr Ala Glu Ala
 440 445 450

ttg ctc agc tcg tcg ccg tat gcc ttg tcc tgg ggg ccg gcc cgc tat 1507
 Leu Leu Ser Ser Ser Pro Tyr Ala Leu Ser Trp Gly Pro Ala Arg Tyr
 455 460 465

ttg atc act ggc tgg gct ggg cca tgg ccg gtg gat gat cga tgg tgg 1555
 Leu Ile Thr Gly Trp Ala Gly Pro Trp Pro Val Asp Asp Arg Trp Trp
 470 475 480 485

gag aaa aac ggc aca aaa tat gcc cgc ctc caa gtg gtg gga cgg gca 1603
 Glu Lys Asn Gly Thr Lys Tyr Ala Arg Leu Gln Val Val Gly Arg Ala
 490 495 500

gta tct gaa gaa agg cag ctc aat gcg tgg ctg ttg atg tgg aaa gac 1651
 Val Ser Glu Glu Arg Gln Leu Asn Ala Trp Leu Leu Met Trp Lys Asp
 505 510 515

aac aag tgg cgg att gag gcc aca tat taggaaacta ctgcgctaaa 1698
 Asn Lys Trp Arg Ile Glu Ala Thr Tyr
 520 525

aca 1701

<210> 1776

<211> 526

<212> PRT

<213> Corynebacterium glutamicum

<400> 1776

Met Ala Leu Trp Phe Pro Asp Trp Pro Val Gln Ala Val His Leu Asp
 1 5 10 15

Glu Asp Ala Pro Ala His Asn Lys Pro Val Ala Ile Ala Ala His Tyr
20 25 30

Arg Ile Gln Val Cys Gly Val Ala Ala Arg Lys Arg Gly Val Arg Arg
35 40 45

Gly Met Lys Val Arg Gln Ala Gln Ala Val Cys Pro Glu Leu Glu Val
50 55 60

Val Asp Ala Asp Ala Asp Arg Asp Ala Arg Met Phe Glu Gly Ile Val
65 70 75 80

Ala Ser Leu Gly Glu Val Ala Ser Ser Val Glu Val Leu Arg Pro Gly
85 90 95

Leu Val Ala Val Asp Ala Gly Ala Ala Ala Arg Tyr Tyr Gly Ser Glu
100 105 110

Asp Ile Ala Ala Gln Met Leu Ile Asp Ala Ala Leu Arg Gln Gly Ile
115 120 125

Asp Val Phe Ala Gly Val Ala Asp Glu Ile Thr Thr Ala Val Ile Ala
130 135 140

Ala Arg Ala Asn Gly Gly Thr Val Val Lys Arg Glu Ala Ser Arg Ser
145 150 155 160

Phe Leu Gln Gln Gln Pro Leu Gly Val Leu Ala Ala Glu Glu Ala Leu
165 170 175

Gly Cys Glu Ala Glu Val Val Arg Ala Leu Ala Asp Leu Gly Met Arg
180 185 190

Thr Leu Gly Glu Leu Ala Glu Leu Pro Val Glu Ala Val Ala Thr Arg
195 200 205

Phe Gly Asn Ala Gly Leu Arg Cys His Asn Ile Ala Arg Ala Arg His
210 215 220

Asp Arg Lys Val Ala Pro Pro Ile Thr His Ala Asp Trp Glu Val Ser
225 230 235 240

His Val Pro Glu Glu Pro Ile Leu Arg Val Asp Ala Ala Ser Phe Val
245 250 255

Ala Arg Asn Leu Ala Ser Arg Leu His Gln Leu Leu Ser Lys Gly Gly
260 265 270

Val Val Cys Gln Leu Leu Lys Val Thr Ala Asp Phe Ser Thr Gly Asp
275 280 285

Thr Val Ser Arg Ile Trp Arg Thr Gly Glu Pro Leu Thr Glu Gln Ala
290 295 300

Thr Ala Asp Arg Val Arg Trp Gln Leu Asp Gly Trp Leu Thr Ala Arg
305 310 315 320

Gly Val His Ser Asp Asp Pro Asn Glu His Asp Gly Ile Thr Ala Leu
325 330 335

Trp Leu Ile Pro Leu Glu Cys Val Pro Pro Asp Met Ala Ser Gly Gly

340	345	350
Leu Trp Asp Thr Gly Arg Ser Gln	Gln His Val Ala Arg Gln Val Ile	
355	360	365
Glu Arg Val Gln Ser Ser Leu Gly Val Asp Ala Val Leu Gln Pro Val		
370	375	380
Pro Ala Gly Gly Arg Gly Val Glu Glu Arg Ile His Phe Val Pro Tyr		
385	390	395
Gly Glu Lys Arg Asp Ala Ile Arg Asn Pro Ala Gly Ser Trp Pro Gly		
405	410	415
Lys Ile Pro Gly Pro Leu Pro Ala Arg Leu Gly Gly Gly Ile Asn His		
420	425	430
Pro Ala Ser Gln Val Thr Met Ile Asp Thr Glu Gly Gln Arg Ile Tyr		
435	440	445
Val Thr Ala Glu Ala Leu Leu Ser Ser Ser Pro Tyr Ala Leu Ser Trp		
450	455	460
Gly Pro Ala Arg Tyr Leu Ile Thr Gly Trp Ala Gly Pro Trp Pro Val		
465	470	475
Asp Asp Arg Trp Trp Glu Lys Asn Gly Thr Lys Tyr Ala Arg Leu Gln		
485	490	495
Val Val Gly Arg Ala Val Ser Glu Glu Arg Gln Leu Asn Ala Trp Leu		
500	505	510
Leu Met Trp Lys Asp Asn Lys Trp Arg Ile Glu Ala Thr Tyr		
515	520	525

<210> 1777

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(760)

<223> RXA00475

<400> 1777

gggggtgtctg taattttcac gtctcctggc gtttttaaga cgaattacaa caattcgttc 60

acgattgagc gaaattgggc gtcttgctta ggtttcgggg	gtg acc cag ggt tac	115
	Val Thr Gln Gly Tyr	
	1 5	

ggt gtg tgc atg att gtg cag cca act tct cat tca aag cat cgt gcc	163
Gly Val Cys Met Ile Val Gln Pro Thr Ser His Ser Lys His Arg Ala	
10 15 20	

cgc ctg aag act cta gcg att gtc ggc gct agc gcg ttg act ctt gcg	211
Arg Leu Lys Thr Leu Ala Ile Val Gly Ala Ser Ala Leu Thr Leu Ala	
25 30 35	

ggt tgt gga acc tcc aat tcc acc acc aac gat gct tct tct gta acc 259
 Gly Cys Gly Thr Ser Asn Ser Thr Thr Asn Asp Ala Ser Ser Val Thr
 40 45 50
 caa act atg tcc gca act gcg gat ggc gca cag ttg tcc aac gaa gct 307
 Gln Thr Met Ser Ala Thr Ala Asp Gly Ala Gln Leu Ser Asn Glu Ala
 55 60 65
 tcc acc ggc cca acc gca ttg ggc gaa gcc gat gta gca atg aag act 355
 Ser Thr Gly Pro Thr Ala Leu Gly Glu Ala Asp Val Ala Met Lys Thr
 70 75 80 85
 ctc cga cct gat gcg cct gca cag ctc atg gtc acc gat gtt cgg att 403
 Leu Arg Pro Asp Ala Pro Ala Gln Leu Met Val Thr Asp Val Arg Ile
 90 95 100
 ggc tct cac agt ggc ttt gac cgc gtg gta ttt gat ctc act ggc acc 451
 Gly Ser His Ser Gly Phe Asp Arg Val Val Phe Asp Leu Thr Gly Thr
 105 110 115
 gga act cct ggt tgg ttc att gat tac acc tcc aat ccc acc cag cag 499
 Gly Thr Pro Gly Trp Phe Ile Asp Tyr Thr Ser Asn Pro Thr Gln Gln
 120 125 130
 ggc agc gga aac acc atc aac ttc acg ggc gat aca gcg ctg aac gta 547
 Gly Ser Gly Asn Thr Ile Asn Phe Thr Gly Asp Thr Ala Leu Asn Val
 135 140 145
 aat att gac ggt act gtt tat cct ttc gat ttg ggc ctt gag gat cca 595
 Asn Ile Asp Gly Thr Val Tyr Pro Phe Asp Leu Gly Leu Glu Asp Pro
 150 155 160 165
 gag atc ggc acc gtg gat ggc tcc ggc agc att gtc acc cag gtc gtc 643
 Glu Ile Gly Thr Val Asp Gly Ser Gly Ser Ile Val Thr Gln Val Val
 170 175 180
 agc gca ggt act ttt gag gga cgc tcc cag ttc gtc atc ggc ctc aac 691
 Ser Ala Gly Thr Phe Glu Gly Arg Ser Gln Phe Val Ile Gly Leu Asn
 185 190 195
 ggc aag cac cgc tac tcg gtc act gag ttg cag gat ccg cac cgt ctc 739
 Gly Lys His Arg Tyr Ser Val Thr Glu Leu Gln Asp Pro His Arg Leu
 200 205 210
 gtt gtg gat gtt tta gcg cag tagtttccta atatgtggcc tca 783
 Val Val Asp Val Leu Ala Gln
 215 220

<210> 1778

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 1778

Val Thr Gln Gly Tyr Gly Val Cys Met Ile Val Gln Pro Thr Ser His
 1 5 10 15

Ser Lys His Arg Ala Arg Leu Lys Thr Leu Ala Ile Val Gly Ala Ser
 20 25 30

gac ggc gga aca ttt gat cct gag ttg act gat caa ttg aag agg cac Asp Gly Gly Thr Phe Asp Pro Glu Leu Thr Asp Gln Leu Lys Arg His 40 45 50	259
ctg aaa gct tcc gga atg ggt ctg caa tta att agg aag ccg gga agg Leu Lys Ala Ser Gly Met Gly Leu Gln Leu Ile Arg Lys Pro Gly Arg 55 60 65	307
gag ggt cga aac gtc gaa aag cat aat ctt ttt ctc gtt ttt gct gag Glu Gly Arg Asn Val Glu Lys His Asn Leu Phe Leu Val Phe Ala Glu 70 75 80 85	355
gcc tca att att gag cac ctg gtg gtg gac gcg ccg gct gat gtt ttg Ala Ser Ile Ile Glu His Leu Val Val Asp Ala Pro Ala Asp Val Leu 90 95 100	403
gat ctt gat tta agc ggg ccg ggc aaa aac aat gcg cag cgc atg gat Asp Leu Asp Leu Ser Gly Pro Gly Lys Asn Asn Ala Gln Arg Met Asp 105 110 115	451
gat ccg atg ctg ctg att tgt acg cat tcg aag cgc gat gtg tgc tgc Asp Pro Met Leu Leu Ile Cys Thr His Ser Lys Arg Asp Val Cys Cys 120 125 130	499
gcg atc aag ggg cgt ccg ctg gca gct gcc gtg gag cca caa ttt ggg Ala Ile Lys Gly Arg Pro Leu Ala Ala Val Glu Pro Gln Phe Gly 135 140 145	547
ccg ctg cat gtg tgg gag gct tcg cac acc aag ggc cac cgt ttt gcg Pro Leu His Val Trp Glu Ala Ser His Thr Lys Gly His Arg Phe Ala 150 155 160 165	595
cca tcg atg ctg ctc atg ccg tgg aat tac tct tat ggc cta ctt gat Pro Ser Met Leu Leu Met Pro Trp Asn Tyr Ser Tyr Gly Leu Leu Asp 170 175 180	643
gag gcc gaa acc gtg cag ctt ttc caa ggc gcg ttg gac aac aaa ctc Glu Ala Glu Thr Val Gln Leu Phe Gln Gly Ala Leu Asp Asn Lys Leu 185 190 195	691
ttc ctg ccg ggc aac cgt ggc cga gga acc tta gat gct cgt ggc cag Phe Leu Pro Gly Asn Arg Gly Arg Gly Thr Leu Asp Ala Arg Gly Gln 200 205 210	739
gtt gca gaa att gcc gtg gcg gaa gct ttc ggc gag gcg gtt gct cct Val Ala Glu Ile Ala Val Ala Glu Ala Phe Gly Glu Ala Val Ala Pro 215 220 225	787
gcg agt ttg cag gtt gaa ttc gaa gat gat tct gtt ttg gtt act cat Ala Ser Leu Gln Val Glu Phe Glu Asp Asp Ser Val Leu Val Thr His 230 235 240 245	835
ccc gat ggg cgc acg tgg gtt gtg gag ctt gaa cgc atc gag gtc gac Pro Asp Gly Arg Thr Trp Val Val Glu Leu Glu Arg Ile Glu Val Asp 250 255 260	883
ggc gtg gtg tcc tcg tgt ggt gat cag ccg aaa act gga aaa gcg tgg Gly Val Val Ser Ser Cys Gly Asp Gln Pro Lys Thr Gly Lys Ala Trp 265 270 275	931

gtg gct agg caa gtt aca gaa ctg atc gga taaaagcaga gttatatctg 981
 Val Ala Arg Gln Val Thr Glu Leu Ile Gly
 280 285

atg 984

<210> 1780

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 1780

Met Thr Leu Arg Cys Ser Asp Val Asn Val Glu Pro Leu Pro Gly Thr
 1 5 10 15

Ala Lys Thr Gly Ser Gly Phe Val Leu Leu Glu His Ala Gly Ser Trp
 20 25 30

Ser Arg Asp Val Leu Asp Gly Gly Thr Phe Asp Pro Glu Leu Thr Asp
 35 40 45

Gln Leu Lys Arg His Leu Lys Ala Ser Gly Met Gly Leu Gln Leu Ile
 50 55 60

Arg Lys Pro Gly Arg Glu Gly Arg Asn Val Glu Lys His Asn Leu Phe
 65 70 75 80

Leu Val Phe Ala Glu Ala Ser Ile Ile Glu His Leu Val Val Asp Ala
 85 90 95

Pro Ala Asp Val Leu Asp Leu Asp Leu Ser Gly Pro Gly Lys Asn Asn
 100 105 110

Ala Gln Arg Met Asp Asp Pro Met Leu Leu Ile Cys Thr His Ser Lys
 115 120 125

Arg Asp Val Cys Cys Ala Ile Lys Gly Arg Pro Leu Ala Ala Ala Val
 130 135 140

Glu Pro Gln Phe Gly Pro Leu His Val Trp Glu Ala Ser His Thr Lys
 145 150 155 160

Gly His Arg Phe Ala Pro Ser Met Leu Leu Met Pro Trp Asn Tyr Ser
 165 170 175

Tyr Gly Leu Leu Asp Glu Ala Glu Thr Val Gln Leu Phe Gln Gly Ala
 180 185 190

Leu Asp Asn Lys Leu Phe Leu Pro Gly Asn Arg Gly Arg Gly Thr Leu
 195 200 205

Asp Ala Arg Gly Gln Val Ala Glu Ile Ala Val Ala Glu Ala Phe Gly
 210 215 220

Glu Ala Val Ala Pro Ala Ser Leu Gln Val Glu Phe Glu Asp Asp Ser
 225 230 235 240

Val Leu Val Thr His Pro Asp Gly Arg Thr Trp Val Val Glu Leu Glu
 245 250 255

Arg Ile Glu Val Asp Gly Val Val Ser Ser Cys Gly Asp Gln Pro Lys
 260 265 270

Thr Gly Lys Ala Trp Val Ala Arg Gln Val Thr Glu Leu Ile Gly
 275 280 285

<210> 1781

<211> 708

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(685)

<223> RXA00481

<400> 1781

gtccataaaa ataatgtgcc tacaagaaat ttatagtatc ccatgagtta atatttttaa 60

aaataaactt tatctgactt tgtagaaaaa ggtgattact atg ctg aat atg cag 115
 Met Leu Asn Met Gln
 1 5

gaa cca gat aaa atc cat ccg gca gaa cct aca ctt cgt aat att tat 163
 Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr Leu Arg Asn Ile Tyr
 10 15 20

gac gtt aaa act agt gat ccc aaa agt gaa tta gtt gat cgt tct ggc 211
 Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu Val Asp Arg Ser Gly
 25 30 35

atg tcg gaa gaa gac att gcg caa att ggg cgg cta atg aaa tcg ttg 259
 Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg Leu Met Lys Ser Leu
 40 45 50

gcc agt ctt cgc gat gtg gaa cgt agt att ggt gaa gcc tcg gca cgt 307
 Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly Glu Ala Ser Ala Arg
 55 60 65

tat atg gag cta agt gcc cct gat atg cga gct ttg cac tat ttg att 355
 Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala Leu His Tyr Leu Ile
 70 75 80 85

gtg gcg ggc aat gcg ggc gaa gtg gtg act cca gga atg ctt gga gct 403
 Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro Gly Met Leu Gly Ala
 90 95 100

cac ctt aag ctt tcc ccg gca tct gta aca aag acg ctt aat agg cta 451
 His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys Thr Leu Asn Arg Leu
 105 110 115

gaa aaa ggt ggg cat att gtt cgt aat gtg cac ccc gtc gac cgc agg 499
 Glu Lys Gly Gly His Ile Val Arg Asn Val His Pro Val Asp Arg Arg
 120 125 130

gct ttc gcc ctc atg gtc act gat gcc act cgt gga gag gcg atg cgg 547
 Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg Gly Glu Ala Met Arg
 135 140 145

acg ctt ggt aag cat cag gcg cgt cgt ttt gat gct gct aaa cga tta 595

Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp Ala Ala Lys Arg Leu
 150 155 160 165

act cca caa gag cgt gaa gtg gtt atc cga ttc ctt cag gat atg gca 643
 Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe Leu Gln Asp Met Ala
 170 175 180

cag gag tta tcc ctt aat aat gca cca tgg ctc aac acg gag 685
 Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu Asn Thr Glu
 185 190 195

tagatgacca tctacgttaa tta 708

<210> 1782

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 1782

Met Leu Asn Met Gln Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr
 1 5 10 15

Leu Arg Asn Ile Tyr Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu
 20 25 30

Val Asp Arg Ser Gly Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg
 35 40 45

Leu Met Lys Ser Leu Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly
 50 55 60

Glu Ala Ser Ala Arg Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala
 65 70 75 80

Leu His Tyr Leu Ile Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro
 85 90 95

Gly Met Leu Gly Ala His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys
 100 105 110

Thr Leu Asn Arg Leu Glu Lys Gly Gly His Ile Val Arg Asn Val His
 115 120 125

Pro Val Asp Arg Arg Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg
 130 135 140

Gly Glu Ala Met Arg Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp
 145 150 155 160

Ala Ala Lys Arg Leu Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe
 165 170 175

Leu Gln Asp Met Ala Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu
 180 185 190

Asn Thr Glu
 195

<210> 1783

<211> 725
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(702)
 <223> RXA00486

<400> 1783

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His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp	
1 5 10 15	
tcg ctg tct gaa gtg tcc gga acg ttg aaa gtc acc tcc ttc caa tcc	96
Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser	
20 25 30	
ctg ctg ttc acc ctt gcc ccg aaa gcc atc gcg cgc ctg acc gag aaa	144
Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys	
35 40 45	
tac cca cac ctg caa gta gaa atc tcc caa cta gaa gtc acc gca gcg	192
Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala	
50 55 60	
ctc gaa gaa ctc cgc gcc cgc cgc gtc gac gtc gca ctc ggc gag gaa	240
Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu	
65 70 75 80	
tac ccc gtg gaa gtc ccc ctt gtt gag gcc agc att cac cgc gaa gtc	288
Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val	
85 90 95	
ctc ttc gaa gac ccc atg ctg ctc gtc acc cca gca agc ggc cca tac	336
Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr	
100 105 110	
tct ggc ctc acc ctg cca gaa ctc cgc gac atc ccc atc gcc atc gat	384
Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp	
115 120 125	
cca ccc gac ctt ccc gcg ggc gaa tgg gtc cat agg ctc tgc cgg cgc	432
Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg	
130 135 140	
gcc ggg ttt gag ccc cgc gtg acc ttt gaa acc agc gat ccc atg ctc	480
Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu	
145 150 155 160	
caa gca cac ctc gtg cgt agc ggc ttg gcc gtg aca ttt tcc ccc aca	528
Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr	
165 170 175	
ctg ctc acc ccg atg ctg gaa agc gtg cac atc cag ccg ctg ccc ggc	576
Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly	
180 185 190	
aac ccc acg cgc acg ctc tac acc gcg gtc agg gaa ggg cgc cag ggg	624
Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly	
195 200 205	

cat cca gcc att aaa gct ttt cga cga gcc ctc gcc cat gtg gcc aaa 672
His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
210 215 220

gaa tct tat ttg gag gct cgt cta gta gag tgagttcttg tgagccttca 722
Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu
225 230

gac 725

<210> 1784

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 1784

His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
1 5 10 15

Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
20 25 30

Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
35 40 45

Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
50 55 60

Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu
65 70 75 80

Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
85 90 95

Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
100 105 110

Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
115 120 125

Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
130 135 140

Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
145 150 155 160

Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
165 170 175

Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
180 185 190

Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
195 200 205

His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
210 215 220

Glu Ser Tyr Leu Glu Ala Arg Leu Val Glu

225

230

<210> 1785

<211> 1026

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA00490

<400> 1785

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gatctagtc ttaaagggttt ctttggcaat aatcaagggc atg aat aaa cag tcc 115
                                         Met Asn Lys Gln Ser
                                         1 5

gct gca gtg ttg atg gtg atg ggt tcc gcc cta tcc ctg caa ttt ggt 163
Ala Ala Val Leu Met Val Met Gly Ser Ala Leu Ser Leu Gln Phe Gly
                        10 15 20

gct gcc att gga acg cag ctt ttc ccc ctc aac ggc ccc tgg gct gtc 211
Ala Ala Ile Gly Thr Gln Leu Phe Pro Leu Asn Gly Pro Trp Ala Val
                        25 30 35

acc tct tta agg ctg ttc atc gca ggc ttg atc atg tgc ctg gtg atc 259
Thr Ser Leu Arg Leu Phe Ile Ala Gly Leu Ile Met Cys Leu Val Ile
                        40 45 50

cgc ccg cga ctt cgt tcc tgg act aaa aaa caa tgg atc gcc gtg ctg 307
Arg Pro Arg Leu Arg Ser Trp Thr Lys Lys Gln Trp Ile Ala Val Leu
                        55 60 65

ctg ttg gga tta tct ctt ggc gga atg aac agc ctg ttt tac gca tcc 355
Leu Leu Gly Leu Ser Leu Gly Gly Met Asn Ser Leu Phe Tyr Ala Ser
                        70 75 80 85

atc gaa ctc atc ccg ctg ggt acc gcc gtg acc att gag ttc ctc ggc 403
Ile Glu Leu Ile Pro Leu Gly Thr Ala Val Thr Ile Glu Phe Leu Gly
                        90 95 100

ccc ctg att ttc tcc gcg gtg tta gcc cgc acg ctg aaa aac gga ttg 451
Pro Leu Ile Phe Ser Ala Val Leu Ala Arg Thr Leu Lys Asn Gly Leu
                        105 110 115

tgc gtg gct tta gcg ttt ctc ggc atg gca cta ctg ggt atc gat tcc 499
Cys Val Ala Leu Ala Phe Leu Gly Met Ala Leu Leu Gly Ile Asp Ser
                        120 125 130

ctc agc ggc gaa acc ctt gac cca ctc ggc gtc att ttc gca gcc gtc 547
Leu Ser Gly Glu Thr Leu Asp Pro Leu Gly Val Ile Phe Ala Ala Val
                        135 140 145

gca gga atc ttc tgg gtg tgc tac atc ctg gca tca aag aaa atc ggc 595
Ala Gly Ile Phe Trp Val Cys Tyr Ile Leu Ala Ser Lys Lys Ile Gly
                        150 155 160 165

caa ctc atc ccc gga aca agc ggc ctg gcc gtc gca ctg att atc ggc 643

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Gln Leu Ile Pro Gly Thr Ser Gly Leu Ala Val Ala Leu Ile Ile Gly
 170 175 180
 gca gtg gca gta ttt cca ctg ggt gct aca cac atg ggc ccg att ttc 691
 Ala Val Ala Val Phe Pro Leu Gly Ala Thr His Met Gly Pro Ile Phe
 185 190 195
 cag acc cca acc cta ctc atc ctg gcg ctt ggc aca gca ctt ctc ggg 739
 Gln Thr Pro Thr Leu Leu Ile Leu Ala Leu Gly Thr Ala Leu Leu Gly
 200 205 210
 tcg ctt atc ccc tat tcg ctg gaa tta tcg gca ctg cgc cga ctc ccc 787
 Ser Leu Ile Pro Tyr Ser Leu Glu Leu Ser Ala Leu Arg Arg Leu Pro
 215 220 225
 gcc ccc att ttc agt att ctg ctc agc ctc gaa ccg gca ttc gcc gcc 835
 Ala Pro Ile Phe Ser Ile Leu Leu Ser Leu Glu Pro Ala Phe Ala Ala
 230 235 240 245
 gcc gtc ggc tgg atc ctg ctt gat caa acc ccc acc gcg ctc aag tgg 883
 Ala Val Gly Trp Ile Leu Leu Asp Gln Thr Pro Thr Ala Leu Lys Trp
 250 255 260
 gcc gcg atc atc ctt gtc atc gcg gcc agc atc ggc gtc acg tgg gag 931
 Ala Ala Ile Ile Leu Val Ile Ala Ala Ser Ile Gly Val Thr Trp Glu
 265 270 275
 cct aaa aag atg ctt gtc gac gcg ccc ctc cac tca aaa tgc aac gcg 979
 Pro Lys Lys Met Leu Val Asp Ala Pro Leu His Ser Lys Cys Asn Ala
 280 285 290
 aag agg cga gta cac aca cct agt taacgtgcag gcttaccttt tgg 1026
 Lys Arg Arg Val His Thr Pro Ser
 295 300

<210> 1786

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 1786

Met Asn Lys Gln Ser Ala Ala Val Leu Met Val Met Gly Ser Ala Leu
 1 5 10 15

Ser Leu Gln Phe Gly Ala Ala Ile Gly Thr Gln Leu Phe Pro Leu Asn
 20 25 30

Gly Pro Trp Ala Val Thr Ser Leu Arg Leu Phe Ile Ala Gly Leu Ile
 35 40 45

Met Cys Leu Val Ile Arg Pro Arg Leu Arg Ser Trp Thr Lys Lys Gln
 50 55 60

Trp Ile Ala Val Leu Leu Leu Gly Leu Ser Leu Gly Gly Met Asn Ser
 65 70 75 80

Leu Phe Tyr Ala Ser Ile Glu Leu Ile Pro Leu Gly Thr Ala Val Thr
 85 90 95

Ile Glu Phe Leu Gly Pro Leu Ile Phe Ser Ala Val Leu Ala Arg Thr

100	105	110
Leu Lys Asn Gly Leu Cys Val Ala 115	Leu Ala Phe 120	Leu Gly Met Ala Leu 125
Leu Gly Ile Asp Ser Leu Ser Gly Glu Thr Leu Asp Pro Leu Gly Val 130	135	140
Ile Phe Ala Ala Val Ala Gly Ile Phe Trp Val Cys Tyr Ile Leu Ala 145	150	155
Ser Lys Lys Ile Gly Gln Leu Ile Pro Gly Thr Ser Gly Leu Ala Val 165	170	175
Ala Leu Ile Ile Gly Ala Val Ala Val Phe Pro Leu Gly Ala Thr His 180	185	190
Met Gly Pro Ile Phe Gln Thr Pro Thr Leu Leu Ile Leu Ala Leu Gly 195	200	205
Thr Ala Leu Leu Gly Ser Leu Ile Pro Tyr Ser Leu Glu Leu Ser Ala 210	215	220
Leu Arg Arg Leu Pro Ala Pro Ile Phe Ser Ile Leu Leu Ser Leu Glu 225	230	235
Pro Ala Phe Ala Ala Ala Val Gly Trp Ile Leu Leu Asp Gln Thr Pro 245	250	255
Thr Ala Leu Lys Trp Ala Ala Ile Ile Leu Val Ile Ala Ala Ser Ile 260	265	270
Gly Val Thr Trp Glu Pro Lys Lys Met Leu Val Asp Ala Pro Leu His 275	280	285
Ser Lys Cys Asn Ala Lys Arg Arg Val His Thr Pro Ser 290	295	300

<210> 1787

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXA00491

<400> 1787

tcctcatagt gtgtccacaa ttatctaaac tttagtagct tgtccttaaa tcggataacc 60

gctgcagctc acacgctatt ccacaaccgg aaatctggca	gtg tat tgg gtt tta	115
	Val Tyr Trp Val Leu	
	1 5	

gca acc tct gcc aat agg gtg gaa gat gtg aac ttt gat gcg atg atg	163
Ala Thr Ser Ala Asn Arg Val Glu Asp Val Asn Phe Asp Ala Met Met	
10 15 20	

ccc cgc gac ccg ttt gcc gat gat ccc aat gac ccg gca tcg ttt att 211

Pro Arg Asp Pro Phe Ala Asp Asp Pro Asn Asp Pro Ala Ser Phe Ile
 25 30 35
 acc gac gat gac cct tat gat cat ccc gaa ccg ctt tct gaa gaa gag 259
 Thr Asp Asp Asp Pro Tyr Asp His Pro Glu Pro Leu Ser Glu Glu Glu
 40 45 50
 cga atc cac gtg agc caa gac ctt cgc ctc gtg atg gaa ttt aaa aaa 307
 Arg Ile His Val Ser Gln Asp Leu Arg Leu Val Met Glu Phe Lys Lys
 55 60 65
 gtt tta ggt ccc cga gga atc gaa ggc gtg ttc ttc atg tgc gaa gac 355
 Val Leu Gly Pro Arg Gly Ile Glu Gly Val Phe Phe Met Cys Glu Asp
 70 75 80 85
 tgc gaa gag ttc cac tac tac gac tgg gac atc atg gca gca aac atg 403
 Cys Glu Glu Phe His Tyr Tyr Asp Trp Asp Ile Met Ala Ala Asn Met
 90 95 100
 cgc gcc acc ttg gct ggg gaa ctc agc ccc gtg cat gaa cca agt gcg 451
 Arg Ala Thr Leu Ala Gly Glu Leu Ser Pro Val His Glu Pro Ser Ala
 105 110 115
 caa ccc aat att gat gcc tat gtg ccg tgg gac tac tgc att ggt tac 499
 Gln Pro Asn Ile Asp Ala Tyr Val Pro Trp Asp Tyr Cys Ile Gly Tyr
 120 125 130
 cta gac gga ctt gaa gcc aaa taaaaactgc tagcaactaa aga 543
 Leu Asp Gly Leu Glu Ala Lys
 135 140

<210> 1788

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 1788

Val Tyr Trp Val Leu Ala Thr Ser Ala Asn Arg Val Glu Asp Val Asn
 1 5 10 15
 Phe Asp Ala Met Met Pro Arg Asp Pro Phe Ala Asp Asp Pro Asn Asp
 20 25 30
 Pro Ala Ser Phe Ile Thr Asp Asp Asp Pro Tyr Asp His Pro Glu Pro
 35 40 45
 Leu Ser Glu Glu Glu Arg Ile His Val Ser Gln Asp Leu Arg Leu Val
 50 55 60
 Met Glu Phe Lys Lys Val Leu Gly Pro Arg Gly Ile Glu Gly Val Phe
 65 70 75 80
 Phe Met Cys Glu Asp Cys Glu Glu Phe His Tyr Tyr Asp Trp Asp Ile
 85 90 95
 Met Ala Ala Asn Met Arg Ala Thr Leu Ala Gly Glu Leu Ser Pro Val
 100 105 110
 His Glu Pro Ser Ala Gln Pro Asn Ile Asp Ala Tyr Val Pro Trp Asp
 115 120 125

Tyr Cys Ile Gly Tyr Leu Asp Gly Leu Glu Ala Lys
 130 135 140

<210> 1789

<211> 347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(324)

<223> RXA00493

<400> 1789

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 Phe Glu Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu
 1 5 10 15

ggc aag cca gcg tac tgg atc gcc tcc aac gca ggt ctt gac ggc tct 96
 Gly Lys Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser
 20 25 30

ggt gtt gtt gca cgc act gct gct ctg cca aac ggc gag ggc ttc aac 144
 Val Val Val Ala Arg Thr Ala Leu Pro Asn Gly Glu Gly Phe Asn
 35 40 45

gct gca act ttg gaa tac gga aac ctg atc aac gac ggt gtc atc gac 192
 Ala Ala Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp
 50 55 60

cca gtc aag gtc acc cat tcc gca gta gtg aat gca acc tct gtt gca 240
 Pro Val Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala
 65 70 75 80

cgc atg gtt ctg acc act gag gct tct gtt gtt gag aag cct gca gaa 288
 Arg Met Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu
 85 90 95

gaa gca gcc gat gca cat gca gga cat cat cac cac taaagttctg 334
 Glu Ala Ala Asp Ala His Ala Gly His His His His
 100 105

tgaaaaaacac cgt 347

<210> 1790

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1790

Phe Glu Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu
 1 5 10 15

Gly Lys Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser
 20 25 30

Val Val Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn
 35 40 45

Ala Ala Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp
 50 55 60

Pro Val Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala
 65 70 75 80

Arg Met Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu
 85 90 95

Glu Ala Ala Asp Ala His Ala Gly His His His His
 100 105

<210> 1791

<211> 536

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(513)

<223> RXA00519

<400> 1791

atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct gct cct	48
Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro	
1 5 10 15	
aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg gat tcc	96
Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser	
20 25 30	
ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag ctc aac	144
Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn	
35 40 45	
aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg gac aag	192
Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys	
50 55 60	
gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc aag gtt	240
Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val	
65 70 75 80	
ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag ttc tgg	288
Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp	
85 90 95	
gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct gct acc	336
Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala Ala Thr	
100 105 110	
ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac atc gat	384
Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp Ile Asp	
115 120 125	
gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt ggc tac	432
Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr	
130 135 140	

tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca gtc gca 480
Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala
145 150 155 160

cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct tcacaaaaaag 533
Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
165 170

cgc 536

<210> 1792

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1792

Met Ala Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro
1 5 10 15

Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp Asp Ser
20 25 30

Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn
35 40 45

Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Lys
50 55 60

Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val
65 70 75 80

Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys Phe Trp
85 90 95

Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala Ala Thr
100 105 110

Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp Ile Asp
115 120 125

Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly Gly Tyr
130 135 140

Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro Val Ala
145 150 155 160

Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
165 170

<210> 1793

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXA00528

<400> 1793

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tcggtcgcgg ccgttatctt tttaagagga gaaatttttag atg agc acg tcc acc 115
                                   Met Ser Thr Ser Thr
                                   1 5

atc agg gtt gcc att gcc gga gtc gga aac tgc gcg acc tcc ctc att 163
Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile
                                   10 15 20

cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg 211
Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro
                                   25 30 35

ggg ttg atg cac gtc aaa ttc ggt gat tac cac gtt ggc gac att gaa 259
Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu
                                   40 45 50

ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt 307
Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu
                                   55 60 65

gcc gac gcc acc gag gct tca caa aac tgc act atc aaa atc gcc gat 355
Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp
                                   70 75 80 85

gtc cca cag acc ggc atc aac gtg ctg cgt ggc ccg act ctc gac ggc 403
Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly
                                   90 95 100

ctg ggc gat cat tac cgc gcg acc atc gac gag tcc acc gcc gag cca 451
Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu Ser Thr Ala Glu Pro
                                   105 110 115

gtc gac gtt gtc cag gcg ctt atc gac gca aaa gcc gat gtt ttg gtg 499
Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys Ala Asp Val Leu Val
                                   120 125 130

tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa 547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln
                                   135 140 145

gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc 595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe
                                   150 155 160 165

atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc 643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile
                                   170 175 180

cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc 691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr
                                   185 190 195

cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat 739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp
                                   200 205 210

cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg 787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met

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215	220	225	
ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca			835
Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala			
230	235	240	245
gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac			883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp			
	250	255	260
cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac			931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp			
	265	270	275
cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt			979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val			
	280	285	290
ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct			1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser			
	295	300	305
gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat			1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp			
310	315	320	325
cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag			1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys			
	330	335	340
tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag			1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu			
	345	350	355
gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg			1212
Ala Phe Ile Ile Glu Ala			
360			

<210> 1794

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 1794

Met	Ser	Thr	Ser	Thr	Ile	Arg	Val	Ala	Ile	Ala	Gly	Val	Gly	Asn	Cys
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Ala	Thr	Ser	Leu	Ile	Gln	Gly	Val	Glu	Tyr	Tyr	Arg	Asn	Ala	Asp	Pro
			20					25					30		

Ser	Glu	Thr	Val	Pro	Gly	Leu	Met	His	Val	Lys	Phe	Gly	Asp	Tyr	His
		35					40					45			

Val	Gly	Asp	Ile	Glu	Phe	Val	Ala	Ala	Phe	Asp	Val	Asp	Ala	Glu	Lys
	50					55					60				

Val	Gly	Ile	Asp	Leu	Ala	Asp	Ala	Thr	Glu	Ala	Ser	Gln	Asn	Cys	Thr
65					70				75						80

Ile	Lys	Ile	Ala	Asp	Val	Pro	Gln	Thr	Gly	Ile	Asn	Val	Leu	Arg	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85					90					95					
Pro	Thr	Leu	Asp	Gly	Leu	Gly	Asp	His	Tyr	Arg	Ala	Thr	Ile	Asp	Glu
			100					105					110		
Ser	Thr	Ala	Glu	Pro	Val	Asp	Val	Val	Gln	Ala	Leu	Ile	Asp	Ala	Lys
		115					120					125			
Ala	Asp	Val	Leu	Val	Ser	Tyr	Leu	Pro	Val	Gly	Ser	Glu	Glu	Ala	Asp
		130					135					140			
Lys	Phe	Tyr	Ala	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Phe	Val	Asn
145						150					155				160
Ala	Leu	Pro	Val	Phe	Ile	Ala	Ser	Asp	Pro	Glu	Trp	Ala	Lys	Lys	Phe
				165					170					175	
Thr	Asp	Ala	Gly	Ile	Pro	Ile	Val	Gly	Asp	Asp	Ile	Lys	Ser	Gln	Ile
			180					185					190		
Gly	Ala	Thr	Ile	Thr	His	Arg	Val	Leu	Ala	Arg	Leu	Phe	Glu	Glu	Arg
		195					200					205			
Gly	Val	Arg	Val	Asp	Arg	Thr	Met	Gln	Leu	Asn	Val	Gly	Gly	Asn	Met
		210					215					220			
Asp	Phe	Lys	Asn	Met	Leu	Asp	Arg	Asn	Arg	Leu	Glu	Ser	Lys	Lys	Val
225						230					235				240
Ser	Lys	Thr	Gln	Ala	Val	Thr	Ser	Asn	Ile	Pro	Asp	Gly	Pro	Leu	Ser
			245						250					255	
Gly	Lys	Val	Glu	Asp	Arg	Asn	Val	His	Ile	Gly	Pro	Ser	Asp	His	Val
		260						265					270		
Gln	Trp	Leu	Asp	Asp	Arg	Lys	Trp	Ala	Tyr	Val	Arg	Leu	Glu	Gly	Thr
		275					280					285			
Ala	Phe	Gly	Gly	Val	Pro	Leu	Asn	Leu	Glu	Tyr	Lys	Leu	Glu	Val	Trp
		290					295					300			
Asp	Ser	Pro	Asn	Ser	Ala	Gly	Ile	Ile	Ile	Asp	Ala	Val	Arg	Ala	Ala
305						310					315				320
Lys	Ile	Ala	Leu	Asp	Arg	Gly	Ile	Gly	Gly	Pro	Ile	Met	Pro	Ala	Ser
			325						330					335	
Ser	Tyr	Leu	Met	Lys	Ser	Pro	Pro	Glu	Gln	Leu	Pro	Asp	Asp	Val	Ala
			340					345					350		
Cys	Glu	Arg	Leu	Glu	Ala	Phe	Ile	Ile	Glu	Ala					
			355				360								

<210> 1795

<211> 666

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(643)

<223> RXA00529

<400> 1795

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                                         Met Lys Leu Lys Trp
                                         1      5

att gca cca att ctt ccg gtt ttg gcc ctt gca ggc tgc gga aac tac 163
Ile Ala Pro Ile Leu Pro Val Leu Ala Leu Ala Gly Cys Gly Asn Tyr
                        10                        15                        20

gtc aac gta gag tcg caa ggg aaa tct gga att tcc cat gat gag gac 211
Val Asn Val Glu Ser Gln Gly Lys Ser Gly Ile Ser His Asp Glu Asp
                        25                        30                        35

gga aat ata agc gtt cac atg tac atc tgt ggt gat aat gcg gtg gat 259
Gly Asn Ile Ser Val His Met Tyr Ile Cys Gly Asp Asn Ala Val Asp
                        40                        45                        50

gaa ctg ata ctt agc ggt ggt ttt tac gat ggc cca cct ggg aca aac 307
Glu Leu Ile Leu Ser Gly Gly Phe Tyr Asp Gly Pro Pro Gly Thr Asn
      55                        60                        65

aac cca gcc ctt ggg atg ttg aaa act tcc aac cct gag tcg ggt tat 355
Asn Pro Ala Leu Gly Met Leu Lys Thr Ser Asn Pro Glu Ser Gly Tyr
      70                        75                        80                        85

gtt gta gtc aac atc gct gat cca gca ccg tgg gaa gtt gtt gag cca 403
Val Val Val Asn Ile Ala Asp Pro Ala Pro Trp Glu Val Val Glu Pro
                        90                        95                        100

atc aat ttg ccc acg gaa cag gga aag tac att att gcc aat ccg agg 451
Ile Asn Leu Pro Thr Glu Gln Gly Lys Tyr Ile Ile Ala Asn Pro Arg
                        105                        110                        115

ttg gta gat aaa ggt tgg ccg att cct ttc gca aaa gaa aag tat atg 499
Leu Val Asp Lys Gly Trp Pro Ile Pro Phe Ala Lys Glu Lys Tyr Met
                        120                        125                        130

ccg agt gtt tcc aca tca gta gga atg ctt gaa gga ata gat cca ggt 547
Pro Ser Val Ser Thr Ser Val Gly Met Leu Glu Gly Ile Asp Pro Gly
      135                        140                        145

cta gtc atg cgg gat atg tat acc gag tcg act cat gtg ttc ggt act 595
Leu Val Met Arg Asp Met Tyr Thr Glu Ser Thr His Val Phe Gly Thr
      150                        155                        160                        165

gcc gaa gac ttt gtt gaa gcc ggt caa cag tgg tgc gag gat tat ttc 643
Ala Glu Asp Phe Val Glu Ala Gly Gln Gln Trp Cys Glu Asp Tyr Phe
                        170                        175                        180

taaaacgtga atctggcaaa aga 666

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<210> 1796

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 1796

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Met Lys Leu Lys Trp Ile Ala Pro Ile Leu Pro Val Leu Ala Leu Ala
 1           5           10           15

Gly Cys Gly Asn Tyr Val Asn Val Glu Ser Gln Gly Lys Ser Gly Ile
          20           25           30

Ser His Asp Glu Asp Gly Asn Ile Ser Val His Met Tyr Ile Cys Gly
          35           40           45

Asp Asn Ala Val Asp Glu Leu Ile Leu Ser Gly Gly Phe Tyr Asp Gly
          50           55           60

Pro Pro Gly Thr Asn Asn Pro Ala Leu Gly Met Leu Lys Thr Ser Asn
          65           70           75           80

Pro Glu Ser Gly Tyr Val Val Val Asn Ile Ala Asp Pro Ala Pro Trp
          85           90           95

Glu Val Val Glu Pro Ile Asn Leu Pro Thr Glu Gln Gly Lys Tyr Ile
          100          105          110

Ile Ala Asn Pro Arg Leu Val Asp Lys Gly Trp Pro Ile Pro Phe Ala
          115          120          125

Lys Glu Lys Tyr Met Pro Ser Val Ser Thr Ser Val Gly Met Leu Glu
          130          135          140

Gly Ile Asp Pro Gly Leu Val Met Arg Asp Met Tyr Thr Glu Ser Thr
          145          150          155          160

His Val Phe Gly Thr Ala Glu Asp Phe Val Glu Ala Gly Gln Gln Trp
          165          170          175

Cys Glu Asp Tyr Phe
          180

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<210> 1797

<211> 1404

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1381)

<223> RXA00530

<400> 1797

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ggggttagat ttcagctgaa gcaactgggg agttggcgct atg agc atc gga ttc 115
                                   Met Ser Ile Gly Phe
                                   1           5

gac cgc gac ctt tat att aag atg cag tcg cag cac atc aat gag cgc 163
Asp Arg Asp Leu Tyr Ile Lys Met Gln Ser Gln His Ile Asn Glu Arg
          10           15           20

cgc gag cag atc ggc ggc aag ctg tat ctg gaa atg ggc ggc aag ctt 211

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Arg	Glu	Gln	Ile	Gly	Gly	Lys	Leu	Tyr	Leu	Glu	Met	Gly	Gly	Lys	Leu		
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ttc	gac	gac	atg	cac	gct	tcc	cgt	gtg	ctg	cca	ggt	ttc	acg	cct	gac	259	
Phe	Asp	Asp	Met	His	Ala	Ser	Arg	Val	Leu	Pro	Gly	Phe	Thr	Pro	Asp		
		40					45					50					
aac	aag	atc	gct	atg	ctc	act	gag	ctt	aaa	gat	gag	ctg	gaa	atc	ctc	307	
Asn	Lys	Ile	Ala	Met	Leu	Thr	Glu	Leu	Lys	Asp	Glu	Leu	Glu	Ile	Leu		
		55				60					65						
gtc	gca	atc	aat	gcg	aag	gat	ctg	gag	cgc	aag	aaa	acc	cgc	gcc	gac	355	
Val	Ala	Ile	Asn	Ala	Lys	Asp	Leu	Glu	Arg	Lys	Lys	Thr	Arg	Ala	Asp		
	70				75				80						85		
ctc	gac	att	tct	tat	gag	gaa	gat	gtt	tta	cgc	ctc	att	gat	gtg	ttc	403	
Leu	Asp	Ile	Ser	Tyr	Glu	Glu	Asp	Val	Leu	Arg	Leu	Ile	Asp	Val	Phe		
				90				95						100			
cgt	gag	ctg	ggc	ttt	ttg	gcg	gag	cat	gtg	gtg	ctc	aca	cag	ttg	gag	451	
Arg	Glu	Leu	Gly	Phe	Leu	Ala	Glu	His	Val	Val	Leu	Thr	Gln	Leu	Glu		
			105					110					115				
gat	gac	aac	tat	cag	gca	ctc	gcg	ttc	aag	cag	cgc	cta	gag	cgc	ctt	499	
Asp	Asp	Asn	Tyr	Gln	Ala	Leu	Ala	Phe	Lys	Gln	Arg	Leu	Glu	Arg	Leu		
		120					125					130					
ggc	ctg	aag	gtt	gct	gtt	cac	cgc	gtg	att	cca	ggt	tac	cca	act	gat	547	
Gly	Leu	Lys	Val	Ala	Val	His	Arg	Val	Ile	Pro	Gly	Tyr	Pro	Thr	Asp		
	135					140					145						
gct	cgc	cgc	att	gtt	agc	gag	gaa	ggt	ttc	ggc	atc	aac	gag	tat	gtg	595	
Ala	Arg	Arg	Ile	Val	Ser	Glu	Glu	Gly	Phe	Gly	Ile	Asn	Glu	Tyr	Val		
	150				155				160						165		
gaa	acc	acc	cgc	aat	ttg	gtt	gtt	gtg	acc	gca	ccg	ggc	cca	ggt	tct	643	
Glu	Thr	Thr	Arg	Asn	Leu	Val	Val	Val	Thr	Ala	Pro	Gly	Pro	Gly	Ser		
				170					175						180		
gga	aag	ctc	gct	acc	tgc	ttg	agc	cag	att	tat	ggc	gat	cac	cag	cgc	691	
Gly	Lys	Leu	Ala	Thr	Cys	Leu	Ser	Gln	Ile	Tyr	Gly	Asp	His	Gln	Arg		
			185					190					195				
gga	atc	aag	tcc	ggc	tac	gca	aag	ttt	gaa	act	ttc	ccc	att	tg	aac	739	
Gly	Ile	Lys	Ser	Gly	Tyr	Ala	Lys	Phe	Glu	Thr	Phe	Pro	Ile	Trp	Asn		
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ctg	cct	ctt	gag	cac	cca	gtt	aac	ttg	gct	tat	gag	gct	gcc	acg	gca	787	
Leu	Pro	Leu	Glu	His	Pro	Val	Asn	Leu	Ala	Tyr	Glu	Ala	Ala	Thr	Ala		
						220					225						
gat	ctc	gat	gac	atc	aac	atc	atc	gat	cct	ttc	cac	ctc	gcc	gcc	tat	835	
Asp	Leu	Asp	Asp	Ile	Asn	Ile	Ile	Asp	Pro	Phe	His	Leu	Ala	Ala	Tyr		
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gac	acc	aaa	gcc	acc	agc	tac	aac	cgc	gac	gtg	gaa	gtc	ttc	ccg	ctg	883	
Asp	Thr	Lys	Ala	Thr	Ser	Tyr	Asn	Arg	Asp	Val	Glu	Val	Phe	Pro	Leu		
				250					255						260		
ctg	aaa	acc	atg	ctg	gaa	atg	ctg	tcg	ggc	tca	tcg	ccg	tac	aaa	tcc	931	
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265	270	275	
ccc acc gac atg ggt gtc aac atg gtc gga agc gca att atc gac gac Pro Thr Asp Met Gly Val Asn Met Val Gly Ser Ala Ile Ile Asp Asp 280 285 290			979
gcc gcg tgc cag gaa gcc gcc cgc caa gaa att gtt cgg cgt tac ttc Ala Ala Cys Gln Glu Ala Ala Arg Gln Glu Ile Val Arg Arg Tyr Phe 295 300 305			1027
aag gcg ctt gtc gac gag cgt cgc gag gag cag gac gat acc att tca Lys Ala Leu Val Asp Glu Arg Arg Glu Glu Gln Asp Asp Thr Ile Ser 310 315 320 325			1075
gcg cgc atc gcc att gtc atg agc aag gcc ggt tgc acc gtt gaa gac Ala Arg Ile Ala Ile Val Met Ser Lys Ala Gly Cys Thr Val Glu Asp 330 335 340			1123
cgc cgc gtg gtt gcc cga gca ctt gat gtt gaa gaa tcc acc ggc gcg Arg Arg Val Val Ala Arg Ala Leu Asp Val Glu Glu Ser Thr Gly Ala 345 350 355			1171
ccg ggt tgt gcc att gaa ctt aac gat ggt cga ctc gtc acc ggc aag Pro Gly Cys Ala Ile Glu Leu Asn Asp Gly Arg Leu Val Thr Gly Lys 360 365 370			1219
act tca gaa ctt ctc gga tgc tcc gca gcg atg gtg ctt aat gca ctg Thr Ser Glu Leu Leu Gly Cys Ser Ala Ala Met Val Leu Asn Ala Leu 375 380 385			1267
aag gaa ctc gct ggc att gat cgc agc gtg gat ctc ctc tcc cct gaa Lys Glu Leu Ala Gly Ile Asp Arg Ser Val Asp Leu Leu Ser Pro Glu 390 395 400 405			1315
tcc atc gag cca atc caa tcg ctg aag acc cag cac ctg gga tcc cgc Ser Ile Glu Pro Ile Gln Ser Leu Lys Thr Gln His Leu Gly Ser Arg 410 415 420			1363
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<210> 1798

<211> 427

<212> PRT

<213> Corynebacterium glutamicum

<400> 1798

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His	Ile	Asn	Glu	Arg	Arg	Glu	Gln	Ile	Gly	Gly	Lys	Leu	Tyr	Leu	Glu
		20					25						30		

Met	Gly	Gly	Lys	Leu	Phe	Asp	Asp	Met	His	Ala	Ser	Arg	Val	Leu	Pro
		35					40					45			

Gly	Phe	Thr	Pro	Asp	Asn	Lys	Ile	Ala	Met	Leu	Thr	Glu	Leu	Lys	Asp
	50					55					60				

Glu Leu Glu Ile Leu Val Ala Ile Asn Ala Lys Asp Leu Glu Arg Lys
65 70 75 80

Lys Thr Arg Ala Asp Leu Asp Ile Ser Tyr Glu Glu Asp Val Leu Arg
85 90 95

Leu Ile Asp Val Phe Arg Glu Leu Gly Phe Leu Ala Glu His Val Val
100 105 110

Leu Thr Gln Leu Glu Asp Asp Asn Tyr Gln Ala Leu Ala Phe Lys Gln
115 120 125

Arg Leu Glu Arg Leu Gly Leu Lys Val Ala Val His Arg Val Ile Pro
130 135 140

Gly Tyr Pro Thr Asp Ala Arg Arg Ile Val Ser Glu Glu Gly Phe Gly
145 150 155 160

Ile Asn Glu Tyr Val Glu Thr Thr Arg Asn Leu Val Val Val Thr Ala
165 170 175

Pro Gly Pro Gly Ser Gly Lys Leu Ala Thr Cys Leu Ser Gln Ile Tyr
180 185 190

Gly Asp His Gln Arg Gly Ile Lys Ser Gly Tyr Ala Lys Phe Glu Thr
195 200 205

Phe Pro Ile Trp Asn Leu Pro Leu Glu His Pro Val Asn Leu Ala Tyr
210 215 220

Glu Ala Ala Thr Ala Asp Leu Asp Asp Ile Asn Ile Ile Asp Pro Phe
225 230 235 240

His Leu Ala Ala Tyr Asp Thr Lys Ala Thr Ser Tyr Asn Arg Asp Val
245 250 255

Glu Val Phe Pro Leu Leu Lys Thr Met Leu Glu Met Leu Ser Gly Ser
260 265 270

Ser Pro Tyr Lys Ser Pro Thr Asp Met Gly Val Asn Met Val Gly Ser
275 280 285

Ala Ile Ile Asp Asp Ala Ala Cys Gln Glu Ala Ala Arg Gln Glu Ile
290 295 300

Val Arg Arg Tyr Phe Lys Ala Leu Val Asp Glu Arg Arg Glu Glu Gln
305 310 315 320

Asp Asp Thr Ile Ser Ala Arg Ile Ala Ile Val Met Ser Lys Ala Gly
325 330 335

Cys Thr Val Glu Asp Arg Arg Val Val Ala Arg Ala Leu Asp Val Glu
340 345 350

Glu Ser Thr Gly Ala Pro Gly Cys Ala Ile Glu Leu Asn Asp Gly Arg
355 360 365

Leu Val Thr Gly Lys Thr Ser Glu Leu Leu Gly Cys Ser Ala Ala Met
370 375 380

Val Leu Asn Ala Leu Lys Glu Leu Ala Gly Ile Asp Arg Ser Val Asp

aac tgg gaa ggc tac ggc cta atc ctc acc gca tta ctt gga aca atc 595
 Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile
 150 155 160 165

 gtg cag cag tat tcc ttt aac gct ggc gaa cta caa aaa tcg cta ccc 643
 Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro
 170 175 180

 gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg 691
 Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu
 185 190 195

 gtt ctg ggc gaa aaa ttc caa gtc gtg gac tgg gaa tgg atc gcc atg 739
 Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met
 200 205 210

 ggc atc gca cta ctg gtg atg att gtt tcc acc att gca ctg tct cgt 787
 Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg
 215 220 225

 aca agc aca atg ccg gcc gga tcg aaa agg taaaactcca aagttccccc 837
 Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
 230 235

 cga 840

<210> 1800

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 1800

Met Trp Trp Ala Gly Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln
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 Thr Val Ala Leu Gly Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu
 20 25 30

 Val Leu Ser Leu Met Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly
 35 40 45

 Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val
 50 55 60

 Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro
 65 70 75 80

 His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala
 85 90 95

 Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp
 100 105 110

 Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val
 115 120 125

 Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile
 130 135 140

Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala
 145 150 155 160
 Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu
 165 170 175
 Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe
 180 185 190
 Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp
 195 200 205
 Glu Trp Ile Ala Met Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr
 210 215 220
 Ile Ala Leu Ser Arg Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
 225 230 235

<210> 1801
 <211> 366
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(343)
 <223> RXA00540

<400> 1801
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 aaacattgtc ctccccattt cttgagtaag ggaaaatacc gtg gcc cgt gta gtt 115
 Val Ala Arg Val Val
 1 5
 gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg 163
 Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp Pro Gln Gly Gln Ala
 10 15 20
 gta cac cgc gcc ctc gga cgt atc gga gtt tct ggc gtt tcc gat gtc 211
 Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val
 25 30 35
 cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa 259
 Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu
 40 45 50
 gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc 307
 Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile
 55 60 65
 gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa 353
 Glu Asp Phe Asp Val Val Gly Val Glu Val Ala Lys
 70 75 80
 aatcgggtgc att 366

<210> 1802
 <211> 81

<212> PRT

<213> Corynebacterium glutamicum

<400> 1802

Val Ala Arg Val Val Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp
 1 5 10 15

Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser
 20 25 30

Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
 35 40 45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
 50 55 60

Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
 65 70 75 80

Lys

<210> 1803

<211> 519

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(496)

<223> RXA00549

<400> 1803

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ttgggtatcg cgaagtcttt gccaaactatc cctgagacac ttg act gaa aac gga 115
 Leu Thr Glu Asn Gly
 1 5

gag acc cct tat gag ggc atc atc ttg ggt cag tat gag tcc cgc cca 163
 Glu Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln Tyr Glu Ser Arg Pro
 10 15 20

ctt gat atg gct tct gcg atg gca act atc gct aat gaa ggt gtc tgg 211
 Leu Asp Met Ala Ser Ala Met Ala Thr Ile Ala Asn Glu Gly Val Trp
 25 30 35

cac cgc ccg cac ttc gtg tcc aag gtg gag act gtc agc ggt gag gtt 259
 His Arg Pro His Phe Val Ser Lys Val Glu Thr Val Ser Gly Glu Val
 40 45 50

ctc tac gag ttc gag gat ggc gac ggc gag cgt cgt gtt tct gaa aag 307
 Leu Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg Arg Val Ser Glu Lys
 55 60 65

gtt gca ctg aat ctg ctc aag gcc atg ggg cca atc gct gca tac tcc 355
 Val Ala Leu Asn Leu Leu Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser
 70 75 80 85

aac gga aac gct ctg gct gat ggc cag gtt tct gca tcc aag act ggt 403

Asn Gly Asn Ala Leu Ala Asp Gly Gln Val Ser Ala Ser Lys Thr Gly
 90 95 100
 acc act cag ctt ggt gat acc ggt gca aac aag gat gcg tgg atg ttg 451
 Thr Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys Asp Ala Trp Met Leu
 105 110 115
 ggt gcg gca cct cag cta gct act gcg gtg tgg gtc gga act gct 496
 Gly Ala Ala Pro Gln Leu Ala Thr Ala Val Trp Val Gly Thr Ala
 120 125 130
 tgataacact gcattgtata aca 519

<210> 1804
 <211> 132
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1804
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 Tyr Glu Ser Arg Pro Leu Asp Met Ala Ser Ala Met Ala Thr Ile Ala
 20 25 30
 Asn Glu Gly Val Trp His Arg Pro His Phe Val Ser Lys Val Glu Thr
 35 40 45
 Val Ser Gly Glu Val Leu Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg
 50 55 60
 Arg Val Ser Glu Lys Val Ala Leu Asn Leu Leu Lys Ala Met Gly Pro
 65 70 75 80
 Ile Ala Ala Tyr Ser Asn Gly Asn Ala Leu Ala Asp Gly Gln Val Ser
 85 90 95
 Ala Ser Lys Thr Gly Thr Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys
 100 105 110
 Asp Ala Trp Met Leu Gly Ala Ala Pro Gln Leu Ala Thr Ala Val Trp
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 Val Gly Thr Ala
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<210> 1805
 <211> 444
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(421)
 <223> RXA00550

<400> 1805
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gcttgataac actgcattgt ataacacctg ggggtggcagt atg tat ggt tct aac 115
Met Tyr Gly Ser Asn
1 5

tcc cct gcc acg atc tgg aag cag acc atg gat aac gcc ctc gag aac 163
Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp Asn Ala Leu Glu Asn
10 15 20

tcc cct ctc gaa act tgg gat atc gct cca gca ttg ggg tac ggt aac 211
Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala Leu Gly Tyr Gly Asn
25 30 35

cca cca gtt ccg gaa tat gtg tgg act cca agt cca aac atc gcg act 259
Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser Pro Asn Ile Ala Thr
40 45 50

aat gat cca gaa gga gca acc gag gaa gct cca gtg gag gat cca aat 307
Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro Val Glu Asp Pro Asn
55 60 65

gca gta atc gat acc cct gct gta gat ccc act gca cct gca gag gag 355
Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr Ala Pro Ala Glu Glu
70 75 80 85

acc ggt aac ggt cag gta gaa atc ctg ccg ggg ctg act atc ccg gga 403
Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly Leu Thr Ile Pro Gly
90 95 100

gat ctc tta ggg atc ggc taaaatccgg tcgtagccta aac 444
Asp Leu Leu Gly Ile Gly
105

<210> 1806

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 1806

Met Tyr Gly Ser Asn Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp
1 5 10 15

Asn Ala Leu Glu Asn Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala
20 25 30

Leu Gly Tyr Gly Asn Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser
35 40 45

Pro Asn Ile Ala Thr Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro
50 55 60

Val Glu Asp Pro Asn Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr
65 70 75 80

Ala Pro Ala Glu Glu Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly
85 90 95

Leu Thr Ile Pro Gly Asp Leu Leu Gly Ile Gly
100 105

Asp Arg Tyr Phe Val Val Thr Gln Trp Ala Asp Glu Asp Ser Tyr Asn
 50 55 60
 Ala Trp Arg Asp Ala Glu Lys Ala Lys Gly Gly His Gly Gln Gly Ala
 65 70 75 80
 His Gly Ser Asp Lys Lys Pro Val Ala Ser Gly Ala Ser Leu Leu Glu
 85 90 95
 Phe Glu Val Val Leu Gly Ser Thr Gly Ala Lys
 100 105

<210> 1809

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXA00554

<400> 1809

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aggactagac ttaagtatgc ctgcaaagga ggacaacttc atg aac acc caa cca 115
 Met Asn Thr Gln Pro
 1 5

gag cat cca gaa aat gat cta gtc gac gaa gcc gat ttt tct aac cgg 163
 Glu His Pro Glu Asn Asp Leu Val Asp Glu Ala Asp Phe Ser Asn Arg
 10 15 20

ccc agg atc tac tcg gac gat cct gat tcc ttg gct gat gcg cca gac 211
 Pro Arg Ile Tyr Ser Asp Asp Pro Asp Ser Leu Ala Asp Ala Pro Asp
 25 30 35

cca gcg ctg gag cat gag aag aac aag aaa tct tca cgc caa gca ctc 259
 Pro Ala Leu Glu His Glu Lys Asn Lys Lys Ser Ser Arg Gln Ala Leu
 40 45 50

att tat ctg ttg cag gtt cca cta gtt aca ttc gtt tct gca tac gta 307
 Ile Tyr Leu Leu Gln Val Pro Leu Val Thr Phe Val Ser Ala Tyr Val
 55 60 65

ttg gcc tgg gtg tca cga ctc cag gcc ggt ccc atc tgt gac gcc ggt 355
 Leu Ala Trp Val Ser Arg Leu Gln Gly Gly Pro Ile Cys Asp Ala Gly
 70 75 80 85

gag gct gtg tgg att tgt tcc cgt gct gca gaa ctg tgg tgg cca att 403
 Glu Ala Val Trp Ile Cys Ser Arg Ala Ala Glu Leu Trp Trp Pro Ile
 90 95 100

acc act agc gtc atc gca ttt ggt gcc atg ctt gga tct gca tgg atc 451
 Thr Thr Ser Val Ile Ala Phe Gly Gly Met Leu Gly Ser Ala Trp Ile
 105 110 115

ctc tat gac aaa tac cga aat tac cta cgc tgg cgt cct tgg atg gcc 499
 Leu Tyr Asp Lys Tyr Arg Asn Tyr Leu Arg Trp Arg Pro Trp Met Gly
 120 125 130

gtg ttg tgg att ttg att cca ttc agc atg ctg tgg gga acc tcg gtg 547
Val Leu Trp Ile Leu Ile Pro Phe Ser Met Leu Trp Gly Thr Ser Val
135 140 145

ctc acc ttg tcc atc ttg ggg cac taaaaacttc acataaatga caa 594
Leu Thr Leu Ser Ile Leu Gly His
150 155

<210> 1810

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 1810

Met Asn Thr Gln Pro Glu His Pro Glu Asn Asp Leu Val Asp Glu Ala
1 5 10 15

Asp Phe Ser Asn Arg Pro Arg Ile Tyr Ser Asp Asp Pro Asp Ser Leu
20 25 30

Ala Asp Ala Pro Asp Pro Ala Leu Glu His Glu Lys Asn Lys Lys Ser
35 40 45

Ser Arg Gln Ala Leu Ile Tyr Leu Leu Gln Val Pro Leu Val Thr Phe
50 55 60

Val Ser Ala Tyr Val Leu Ala Trp Val Ser Arg Leu Gln Gly Gly Pro
65 70 75 80

Ile Cys Asp Ala Gly Glu Ala Val Trp Ile Cys Ser Arg Ala Ala Glu
85 90 95

Leu Trp Trp Pro Ile Thr Thr Ser Val Ile Ala Phe Gly Gly Met Leu
100 105 110

Gly Ser Ala Trp Ile Leu Tyr Asp Lys Tyr Arg Asn Tyr Leu Arg Trp
115 120 125

Arg Pro Trp Met Gly Val Leu Trp Ile Leu Ile Pro Phe Ser Met Leu
130 135 140

Trp Gly Thr Ser Val Leu Thr Leu Ser Ile Leu Gly His
145 150 155

<210> 1811

<211> 2762

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2739)

<223> RXA00563

<400> 1811

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Phe Tyr Lys Asp Leu Tyr Ala Arg Ser Ala Arg Gly Thr Ala Ala Leu
1 5 10 15

tgg atc gtg gcg gct aac ttg agc tcc tac tca gac atc gac gcc atc	96
Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile	
20 25 30	
atc aac tgg gtc gga tcc gag cag acc acc acc gtc aac ggc gca tcc	144
Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser	
35 40 45	
aag ctg gtc aag cca gct ttg gtc cct acc ttg ctg ttc cca ttc gcg	192
Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala	
50 55 60	
gca cct cgc gtg tcc gga tcc atg gca gat gca ggc cca cag gca gaa	240
Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu	
65 70 75 80	
tcc cag atg cga ctt ctg ctc tgg tct gtt gag cgc ctc atc gca ggt	288
Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly	
85 90 95	
ctt gcg cca ttg ggc tcc tcc atc aac gtg ggt cac cgc ctg cac gtg	336
Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val	
100 105 110	
gtc atc cca ggt tca cca aac cgt gga cgc ttc ggt ggc gat ggt gca	384
Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala	
115 120 125	
tac ggt gaa tcc aag gca gct ctc gac gcc gtg gtt acc cgt tgg aac	432
Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn	
130 135 140	
gca gag caa gct gca tgg gga gca cac acc tcc ctc gtg cac gct cac	480
Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His	
145 150 155 160	
atc ggt tgg gtt cgc ggc acc ggc ctc atg ggc ggc aac gat cct ttg	528
Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu	
165 170 175	
gtc aag gca gct gaa gaa gca ggc gtg gaa acc tac tcc acc caa gaa	576
Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu	
180 185 190	
att gca gag aaa ctg ctg tcc cag gca act tcc act gtt cgc gag cag	624
Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln	
195 200 205	
gca gca tcc gcg cca atc acc gtc gac ttc act ggc gga ctt ggt gaa	672
Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu	
210 215 220	
tct gat ctg aac ctg gcg gaa atg gca cgt gca gaa gca gct aag gca	720
Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala	
225 230 235 240	
gct aac gca cca gtg gtt gag gct cca cgc aca gtg gca gca ctg cca	768
Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro	
245 250 255	

act cct tac cga cca gtg gtt caa acc acc cct gat ttc gca ggt caa	816
Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln	
260 265 270	
gtc acc caa aac ctt gac gag atg gtc gtc atc gtt ggc gcc ggc gag	864
Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu	
275 280 285	
ctc ggc cca ctg ggt tct gca cgt acg cgt ttc gac gcc gaa ctc aac	912
Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn	
290 295 300	
ggg tcc ctc tcc gcc gcg ggt gtc atc gaa ctt gca tgg acg atg gga	960
Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly	
305 310 315 320	
ctt atc cac tgg gat gaa gat cca aag cca ggc tgg tac gac gac tcc	1008
Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser	
325 330 335	
gac gac gca gtg gcc gaa gaa gac atc ttc gac cgc tac cac gac gaa	1056
Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu	
340 345 350	
gtc atg gca cgc gtt ggt gtc cgc aag tac aat gac atg cct gag tac	1104
Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr	
355 360 365	
ggc atg atc gac aac ttt gca cca gag ctg acc acc gtc tac ctc gac	1152
Gly Met Ile Asp Asn Phe Ala Pro Glu Leu Thr Thr Val Tyr Leu Asp	
370 375 380	
cag gac ctc acc ttc aac gtg gga tcc cgc gaa gag gca ctg acc tac	1200
Gln Asp Leu Thr Phe Asn Val Gly Ser Arg Glu Glu Ala Leu Thr Tyr	
385 390 395 400	
gtc gac tcc gag cca gaa ctc acc ttt gct tct ttc gac gaa gca gca	1248
Val Asp Ser Glu Pro Glu Leu Thr Phe Ala Ser Phe Asp Glu Ala Ala	
405 410 415	
ggg gag tgg aag gtc act cgc aag gca ggc tcc gca atc cgc gta cct	1296
Gly Glu Trp Lys Val Thr Arg Lys Ala Gly Ser Ala Ile Arg Val Pro	
420 425 430	
cgc cgc atg gcg atg acc cgc ttc gtt ggt gga cag gtt cct aag gac	1344
Arg Arg Met Ala Met Thr Arg Phe Val Gly Gly Gln Val Pro Lys Asp	
435 440 445	
ttc gac cca gct gtg tgg ggc att cca gct gac atg gtg gac aac ctg	1392
Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu	
450 455 460	
gac acc gtc gcg ctg tgg aac att gtc tgt act gtc gac gcc ttc ctg	1440
Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu	
465 470 475 480	
tcc gct gga ttc acc cca gca gag ctg ctt gct tcc gtt cac cca gca	1488
Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala	
485 490 495	
cgc gtg tcc tct acc caa ggc acc ggc atg ggc ggc atg gaa tcc ctc	1536

Arg	Val	Ser	Ser	Thr	Gln	Gly	Thr	Gly	Met	Gly	Gly	Met	Glu	Ser	Leu		
			500					505					510				
cgt	ggc	atc	tac	gtc	gac	cgc	att	ctg	gca	gag	cca	cgc	gcc	aac	gac	1584	
Arg	Gly	Ile	Tyr	Val	Asp	Arg	Ile	Leu	Ala	Glu	Pro	Arg	Ala	Asn	Asp		
		515					520					525					
gtt	ctg	cag	gaa	gca	ctg	ccc	aac	gtt	gtt	gca	gct	cac	gtc	atg	cag	1632	
Val	Leu	Gln	Glu	Ala	Leu	Pro	Asn	Val	Val	Ala	Ala	His	Val	Met	Gln		
	530					535				540							
tcc	tac	gtc	ggc	ggc	tac	gga	cag	atg	atc	cac	cca	gtc	gca	gct	tgt	1680	
Ser	Tyr	Val	Gly	Gly	Tyr	Gly	Gln	Met	Ile	His	Pro	Val	Ala	Ala	Cys		
545					550				555						560		
gca	acc	gca	gct	gtt	tct	gtg	gaa	gaa	gca	ctg	gac	aag	atc	cgc	atc	1728	
Ala	Thr	Ala	Ala	Val	Ser	Val	Glu	Glu	Ala	Leu	Asp	Lys	Ile	Arg	Ile		
				565					570					575			
ggc	aag	tcc	gac	ttc	gtt	gtc	gca	ggc	ggc	ttc	gat	gcc	ctg	tcc	gtt	1776	
Gly	Lys	Ser	Asp	Phe	Val	Val	Ala	Gly	Gly	Phe	Asp	Ala	Leu	Ser	Val		
			580					585					590				
gaa	ggc	atc	acc	ggc	ttc	ggc	gac	atg	gca	gca	acc	gcc	gac	tcc	gca	1824	
Glu	Gly	Ile	Thr	Gly	Phe	Gly	Asp	Met	Ala	Ala	Thr	Ala	Asp	Ser	Ala		
		595					600					605					
gag	atg	gaa	ggc	aag	gga	att	gag	cac	cgc	ttc	ttc	tcc	cgc	gcc	aac	1872	
Glu	Met	Glu	Gly	Lys	Gly	Ile	Glu	His	Arg	Phe	Phe	Ser	Arg	Ala	Asn		
	610					615					620						
gac	cgg	cgc	cgc	ggc	gga	ttc	atc	gaa	tcc	gaa	ggc	ggc	gga	acc	gtc	1920	
Asp	Arg	Arg	Arg	Gly	Gly	Phe	Ile	Glu	Ser	Glu	Gly	Gly	Gly	Thr	Val		
625					630					635					640		
ctt	ctg	gca	cgc	gga	tca	ctc	gca	gct	gac	ctg	ggc	ctt	cca	gta	ctc	1968	
Leu	Leu	Ala	Arg	Gly	Ser	Leu	Ala	Ala	Asp	Leu	Gly	Leu	Pro	Val	Leu		
				645					650					655			
ggc	gtc	atc	gga	ttc	gca	gag	tcc	ttt	gca	gat	ggc	gcc	cac	acc	tcc	2016	
Gly	Val	Ile	Gly	Phe	Ala	Glu	Ser	Phe	Ala	Asp	Gly	Ala	His	Thr	Ser		
			660					665					670				
atc	cca	gcc	cca	ggc	ctc	ggc	ctt	ggc	gct	gct	cgc	gat	ggc	gtg		2064	
Ile	Pro	Ala	Pro	Gly	Leu	Gly	Ala	Leu	Gly	Ala	Ala	Arg	Asp	Gly	Val		
		675				680						685					
gaa	tct	cgc	ctt	gca	gta	gca	ctg	cgt	tcc	gtc	ggc	gtc	tct	gct	gat	2112	
Glu	Ser	Arg	Leu	Ala	Val	Ala	Leu	Arg	Ser	Val	Gly	Val	Ser	Ala	Asp		
		690				695					700						
gag	atc	tcc	att	atc	tcc	aag	cac	gac	acc	tcc	acc	aac	gcg	aat	gat	2160	
Glu	Ile	Ser	Ile	Ile	Ser	Lys	His	Asp	Thr	Ser	Thr	Asn	Ala	Asn	Asp		
	705				710					715					720		
cca	aac	gag	tcc	gac	ctg	cac	gag	cgc	atc	gca	tcc	gct	atc	ggc	cgt	2208	
Pro	Asn	Glu	Ser	Asp	Leu	His	Glu	Arg	Ile	Ala	Ser	Ala	Ile	Gly	Arg		
				725				730						735			
gca	gac	ggc	aac	ccg	atg	tac	gtg	att	tcc	cag	aag	tca	ctc	acc	gga	2256	
Ala	Asp	Gly	Asn	Pro	Met	Tyr	Val	Ile	Ser	Gln	Lys	Ser	Leu	Thr	Gly		

740	745	750	
cac gcc aag ggt ggt gca gca gca ttc cag atg atc ggt ctc acc cag			2304
His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln			
755	760	765	
gtc ctc cga tcc gga ctg gtg cca gcc aac cgc gca ctc gac tgc gtt			2352
Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val			
770	775	780	
gac cca gta ctg tcc aag cat tcc cac ctc gtc tgg ctg cgc aag cca			2400
Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro			
785	790	795	800
cta gac ctt cgt gcg aag gca cca aag gca ggt ctt gtt acc tcc ctt			2448
Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu			
805	810	815	
ggc ttc gga cac gtc tcc gct ctg gtt gcg att gtt cac cca gac gcc			2496
Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala			
820	825	830	
ttc tat gag gca gtt cgt gtg gca cgt ggt gct gag gca gct gac gta			2544
Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val			
835	840	845	
tgg cgc gca tcc gcg atc gct cgc gaa gaa gca ggc ctt cgt acc atc			2592
Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile			
850	855	860	
gtc gcc ggt atg cac ggt ggc gta ctg tac gaa cgc cca gtc gag cgc			2640
Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg			
865	870	875	880
aac ctc ggt gtc cac gga gac gca gct aag gaa gtt gaa gct gca gtc			2688
Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val			
885	890	895	
ctc ctg gat tcc cgc gcc cgc cta gtt gac ggt gtc ctc cgc gcc gaa			2736
Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu			
900	905	910	
ggc tagttggtta ttgcgttgag ccc			2762
Gly			

<210> 1812

<211> 913

<212> PRT

<213> Corynebacterium glutamicum

<400> 1812

Phe	Tyr	Lys	Asp	Leu	Tyr	Ala	Arg	Ser	Ala	Arg	Gly	Thr	Ala	Ala	Leu
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Trp	Ile	Val	Ala	Ala	Asn	Leu	Ser	Ser	Tyr	Ser	Asp	Ile	Asp	Ala	Ile
			20					25					30		

Ile	Asn	Trp	Val	Gly	Ser	Glu	Gln	Thr	Thr	Thr	Val	Asn	Gly	Ala	Ser
			35				40					45			

Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
50 55 60

Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
65 70 75 80

Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
85 90 95

Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
100 105 110

Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
115 120 125

Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
130 135 140

Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
145 150 155 160

Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
165 170 175

Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
180 185 190

Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln
195 200 205

Ala Ala Ser Ala Pro Ile Thr Val Asp Phe Thr Gly Gly Leu Gly Glu
210 215 220

Ser Asp Leu Asn Leu Ala Glu Met Ala Arg Ala Glu Ala Ala Lys Ala
225 230 235 240

Ala Asn Ala Pro Val Val Glu Ala Pro Arg Thr Val Ala Ala Leu Pro
245 250 255

Thr Pro Tyr Arg Pro Val Val Gln Thr Thr Pro Asp Phe Ala Gly Gln
260 265 270

Val Thr Gln Asn Leu Asp Glu Met Val Val Ile Val Gly Ala Gly Glu
275 280 285

Leu Gly Pro Leu Gly Ser Ala Arg Thr Arg Phe Asp Ala Glu Leu Asn
290 295 300

Gly Ser Leu Ser Ala Ala Gly Val Ile Glu Leu Ala Trp Thr Met Gly
305 310 315 320

Leu Ile His Trp Asp Glu Asp Pro Lys Pro Gly Trp Tyr Asp Asp Ser
325 330 335

Asp Asp Ala Val Ala Glu Glu Asp Ile Phe Asp Arg Tyr His Asp Glu
340 345 350

Val Met Ala Arg Val Gly Val Arg Lys Tyr Asn Asp Met Pro Glu Tyr
355 360 365

Gly Met Ile Asp Asn Phe Ala Pro Glu Leu Thr Thr Val Tyr Leu Asp
370 375 380

Gln Asp Leu Thr Phe Asn Val Gly Ser Arg Glu Glu Ala Leu Thr Tyr
385 390 395 400

Val Asp Ser Glu Pro Glu Leu Thr Phe Ala Ser Phe Asp Glu Ala Ala
405 410 415

Gly Glu Trp Lys Val Thr Arg Lys Ala Gly Ser Ala Ile Arg Val Pro
420 425 430

Arg Arg Met Ala Met Thr Arg Phe Val Gly Gly Gln Val Pro Lys Asp
435 440 445

Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu
450 455 460

Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu
465 470 475 480

Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala
485 490 495

Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu
500 505 510

Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp
515 520 525

Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln
530 535 540

Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys
545 550 555 560

Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile
565 570 575

Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val
580 585 590

Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala
595 600 605

Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn
610 615 620

Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val
625 630 635 640

Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu
645 650 655

Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser
660 665 670

Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val
675 680 685

Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp

690	695	700
Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp 705	710	715 720
Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg 725	730	735
Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly 740	745	750
His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln 755	760	765
Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val 770	775	780
Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro 785	790	795 800
Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu 805	810	815
Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala 820	825	830
Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val 835	840	845
Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile 850	855	860
Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg 865	870	875 880
Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val 885	890	895
Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu 900	905	910

Gly

<210> 1813

<211> 528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(505)

<223> RXA00564

<400> 1813

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aaaaacggat ggaaccagta ttgggaaaag gatggttgcg atg aaa tac aac gtc 115

Met Lys Tyr Asn Val

1

5

gat gtc tct cgt gaa agc gag gac tgg ctc gcc acc gtc acc aat ctc 163
Asp Val Ser Arg Glu Ser Glu Asp Trp Leu Ala Thr Val Thr Asn Leu
10 15 20
gaa ggc gta tcc acg tgg gcg aca acc ttc gcc aac ctt gat cgc aac 211
Glu Gly Val Ser Thr Trp Ala Thr Thr Phe Ala Asn Leu Asp Arg Asn
25 30 35
ggc cgg gaa gcc att gct cta gct gaa gat ctc ccc gaa ggt gcg gaa 259
Gly Arg Glu Ala Ile Ala Leu Ala Glu Asp Leu Pro Glu Gly Ala Glu
40 45 50
agc tca ctg acc atc tct tgg tcg gtt cct aca gat tcc cac ccc gaa 307
Ser Ser Leu Thr Ile Ser Trp Ser Val Pro Thr Asp Ser His Pro Glu
55 60 65
ctg gac act gca att caa att gct caa cag cgt cgc tat cta gtg caa 355
Leu Asp Thr Ala Ile Gln Ile Ala Gln Gln Arg Arg Tyr Leu Val Gln
70 75 80 85
gcc caa caa gac tta gag ccc aaa gtt cga tcc gct att tcc gct ctc 403
Ala Gln Gln Asp Leu Glu Pro Lys Val Arg Ser Ala Ile Ser Ala Leu
90 95 100
acc caa gct gcg ctg cta ggt atg act gca ggt cga gta tcc cca act 451
Thr Gln Ala Ala Leu Leu Gly Met Thr Ala Gly Arg Val Ser Pro Thr
105 110 115
cac aac ccg ggt agc aga gct atc tca ttg gat cag gtg tca gga gtt 499
His Asn Pro Gly Ser Arg Ala Ile Ser Leu Asp Gln Val Ser Gly Val
120 125 130
tta aac tagcgtgcgc aattcccgtg tga 528
Leu Asn
135

<210> 1814

<211> 135

<212> PRT

<213> Corynebacterium glutamicum

<400> 1814

Met Lys Tyr Asn Val Asp Val Ser Arg Glu Ser Glu Asp Trp Leu Ala
1 5 10 15
Thr Val Thr Asn Leu Glu Gly Val Ser Thr Trp Ala Thr Thr Phe Ala
20 25 30
Asn Leu Asp Arg Asn Gly Arg Glu Ala Ile Ala Leu Ala Glu Asp Leu
35 40 45
Pro Glu Gly Ala Glu Ser Ser Leu Thr Ile Ser Trp Ser Val Pro Thr
50 55 60
Asp Ser His Pro Glu Leu Asp Thr Ala Ile Gln Ile Ala Gln Gln Arg
65 70 75 80
Arg Tyr Leu Val Gln Ala Gln Gln Asp Leu Glu Pro Lys Val Arg Ser
85 90 95

Ala Ile Ser Ala Leu Thr Gln Ala Ala Leu Leu Gly Met Thr Ala Gly
 100 105 110

Arg Val Ser Pro Thr His Asn Pro Gly Ser Arg Ala Ile Ser Leu Asp
 115 120 125

Gln Val Ser Gly Val Leu Asn
 130 135

<210> 1815

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA00573

<400> 1815

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atcgtgacca cccttgacgc tcatgaggtt caggtttccc atg ctc gtt agg cca 115
 Met Leu Val Arg Pro
 1 5

tgt ggt gag caa gca gtc atc atc gat ttg ctt gct gaa gat gcc gaa 163
 Cys Gly Glu Gln Ala Val Ile Ile Asp Leu Leu Ala Glu Asp Ala Glu
 10 15 20

gcc gtc caa ggc agc atc ttg gat gct gtt ctt gca ctc aac cgc tct 211
 Ala Val Gln Gly Ser Ile Leu Asp Ala Val Leu Ala Leu Asn Arg Ser
 25 30 35

ttg gtg ggc atg cag gtc cct gga atc atc gat act att ccc gct gcg 259
 Leu Val Gly Met Gln Val Pro Gly Ile Ile Asp Thr Ile Pro Ala Ala
 40 45 50

caa aca ctg tta gtg acg ttt gac acc aag cag atc acc ccg aat cgt 307
 Gln Thr Leu Leu Val Thr Phe Asp Thr Lys Gln Ile Thr Pro Asn Arg
 55 60 65

ttc gca gag atc gtt gat tca att gcg ctg acc cca gcc gca aag ggc 355
 Phe Ala Glu Ile Val Asp Ser Ile Ala Leu Thr Pro Ala Ala Lys Gly
 70 75 80 85

gca gca gag ctt acc gac acc att gag att ccc gtg gtc tac gac ggc 403
 Ala Ala Glu Leu Thr Asp Thr Ile Glu Ile Pro Val Val Tyr Asp Gly
 90 95 100

cct gat cta gaa acc gta gct caa cac aca ggt ctg agc gtg gag gaa 451
 Pro Asp Leu Glu Thr Val Ala Gln His Thr Gly Leu Ser Val Glu Glu
 105 110 115

gtt atc gcc acg cat tct ggc acc gtg tgg act gct gct ttc ggt gga 499
 Val Ile Ala Thr His Ser Gly Thr Val Trp Thr Ala Ala Phe Gly Gly
 120 125 130

ttt gca cca ggt ttt tac tat ctg atc ccc cag act ccc ctg tgg gat 547

Phe Ala Pro Gly Phe Tyr Tyr Leu Ile Pro Gln Thr Pro Leu Trp Asp
 135 140 145

att ccc cgc ttg gaa tcg cca cgc acc aag att cct gca ggt tct gtc 595
 Ile Pro Arg Leu Glu Ser Pro Arg Thr Lys Ile Pro Ala Gly Ser Val
 150 155 160 165

gca gtg gcc ggt gaa ttc agc gct gtg tac ccg cag cag tcc cct ggt 643
 Ala Val Ala Gly Glu Phe Ser Ala Val Tyr Pro Gln Gln Ser Pro Gly
 170 175 180

ggt tgg caa ctg ctg ggc act act gag att ccc atg tgg gat gtg gac 691
 Gly Trp Gln Leu Leu Gly Thr Thr Glu Ile Pro Met Trp Asp Val Asp
 185 190 195

cgg tgg caa cca tcg ctt ctc aag ccc ggt gat tca gtt cga ttt gtg 739
 Arg Trp Gln Pro Ser Leu Leu Lys Pro Gly Asp Ser Val Arg Phe Val
 200 205 210

cag gtg aag aaa tgagcttcaa agtaatttcc act 774
 Gln Val Lys Lys
 215

<210> 1816

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 1816

Met Leu Val Arg Pro Cys Gly Glu Gln Ala Val Ile Ile Asp Leu Leu
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Ala Glu Asp Ala Glu Ala Val Gln Gly Ser Ile Leu Asp Ala Val Leu
 20 25 30

Ala Leu Asn Arg Ser Leu Val Gly Met Gln Val Pro Gly Ile Ile Asp
 35 40 45

Thr Ile Pro Ala Ala Gln Thr Leu Leu Val Thr Phe Asp Thr Lys Gln
 50 55 60

Ile Thr Pro Asn Arg Phe Ala Glu Ile Val Asp Ser Ile Ala Leu Thr
 65 70 75 80

Pro Ala Ala Lys Gly Ala Ala Glu Leu Thr Asp Thr Ile Glu Ile Pro
 85 90 95

Val Val Tyr Asp Gly Pro Asp Leu Glu Thr Val Ala Gln His Thr Gly
 100 105 110

Leu Ser Val Glu Glu Val Ile Ala Thr His Ser Gly Thr Val Trp Thr
 115 120 125

Ala Ala Phe Gly Gly Phe Ala Pro Gly Phe Tyr Tyr Leu Ile Pro Gln
 130 135 140

Thr Pro Leu Trp Asp Ile Pro Arg Leu Glu Ser Pro Arg Thr Lys Ile
 145 150 155 160

Pro Ala Gly Ser Val Ala Val Ala Gly Glu Phe Ser Ala Val Tyr Pro

				165						170					175
Gln	Gln	Ser	Pro	Gly	Gly	Trp	Gln	Leu	Leu	Gly	Thr	Thr	Glu	Ile	Pro
			180					185					190		
Met	Trp	Asp	Val	Asp	Arg	Trp	Gln	Pro	Ser	Leu	Leu	Lys	Pro	Gly	Asp
		195					200					205			
Ser	Val	Arg	Phe	Val	Gln	Val	Lys	Lys							
	210					215									

<210> 1817

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(772)

<223> RXA00576

<400> 1817

acagtcgcgag cttcttagcg gcggtctgtg gcttcatagc cctgcccgat ggctggcgta 60

cagattcttc	gttcacgccc	acaacggtag	cattgttttc	atg	ctg	acc	tta	agt	115
				Met	Leu	Thr	Leu	Ser	
				1				5	

ttc	atc	act	ggc	acg	gag	cca	gga	aag	tgg	ttt	acc	cga	ttc	cga	gat	163
Phe	Ile	Thr	Gly	Thr	Glu	Pro	Gly	Lys	Trp	Phe	Thr	Arg	Phe	Arg	Asp	
			10					15					20			

cgg	act	cat	cac	ggt	gga	ctt	gag	acc	ctt	gat	tcg	gac	gac	gcc	cta	211
Arg	Thr	His	His	Gly	Gly	Leu	Glu	Thr	Leu	Asp	Ser	Asp	Asp	Ala	Leu	
			25				30					35				

ggc	ctc	atg	ctc	gct	ggc	cag	gca	caa	ctc	gcc	tta	acc	agg	ctt	cca	259
Gly	Leu	Met	Leu	Ala	Gly	Gln	Ala	Gln	Leu	Ala	Leu	Thr	Arg	Leu	Pro	
		40				45						50				

gat	gcg	cgt	atc	gac	gcc	tcc	ctc	cac	gtg	gtc	act	ctt	tat	cag	gaa	307
Asp	Ala	Arg	Ile	Asp	Ala	Ser	Leu	His	Val	Val	Thr	Leu	Tyr	Gln	Glu	
	55					60					65					

caa	ccc	gga	gtc	gct	ttt	cca	aaa	gac	ttt	ttc	ctc	agt	gcc	gaa	gaa	355
Gln	Pro	Gly	Val	Ala	Phe	Pro	Lys	Asp	Phe	Phe	Leu	Ser	Ala	Glu	Glu	
	70				75					80				85		

ggc	gcg	gtg	gac	ctt	gcg	gac	tta	gat	ggg	gag	atc	atc	aac	tgg	tcc	403
Gly	Ala	Val	Asp	Leu	Ala	Asp	Leu	Asp	Gly	Glu	Ile	Ile	Asn	Trp	Ser	
			90						95					100		

atg	ccc	gat	agt	ggg	gaa	gtc	gat	gcc	gct	gct	gtt	cgc	gat	gct	ctg	451
Met	Pro	Asp	Ser	Gly	Glu	Val	Asp	Ala	Ala	Ala	Val	Arg	Asp	Ala	Leu	
			105					110					115			

caa	atc	gtg	gca	gcg	aac	gtc	ggt	gtg	gtg	atc	gcc	ccc	agg	cca	ctt	499
Gln	Ile	Val	Ala	Ala	Asn	Val	Gly	Val	Val	Ile	Ala	Pro	Arg	Pro	Leu	
		120					125						130			

ctc aag gtg ttg agc aag aaa ttg gtg gag cac cgg gac atc aag ggt 547
 Leu Lys Val Leu Ser Lys Lys Leu Val Glu His Arg Asp Ile Lys Gly
 135 140 145

gga act gaa aca tct atc gcc ctg gta tgg aag aaa gat gag gat tct 595
 Gly Thr Glu Thr Ser Ile Ala Leu Val Trp Lys Lys Asp Glu Asp Ser
 150 155 160 165

gaa gag att caa gac ttc gtc ggt att gct cgc ggt cga acg cgg aat 643
 Glu Glu Ile Gln Asp Phe Val Gly Ile Ala Arg Gly Arg Thr Arg Asn
 170 175 180

tcc agc agg cag caa acg gta aag ctc agt gct cgt gaa aaa aca ctg 691
 Ser Ser Arg Gln Gln Thr Val Lys Leu Ser Ala Arg Glu Lys Thr Leu
 185 190 195

gca aaa caa gcc cgc agg cag ggg gag aaa cca aaa act ccg aag cgt 739
 Ala Lys Gln Ala Arg Arg Gln Gly Glu Lys Pro Lys Thr Pro Lys Arg
 200 205 210

ccg cag gca aga aaa cgt ccc gga aaa cgg cga taggggtcac ccgcgcatgt 792
 Pro Gln Ala Arg Lys Arg Pro Gly Lys Arg Arg
 215 220

ccg 795

<210> 1818

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1818

Met Leu Thr Leu Ser Phe Ile Thr Gly Thr Glu Pro Gly Lys Trp Phe
 1 5 10 15

Thr Arg Phe Arg Asp Arg Thr His His Gly Gly Leu Glu Thr Leu Asp
 20 25 30

Ser Asp Asp Ala Leu Gly Leu Met Leu Ala Gly Gln Ala Gln Leu Ala
 35 40 45

Leu Thr Arg Leu Pro Asp Ala Arg Ile Asp Ala Ser Leu His Val Val
 50 55 60

Thr Leu Tyr Gln Glu Gln Pro Gly Val Ala Phe Pro Lys Asp Phe Phe
 65 70 75 80

Leu Ser Ala Glu Glu Gly Ala Val Asp Leu Ala Asp Leu Asp Gly Glu
 85 90 95

Ile Ile Asn Trp Ser Met Pro Asp Ser Gly Glu Val Asp Ala Ala Ala
 100 105 110

Val Arg Asp Ala Leu Gln Ile Val Ala Ala Asn Val Gly Val Val Ile
 115 120 125

Ala Pro Arg Pro Leu Leu Lys Val Leu Ser Lys Lys Leu Val Glu His
 130 135 140

Arg Asp Ile Lys Gly Gly Thr Glu Thr Ser Ile Ala Leu Val Trp Lys

145	150	155	160
Lys Asp Glu Asp Ser Glu Glu Ile Gln Asp Phe Val Gly Ile Ala Arg	165	170	175
Gly Arg Thr Arg Asn Ser Ser Arg Gln Gln Thr Val Lys Leu Ser Ala	180	185	190
Arg Glu Lys Thr Leu Ala Lys Gln Ala Arg Arg Gln Gly Glu Lys Pro	195	200	205
Lys Thr Pro Lys Arg Pro Gln Ala Arg Lys Arg Pro Gly Lys Arg Arg	210	215	220

<210> 1819

<211> 471

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(448)

<223> RXA00577

<400> 1819

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ctggctccgt gccagtgatg aaacttaagg tcagcatgaa aacaatgcta ccgttgtggg 60
cgtgaacgaa gaatctgtac gccagccatc gggcagggct atg aag cca cag acc 115
                               Met Lys Pro Gln Thr
                               1           5

gcc gct aag aag ctc gga ctg ttt ttg ccc gcc acg cca gag gag ttc 163
Ala Ala Lys Lys Leu Gly Leu Phe Leu Pro Ala Thr Pro Glu Glu Phe
          10           15           20

caa aca ggt gca ttg act cac caa gag ttc aag aac ctg cag gaa aac 211
Gln Thr Gly Ala Leu Thr His Gln Glu Phe Lys Asn Leu Gln Glu Asn
          25           30           35

cca ccg gag tgg ctc caa acc cta cgc cgc gag ggc cca cac cct cgt 259
Pro Pro Glu Trp Leu Gln Thr Leu Arg Arg Glu Gly Pro His Pro Arg
          40           45           50

cca gtg gtc gcc caa aaa ttg ggc atc acc atc gcg gct ctg aaa aag 307
Pro Val Val Ala Gln Lys Leu Gly Ile Thr Ile Ala Ala Leu Lys Lys
          55           60           65

aac gac atg gac aaa cca ctg acc acc gcc gag atc aag gca ctt ctg 355
Asn Asp Met Asp Lys Pro Leu Thr Thr Ala Glu Ile Lys Ala Leu Leu
          70           75           80           85

gaa aac cag cca gaa tgg ttg cgc acc gca cgc aca cag ctt gct gaa 403
Glu Asn Gln Pro Glu Trp Leu Arg Thr Ala Arg Thr Gln Leu Ala Glu
          90           95           100

ggt cgc gaa acc gca aag aaa gaa act gaa gaa act acc gaa gac 448
Gly Arg Glu Thr Ala Lys Lys Glu Thr Glu Glu Thr Thr Glu Asp
          105           110           115

taaattctca caaagactgc gct 471

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<210> 1820

<211> 116

<212> PRT

<213> Corynebacterium glutamicum

<400> 1820

Met Lys Pro Gln Thr Ala Ala Lys Lys Leu Gly Leu Phe Leu Pro Ala
 1 5 10 15

Thr Pro Glu Glu Phe Gln Thr Gly Ala Leu Thr His Gln Glu Phe Lys
 20 25 30

Asn Leu Gln Glu Asn Pro Pro Glu Trp Leu Gln Thr Leu Arg Arg Glu
 35 40 45

Gly Pro His Pro Arg Pro Val Val Ala Gln Lys Leu Gly Ile Thr Ile
 50 55 60

Ala Ala Leu Lys Lys Asn Asp Met Asp Lys Pro Leu Thr Thr Ala Glu
 65 70 75 80

Ile Lys Ala Leu Leu Glu Asn Gln Pro Glu Trp Leu Arg Thr Ala Arg
 85 90 95

Thr Gln Leu Ala Glu Gly Arg Glu Thr Ala Lys Lys Glu Thr Glu Glu
 100 105 110

Thr Thr Glu Asp
 115

<210> 1821

<211> 846

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(823)

<223> RXA00578

<400> 1821

tgggcggtgc acttcttgct ctgtctgata cggaggctga gtgggaggaa atccgcgtta 60

aatcacggcc tctgctgaat ttgtttgggg ttgaattccc atg acg tac ctc gtg 115
 Met Thr Tyr Leu Val
 1 5

tgg gac ggt gca aca ctc gta gaa ggc gcg ctg gaa tca aca ccc aca 163
 Trp Asp Gly Ala Thr Leu Val Glu Gly Ala Leu Glu Ser Thr Pro Thr
 10 15 20

gtt gtt gat tcc tac cta gcc aaa gac cac cgc gtg gtg cgc tgg gat 211
 Val Val Asp Ser Tyr Leu Ala Lys Asp His Arg Val Val Arg Trp Asp
 25 30 35

ctt cat gaa cag cgc ttc gcc act agc gtg gac gtg gac ccg tgg gat 259
 Leu His Glu Gln Arg Phe Ala Thr Ser Val Asp Val Asp Pro Trp Asp
 40 45 50

ttt ctc cac gca gta agg gaa gca att cca cgc cag ggc tca tgg ttt 307
 Phe Leu His Ala Val Arg Glu Ala Ile Pro Arg Gln Gly Ser Trp Phe
 55 60 65
 ccc aaa gtt gaa tgg cat ggc gat gat ctt ttc gca gtc aat att cgc 355
 Pro Lys Val Glu Trp His Gly Asp Asp Leu Phe Ala Val Asn Ile Arg
 70 75 80 85
 ccg gca cca aca ctg cga aag gcc aca tca ttg tgg ctt tcc gaa gac 403
 Pro Ala Pro Thr Leu Arg Lys Ala Thr Ser Leu Trp Leu Ser Glu Asp
 90 95 100
 cca gat cca cgc aca cag cca acc att aaa ggc cca gac cta gat gtg 451
 Pro Asp Pro Arg Thr Gln Pro Thr Ile Lys Gly Pro Asp Leu Asp Val
 105 110 115
 ctt gct cac ctt cgc agt cgc gcc aac gat aac ggc tgc gat gat gcg 499
 Leu Ala His Leu Arg Ser Arg Ala Asn Asp Asn Gly Cys Asp Asp Ala
 120 125 130
 ctg ttg atc agc gcg gat ggg ttc att ctg gaa gct gcc aac gcc acc 547
 Leu Leu Ile Ser Ala Asp Gly Phe Ile Leu Glu Ala Ala Asn Ala Thr
 135 140 145
 gtg gtg ttt tgg gcg gat cca cag acg gtc atc gtg ccc agg gga gat 595
 Val Val Phe Trp Ala Asp Pro Gln Thr Val Ile Val Pro Arg Gly Asp
 150 155 160 165
 gtg ctc cca tcg gtg aca ctc gcc gca acc att ccg ctg tgg gaa aaa 643
 Val Leu Pro Ser Val Thr Leu Ala Ala Thr Ile Pro Leu Trp Glu Lys
 170 175 180
 gcc gga atc aca ttg cgc tat caa aac att ccg cac att ggt ttt ccc 691
 Ala Gly Ile Thr Leu Arg Tyr Gln Asn Ile Arg His Ile Gly Phe Pro
 185 190 195
 gcg tgg tgc ggt agt tcg ctg cat ggt tgg aca cct gtg gtc agt tgg 739
 Ala Trp Cys Gly Ser Ser Leu His Gly Trp Thr Pro Val Val Ser Trp
 200 205 210
 ggc agg gga ttg ggc aaa att gca gca gcg aaa gct cca tcg gtg aag 787
 Gly Arg Gly Leu Gly Lys Ile Ala Ala Ala Lys Ala Pro Ser Val Lys
 215 220 225
 ccc tgg aat gaa aaa ttg cgc cca acc att ttt ctg tgaggaaaag 833
 Pro Trp Asn Glu Lys Leu Arg Pro Thr Ile Phe Leu
 230 235 240
 gttgagcgca gtc 846

<210> 1822

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 1822

Met Thr Tyr Leu Val Trp Asp Gly Ala Thr Leu Val Glu Gly Ala Leu
 1 5 10 15

Glu	Ser	Thr	Pro	Thr	Val	Val	Asp	Ser	Tyr	Leu	Ala	Lys	Asp	His	Arg
			20				25						30		
Val	Val	Arg	Trp	Asp	Leu	His	Glu	Gln	Arg	Phe	Ala	Thr	Ser	Val	Asp
			35				40						45		
Val	Asp	Pro	Trp	Asp	Phe	Leu	His	Ala	Val	Arg	Glu	Ala	Ile	Pro	Arg
		50				55					60				
Gln	Gly	Ser	Trp	Phe	Pro	Lys	Val	Glu	Trp	His	Gly	Asp	Asp	Leu	Phe
		65				70					75		80		
Ala	Val	Asn	Ile	Arg	Pro	Ala	Pro	Thr	Leu	Arg	Lys	Ala	Thr	Ser	Leu
			85						90			95			
Trp	Leu	Ser	Glu	Asp	Pro	Asp	Pro	Arg	Thr	Gln	Pro	Thr	Ile	Lys	Gly
			100						105			110			
Pro	Asp	Leu	Asp	Val	Leu	Ala	His	Leu	Arg	Ser	Arg	Ala	Asn	Asp	Asn
		115					120					125			
Gly	Cys	Asp	Asp	Ala	Leu	Leu	Ile	Ser	Ala	Asp	Gly	Phe	Ile	Leu	Glu
		130					135					140			
Ala	Ala	Asn	Ala	Thr	Val	Val	Phe	Trp	Ala	Asp	Pro	Gln	Thr	Val	Ile
145					150					155		160			
Val	Pro	Arg	Gly	Asp	Val	Leu	Pro	Ser	Val	Thr	Leu	Ala	Ala	Thr	Ile
			165						170			175			
Pro	Leu	Trp	Glu	Lys	Ala	Gly	Ile	Thr	Leu	Arg	Tyr	Gln	Asn	Ile	Arg
			180						185			190			
His	Ile	Gly	Phe	Pro	Ala	Trp	Cys	Gly	Ser	Ser	Leu	His	Gly	Trp	Thr
		195					200					205			
Pro	Val	Val	Ser	Trp	Gly	Arg	Gly	Leu	Gly	Lys	Ile	Ala	Ala	Ala	Lys
		210					215					220			
Ala	Pro	Ser	Val	Lys	Pro	Trp	Asn	Glu	Lys	Leu	Arg	Pro	Thr	Ile	Phe
225					230					235		240			
Leu															

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<210> 1823
<211> 642
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(619)  
<223> RXA00582
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<400> 1823
actggccagc cttccgacgc atcgacttcc tccgcgccat tgcgcactac tcgcagcgca 60
gcagaagatt cggtaaataa cttattctcc aaggagagac atg tct gac tac atc 115
Met Ser Asp Tyr Ile

```

1

5

gtc gca ttt gaa tcc gca tac ggc tct acc aag cag tac gca gaa tct 163
 Val Ala Phe Glu Ser Ala Tyr Gly Ser Thr Lys Gln Tyr Ala Glu Ser
 10 15 20

ctg gcg caa cgc ctc ggc gta gat gcc tta aat ttt gaa caa gcg tgt 211
 Leu Ala Gln Arg Leu Gly Val Asp Ala Leu Asn Phe Glu Gln Ala Cys
 25 30 35

gcg gaa ctc gcg gcg aac ccg acc gca gca atc gtg gtt ttg agc ttt 259
 Ala Glu Leu Ala Ala Asn Pro Thr Ala Ala Ile Val Val Leu Ser Phe
 40 45 50

gtt cac ggc cca tcc cat cca ggt gcg aaa ttc att acc gat acc gat 307
 Val His Gly Pro Ser His Pro Gly Ala Lys Phe Ile Thr Asp Thr Asp
 55 60 65

ctc tcc ggc cac cgc gtc gca ctg tgc acc gtc ggc atg acg ctt gat 355
 Leu Ser Gly His Arg Val Ala Leu Cys Thr Val Gly Met Thr Leu Asp
 70 75 80 85

gat gtc gtg caa aag aag gac ggc gca gct cga tca ctg gga aac aag 403
 Asp Val Val Gln Lys Lys Asp Gly Ala Ala Arg Ser Leu Gly Asn Lys
 90 95 100

gca gac gat gtc acc cgt ttc tac ctt ccg gga cgc ctt aat tac tca 451
 Ala Asp Asp Val Thr Arg Phe Tyr Leu Pro Gly Arg Leu Asn Tyr Ser
 105 110 115

gag ctc tcg acc gcg cac cgc acc acc atg tgg acg atc gtc aac atg 499
 Glu Leu Ser Thr Ala His Arg Thr Thr Met Trp Thr Ile Val Asn Met
 120 125 130

ctg aaa gcg aag ccg ttg aag aat gac aac gac aaa atg atg atc aac 547
 Leu Lys Ala Lys Pro Leu Lys Asn Asp Asn Asp Lys Met Met Ile Asn
 135 140 145

act ttt gat acc gat gtt gac cgc gtc gat gag tcc cgc ctg gac gca 595
 Thr Phe Asp Thr Asp Val Asp Arg Val Asp Glu Ser Arg Leu Asp Ala
 150 155 160 165

gtg gag gag tgg gcg agg ggc ctc tagagtgggc gttgcaaaaa ctc 642
 Val Glu Glu Trp Ala Arg Gly Leu
 170

<210> 1824

<211> 173

<212> PRT

<213> Corynebacterium glutamicum

<400> 1824

Met Ser Asp Tyr Ile Val Ala Phe Glu Ser Ala Tyr Gly Ser Thr Lys
 1 5 10 15

Gln Tyr Ala Glu Ser Leu Ala Gln Arg Leu Gly Val Asp Ala Leu Asn
 20 25 30

Phe Glu Gln Ala Cys Ala Glu Leu Ala Ala Asn Pro Thr Ala Ala Ile
 35 40 45

Val Val Leu Ser Phe Val His Gly Pro Ser His Pro Gly Ala Lys Phe
50 55 60

Ile Thr Asp Thr Asp Leu Ser Gly His Arg Val Ala Leu Cys Thr Val
65 70 75 80

Gly Met Thr Leu Asp Asp Val Val Gln Lys Lys Asp Gly Ala Ala Arg
85 90 95

Ser Leu Gly Asn Lys Ala Asp Asp Val Thr Arg Phe Tyr Leu Pro Gly
100 105 110

Arg Leu Asn Tyr Ser Glu Leu Ser Thr Ala His Arg Thr Thr Met Trp
115 120 125

Thr Ile Val Asn Met Leu Lys Ala Lys Pro Leu Lys Asn Asp Asn Asp
130 135 140

Lys Met Met Ile Asn Thr Phe Asp Thr Asp Val Asp Arg Val Asp Glu
145 150 155 160

Ser Arg Leu Asp Ala Val Glu Glu Trp Ala Arg Gly Leu
165 170

<210> 1825

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXA00585

<400> 1825

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atgcagttag accacatcct ttaggaagga ccttttcggc gtg att gac ctc agc 115
Val Ile Asp Leu Ser
1 5

cct gta ttc aat aca gct gcc ggc gta tac aac gac acc aac gca atc 163
Pro Val Phe Asn Thr Ala Ala Gly Val Tyr Asn Asp Thr Asn Ala Ile
10 15 20

atc ttg gct cag cag cag caa ggt gga cca ctt gga cct gag ttt gga 211
Ile Leu Ala Gln Gln Gln Gln Gly Gly Pro Leu Gly Pro Glu Phe Gly
25 30 35

aag gcc tcg ccg gtt ggt ttg cta ctg atc gtc gcg atg ctc gtt gcc 259
Lys Ala Ser Pro Val Gly Leu Leu Ile Val Ala Met Leu Val Ala
40 45 50

att ctt gtt ctc ggc tgg gcg ttc cac cga cgc tgg tca cgg atg aat 307
Ile Leu Val Leu Gly Trp Ala Phe His Arg Arg Trp Ser Arg Met Asn
55 60 65

cgt cgt cgt att ttc gca gag cgc aac ggc ctt gat ccc ttc gat att 355
Arg Arg Arg Ile Phe Ala Glu Arg Asn Gly Leu Asp Pro Phe Asp Ile

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70              75              80              85
gag ggt gtt cgc aag gca atg gct gag gcc ggc ttg aat gaa aag tcc 403
Glu Gly Val Arg Lys Ala Met Ala Glu Ala Gly Leu Asn Glu Lys Ser
              90              95              100

aaa aag ggc ttc ctt taaaaagaaa gtgtgttaag gtt 441
Lys Lys Gly Phe Leu
              105

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<210> 1826
 <211> 106
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 1826
Val Ile Asp Leu Ser Pro Val Phe Asn Thr Ala Ala Gly Val Tyr Asn
  1              5              10              15

Asp Thr Asn Ala Ile Ile Leu Ala Gln Gln Gln Gln Gly Gly Pro Leu
              20              25              30

Gly Pro Glu Phe Gly Lys Ala Ser Pro Val Gly Leu Leu Leu Ile Val
              35              40              45

Ala Met Leu Val Ala Ile Leu Val Leu Gly Trp Ala Phe His Arg Arg
              50              55              60

Trp Ser Arg Met Asn Arg Arg Arg Ile Phe Ala Glu Arg Asn Gly Leu
              65              70              75              80

Asp Pro Phe Asp Ile Glu Gly Val Arg Lys Ala Met Ala Glu Ala Gly
              85              90              95

Leu Asn Glu Lys Ser Lys Lys Gly Phe Leu
              100              105

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<210> 1827
 <211> 1005
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(982)
 <223> RXA00586

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<400> 1827
tcatccaagg ggtaaatagg tatgacggcg gaaacgacta tcatgaatgc aatacacatc 60

aactaaaccc tgcggaagca tataaagctt caaggaaagg atg aaa cac gtg agt 115
              Met Lys His Val Ser
              1              5

ggt cta cgc cta atg gcg atc cac gcc cac cct gac gac gag tca agc 163
Gly Leu Arg Leu Met Ala Ile His Ala His Pro Asp Asp Glu Ser Ser
              10              15              20

aag ggc gca gca acc atg gcg cgc tat gca gct gag ggc aat caa gta 211

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Lys	Gly	Ala	Ala	Thr	Met	Ala	Arg	Tyr	Ala	Ala	Glu	Gly	Asn	Gln	Val		
			25					30					35				
atg	gtt	gtt	acc	tgc	act	ggt	ggt	gag	cgt	gga	gac	att	ctc	aac	cct	259	
Met	Val	Val	Thr	Cys	Thr	Gly	Gly	Glu	Arg	Gly	Asp	Ile	Leu	Asn	Pro		
		40					45					50					
gct	atg	gat	aag	cca	gga	atc	ctg	gac	aat	att	ttt	gct	gtg	cgt	cag	307	
Ala	Met	Asp	Lys	Pro	Gly	Ile	Leu	Asp	Asn	Ile	Phe	Ala	Val	Arg	Gln		
	55					60					65						
gaa	gag	atg	gcg	aag	gcc	atg	gaa	att	ctt	ggc	act	gag	cac	aga	tgg	355	
Glu	Glu	Met	Ala	Lys	Ala	Met	Glu	Ile	Leu	Gly	Thr	Glu	His	Arg	Trp		
70					75					80					85		
cta	ggt	tat	gag	gac	tct	ggg	ctg	ccc	caa	ggt	gat	cct	ttg	cct	cct	403	
Leu	Gly	Tyr	Glu	Asp	Ser	Gly	Leu	Pro	Gln	Gly	Asp	Pro	Leu	Pro	Pro		
				90				95						100			
ctg	cct	gag	ggc	tgt	ttt	gct	tta	gaa	gac	tcg	gat	aaa	gtc	acc	caa	451	
Leu	Pro	Glu	Gly	Cys	Phe	Ala	Leu	Glu	Asp	Ser	Asp	Lys	Val	Thr	Gln		
			105					110					115				
gat	tta	gtg	aag	att	ctg	cgc	gag	ttc	cgc	cca	cac	gtc	atc	att	acc	499	
Asp	Leu	Val	Lys	Ile	Leu	Arg	Glu	Phe	Arg	Pro	His	Val	Ile	Ile	Thr		
		120					125					130					
tat	gat	gag	aac	ggc	ggt	tac	cca	cac	ccg	gat	cac	ctc	aag	gtt	cat	547	
Tyr	Asp	Glu	Asn	Gly	Gly	Tyr	Pro	His	Pro	Asp	His	Leu	Lys	Val	His		
	135					140					145						
gag	gtg	tcg	atg	ctt	gca	tgg	gag	aag	tcc	ggc	gat	gca	gcg	tat	gca	595	
Glu	Val	Ser	Met	Leu	Ala	Trp	Glu	Lys	Ser	Gly	Asp	Ala	Ala	Tyr	Ala		
150					155				160						165		
cct	gag	ttg	ggc	gca	ccg	tgg	gag	cca	ctg	aag	ctt	tat	tac	acc	cac	643	
Pro	Glu	Leu	Gly	Ala	Pro	Trp	Glu	Pro	Leu	Lys	Leu	Tyr	Tyr	Thr	His		
				170					175					180			
ggc	ttt	atc	cgt	cag	cgc	atg	gaa	atg	ttc	cat	gat	ctg	ctc	att	gaa	691	
Gly	Phe	Ile	Arg	Gln	Arg	Met	Glu	Met	Phe	His	Asp	Leu	Leu	Ile	Glu		
			185					190					195				
cag	ggc	aag	ccc	agc	cca	tac	acc	ccg	atg	ctt	gag	cgt	tgg	aag	gca	739	
Gln	Gly	Lys	Pro	Ser	Pro	Tyr	Thr	Pro	Met	Leu	Glu	Arg	Trp	Lys	Ala		
		200					205					210					
aat	gag	gct	gat	gtg	atg	gct	cga	gtt	acc	act	cag	gtt	cct	tgt	gag	787	
Asn	Glu	Ala	Asp	Val	Met	Ala	Arg	Val	Thr	Thr	Gln	Val	Pro	Cys	Glu		
	215					220					225						
cgc	ttc	ttt	gat	cag	cgt	gat	gac	gcc	ctg	cgt	gcg	cac	gca	act	cag	835	
Arg	Phe	Phe	Asp	Gln	Arg	Asp	Asp	Ala	Leu	Arg	Ala	His	Ala	Thr	Gln		
230					235					240					245		
att	gat	cct	gcg	ggt	gct	ttc	ttt	gga	act	ccc	gtt	gag	gtg	cag	cgt	883	
Ile	Asp	Pro	Ala	Gly	Ala	Phe	Phe	Gly	Thr	Pro	Val	Glu	Val	Gln	Arg		
				250					255					260			
cgc	ctg	tgg	ccg	act	gaa	gag	ttc	gaa	tta	gct	aaa	act	cgt	gtg	aag	931	
Arg	Leu	Trp	Pro	Thr	Glu	Glu	Phe	Glu	Leu	Ala	Lys	Thr	Arg	Val	Lys		

265 270 275
 acg tcg atc cca gaa gat gac ctg ttt gcc gga atc aca ccc gat gca 979
 Thr Ser Ile Pro Glu Asp Asp Leu Phe Ala Gly Ile Thr Pro Asp Ala
 280 285 290

gaa taatgcagtt agaccacatc ctt 1005
 Glu

<210> 1828

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 1828

Met Lys His Val Ser Gly Leu Arg Leu Met Ala Ile His Ala His Pro
 1 5 10 15

Asp Asp Glu Ser Ser Lys Gly Ala Ala Thr Met Ala Arg Tyr Ala Ala
 20 25 30

Glu Gly Asn Gln Val Met Val Val Thr Cys Thr Gly Gly Glu Arg Gly
 35 40 45

Asp Ile Leu Asn Pro Ala Met Asp Lys Pro Gly Ile Leu Asp Asn Ile
 50 55 60

Phe Ala Val Arg Gln Glu Glu Met Ala Lys Ala Met Glu Ile Leu Gly
 65 70 75 80

Thr Glu His Arg Trp Leu Gly Tyr Glu Asp Ser Gly Leu Pro Gln Gly
 85 90 95

Asp Pro Leu Pro Pro Leu Pro Glu Gly Cys Phe Ala Leu Glu Asp Ser
 100 105 110

Asp Lys Val Thr Gln Asp Leu Val Lys Ile Leu Arg Glu Phe Arg Pro
 115 120 125

His Val Ile Ile Thr Tyr Asp Glu Asn Gly Gly Tyr Pro His Pro Asp
 130 135 140

His Leu Lys Val His Glu Val Ser Met Leu Ala Trp Glu Lys Ser Gly
 145 150 155 160

Asp Ala Ala Tyr Ala Pro Glu Leu Gly Ala Pro Trp Glu Pro Leu Lys
 165 170 175

Leu Tyr Tyr Thr His Gly Phe Ile Arg Gln Arg Met Glu Met Phe His
 180 185 190

Asp Leu Leu Ile Glu Gln Gly Lys Pro Ser Pro Tyr Thr Pro Met Leu
 195 200 205

Glu Arg Trp Lys Ala Asn Glu Ala Asp Val Met Ala Arg Val Thr Thr
 210 215 220

Gln Val Pro Cys Glu Arg Phe Phe Asp Gln Arg Asp Asp Ala Leu Arg
 225 230 235 240

120 125 130
tcc acg ctg atc ccc acc cgc gaa cca gca gtt tcc ggt ggt gtt tac 547
Ser Thr Leu Ile Pro Thr Arg Glu Pro Ala Val Ser Gly Gly Val Tyr
135 140 145
ggt tgt tca acc gtg atc cca tca cat atg aac ctg taaaactaga 593
Gly Cys Ser Thr Val Ile Pro Ser His Met Asn Leu
150 155 160
aaattttgtct gtg 606

<210> 1830

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 1830

Met Ser Thr Asn Ser Asn Ser Pro Ser Asn Ala Ser Gly Ala Ser Asn
1 5 10 15
Ile Pro Asn Thr Gln Arg Pro Ala Ser Arg Tyr Asn Ser Pro Arg Pro
20 25 30
Glu Ala Ala Ala Gly Arg Asn Ile Ser Gly Lys Ile Ile Ala Val Ile
35 40 45
Gly Val Leu Leu Val Ile Ala Ile Val Ile Val Gly Ala Asn Phe Leu
50 55 60
Lys Asn Arg Asp Ala Gln Thr Val Ser Gly Gln Met Gly Ser Phe Glu
65 70 75 80
Arg Ile Asp Asp Asp Thr Phe Arg Phe Glu Val Asp Val Thr Arg Asp
85 90 95
Asp Pro Ser Gln Val Ala Tyr Cys Ile Val Thr Ala Lys Asp Tyr Ser
100 105 110
His Ala Glu Val Gly Arg Arg Glu Val Leu Val Glu Pro Ser Asp His
115 120 125
Ser Thr Val Arg Ile Ser Thr Leu Ile Pro Thr Arg Glu Pro Ala Val
130 135 140
Ser Gly Gly Val Tyr Gly Cys Ser Thr Val Ile Pro Ser His Met Asn
145 150 155 160
Leu

<210> 1831

<211> 353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(330)

<223> RXA00595

<400> 1831

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cgc aat att gca gca tgg atc gca atc gcc gcc atc atc atc gcc agc 48
Arg Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
  1             5             10             15

ctg ggc gca ctg ctc tgc atg atc cgc gtg tgg cgt gaa gtc ttc tgg 96
Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
          20             25             30

ggt ggc gca atg cac cag cgc ggc gtc tgc ccg cag ctg cgc atc agc 144
Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
          35             40             45

cca gca aaa atc gcc cca gcg ctc agc ctg atc att tta tgc gta ggc 192
Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
          50             55             60

atg ttc atc ttc gcg ggc ccg ctt atc gac gcg acc ctc acc gcc acc 240
Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
          65             70             75             80

gac ggc ctc ttg aac acc gat gca tac caa cag gct gtg ctc ggt gaa 288
Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu
          85             90             95

aat gcc atc gga gtg cca agc cct agc tac cag gga gga aac 330
Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
          100             105             110

taatgcttaa cgccctgaaa ttc 353

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<210> 1832

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 1832

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Arg Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
  1             5             10             15

Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
          20             25             30

Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
          35             40             45

Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
          50             55             60

Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
          65             70             75             80

Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu
          85             90             95

Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
          100             105             110

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<210> 1833
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXA00597

<400> 1833
caaggagatc cgccccagcg atgctgagtg gccaaagtcgc gagatcgctg acaccgccca 60
aaacaccgtc agccaagaca agagggagtt ttaaaacaac atg act gct ttt gga 115
Met Thr Ala Phe Gly
1 5
att gtc acc aca gtt ggc atc tgc atg ttt gcg ttc tcc ctc tta tct 163
Ile Val Thr Thr Val Gly Ile Cys Met Phe Ala Phe Ser Leu Leu Ser
10 15 20
gcc ctg gtc ctt att ctg cgc acc aaa gat ttc ctc acc cgc gtg gtg 211
Ala Leu Val Leu Ile Leu Arg Thr Lys Asp Phe Leu Thr Arg Val Val
25 30 35
ctt tcc gac atg gtt ttc tac tct atg atc gcg atc tac ctc atc tgg 259
Leu Ser Asp Met Val Phe Tyr Ser Met Ile Ala Ile Tyr Leu Ile Trp
40 45 50
gtg ctc aac aac cca acc tca atc gcc ttt gag att gct ctt ctc gca 307
Val Leu Asn Asn Pro Thr Ser Ile Ala Phe Glu Ile Ala Leu Leu Ala
55 60 65
gca gtc ctc ggc ggc gta ctt cca acc ctg tcc atg gct cgc atc att 355
Ala Val Leu Gly Gly Val Leu Pro Thr Leu Ser Met Ala Arg Ile Ile
70 75 80 85
tcg aag gga cgc agg taaatgacca ttccagagat cat 393
Ser Lys Gly Arg Arg
90

<210> 1834
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 1834
Met Thr Ala Phe Gly Ile Val Thr Thr Val Gly Ile Cys Met Phe Ala
1 5 10 15
Phe Ser Leu Leu Ser Ala Leu Val Leu Ile Leu Arg Thr Lys Asp Phe
20 25 30
Leu Thr Arg Val Val Leu Ser Asp Met Val Phe Tyr Ser Met Ile Ala
35 40 45
Ile Tyr Leu Ile Trp Val Leu Asn Asn Pro Thr Ser Ile Ala Phe Glu
50 55 60

Ile Ala Leu Leu Ala Ala Val Leu Gly Gly Val Leu Pro Thr Leu Ser
 65 70 75 80

Met Ala Arg Ile Ile Ser Lys Gly Arg Arg
 85 90

<210> 1835

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXA00598

<400> 1835

aacctcaatc gcctttgaga ttgctcttct cgcagcagtc ctcggcgggcg tacttccaac 60

cctgtccatg gctcgcacatca tttcgaaggg acgcaggtaa atg acc att cca gag 115
 Met Thr Ile Pro Glu
 1 5

atc atc gtc tcc atc ctc gtg atc ctc gca ggc ctg ttt tct cta ggt 163
 Ile Ile Val Ser Ile Leu Val Ile Leu Ala Gly Leu Phe Ser Leu Gly
 10 15 20

act gca atc gct ttg tgg cgc gca ccg gat ccg ctc acc cga gcc aac 211
 Thr Ala Ile Ala Leu Trp Arg Ala Pro Asp Pro Leu Thr Arg Ala Asn
 25 30 35

ctg ctt ggc acc acc gtg ggt gtc tcc ata ccg ctg ctc atc att gcg 259
 Leu Leu Gly Thr Thr Val Gly Val Ser Ile Pro Leu Leu Ile Ile Ala
 40 45 50

ctg ctg att cac acc tgg tcc gtc gac gga ttt aac ccc aac aat ttc 307
 Leu Leu Ile His Thr Trp Ser Val Asp Gly Phe Asn Pro Asn Asn Phe
 55 60 65

atc cga gcg atc atc gcc atc atc ggc gtc tgg gtc atc ggt tcc gtt 355
 Ile Arg Ala Ile Ile Ala Ile Ile Gly Val Trp Val Ile Gly Ser Val
 70 75 80 85

ggc tcc tac tac atg gga cgc gcc atc tat ggt gtg acc gta gtg gat 403
 Gly Ser Tyr Tyr Met Gly Arg Ala Ile Tyr Gly Val Thr Val Val Asp
 90 95 100

aac aga cga tcc aaa taaactgctt ttagaaaaaa agg 441
 Asn Arg Arg Ser Lys
 105

<210> 1836

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1836

Met Thr Ile Pro Glu Ile Ile Val Ser Ile Leu Val Ile Leu Ala Gly
 1 5 10 15

Leu Phe Ser Leu Gly Thr Ala Ile Ala Leu Trp Arg Ala Pro Asp Pro
 20 25 30
 Leu Thr Arg Ala Asn Leu Leu Gly Thr Thr Val Gly Val Ser Ile Pro
 35 40 45
 Leu Leu Ile Ile Ala Leu Leu Ile His Thr Trp Ser Val Asp Gly Phe
 50 55 60
 Asn Pro Asn Asn Phe Ile Arg Ala Ile Ile Ala Ile Ile Gly Val Trp
 65 70 75 80
 Val Ile Gly Ser Val Gly Ser Tyr Tyr Met Gly Arg Ala Ile Tyr Gly
 85 90 95
 Val Thr Val Val Asp Asn Arg Arg Ser Lys
 100 105

<210> 1837

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXA00601

<400> 1837

tagatataga acacattcta ttgcaggga ttatcaagtt tcatacattg tcctcgtagg 60
 ggcaagtata tttcccatgc aatatttttt aggagtccca atg cgt ttc aag tca 115
 Met Arg Phe Lys Ser
 1 5
 gtt gca gct atc gca ctt tcc acc gca atg atc agg ggt gga acc gca 163
 Val Ala Ala Ile Ala Leu Ser Thr Ala Met Ile Arg Gly Gly Thr Ala
 10 15 20
 agc gtt gct aat gct cag cag gtt agc cct agt tcc acg att gag atc 211
 Ser Val Ala Asn Ala Gln Gln Val Ser Pro Ser Ser Thr Ile Glu Ile
 25 30 35
 cct caa gaa ttc gtc cac acc gtg cag aac ttc gtg cca ggt atg act 259
 Pro Gln Glu Phe Val His Thr Val Gln Asn Phe Val Pro Gly Met Thr
 40 45 50
 tac ggc gat gca ggg tcc gct atc cag agc acc gct ggt tct gtg gca 307
 Tyr Gly Asp Ala Gly Ser Ala Ile Gln Ser Thr Ala Gly Ser Val Ala
 55 60 65
 ctg aac agt acc gct gga atc atc ctt cca atc gtt ctt cca ttc ctt 355
 Leu Asn Ser Thr Ala Gly Ile Ile Leu Pro Ile Val Leu Pro Phe Leu
 70 75 80 85
 ggt ctg gga gct gtt ggt tct gca gcg ctg tct gct taagcctttt 401
 Gly Leu Gly Ala Val Gly Ser Ala Ala Leu Ser Ala
 90 95

ctaggttcct taa

414

<210> 1838

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 1838

Met Arg Phe Lys Ser Val Ala Ala Ile Ala Leu Ser Thr Ala Met Ile
 1 5 10 15

Arg Gly Gly Thr Ala Ser Val Ala Asn Ala Gln Gln Val Ser Pro Ser
 20 25 30

Ser Thr Ile Glu Ile Pro Gln Glu Phe Val His Thr Val Gln Asn Phe
 35 40 45

Val Pro Gly Met Thr Tyr Gly Asp Ala Gly Ser Ala Ile Gln Ser Thr
 50 55 60

Ala Gly Ser Val Ala Leu Asn Ser Thr Ala Gly Ile Ile Leu Pro Ile
 65 70 75 80

Val Leu Pro Phe Leu Gly Leu Gly Ala Val Gly Ser Ala Ala Leu Ser
 85 90 95

Ala

<210> 1839

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXA00602

<400> 1839

gcgcgatcaa tggaatctag cttcatatat tgcacaatag cctagttgag gtgcgcaaac 60

tggcaacaaa actaccggc aattgtgtga tgattgtagt gtg caa aaa acg caa 115
 Val Gln Lys Thr Gln
 1 5

gag att cat tca agc ctg gag gtg tcg cca tcc aag gca gcc ctg gaa 163
 Glu Ile His Ser Ser Leu Glu Val Ser Pro Ser Lys Ala Ala Leu Glu
 10 15 20

cca gat gat aaa ggt tat cgg cgc tac gaa atc gcg caa ggt cta aaa 211
 Pro Asp Asp Lys Gly Tyr Arg Arg Tyr Glu Ile Ala Gln Gly Leu Lys
 25 30 35

acc tcc ctt gct gca ggt ttg ggc atg tac ccg att ggt att gcg ttt 259
 Thr Ser Leu Ala Ala Gly Leu Gly Met Tyr Pro Ile Gly Ile Ala Phe
 40 45 50

ggt ctc ttg gtt att caa tac ggc tac gaa tgg tgg gca gcc cca ctg 307

Gly Leu Leu Val Ile Gln Tyr Gly Tyr Glu Trp Trp Ala Ala Pro Leu
 55 60 65
 ttt tcc ggc ctg att ttc gcg ggc tcc acc gaa atg ctg gtc atc gcc 355
 Phe Ser Gly Leu Ile Phe Ala Gly Ser Thr Glu Met Leu Val Ile Ala
 70 75 80 85
 ctc gtt gtg ggc gca gcg ccc ctg ggc gcc atc gcg ctc acc aca ttg 403
 Leu Val Val Gly Ala Ala Pro Leu Gly Ala Ile Ala Leu Thr Thr Leu
 90 95 100
 ctg gtg aac ttc cgc cac gta ttc tat gcg ttt tca ttc ccg ctg cat 451
 Leu Val Asn Phe Arg His Val Phe Tyr Ala Phe Ser Phe Pro Leu His
 105 110 115
 gtg gtc aaa aac ccc att gcc cgt ttc tat tcg gtt ttc gcg ctt atc 499
 Val Val Lys Asn Pro Ile Ala Arg Phe Tyr Ser Val Phe Ala Leu Ile
 120 125 130
 gac gaa gcc tac gca gtc act gcg gcc agg ccc gca ggc tgg tcg gcg 547
 Asp Glu Ala Tyr Ala Val Thr Ala Ala Arg Pro Ala Gly Trp Ser Ala
 135 140 145
 tgg cga ctt atc tca atg caa ata gcg ttt cac tcc tac tgg gta ttc 595
 Trp Arg Leu Ile Ser Met Gln Ile Ala Phe His Ser Tyr Trp Val Phe
 150 155 160 165
 ggc ggt ctc acc gga gtg gcg atc gca gag ttg att cct ttt gaa att 643
 Gly Gly Leu Thr Gly Val Ala Ile Ala Glu Leu Ile Pro Phe Glu Ile
 170 175 180
 aag ggc ctc gag ttc gcc ctt tgc tct ctc ttt gtc acg ctg act ttg 691
 Lys Gly Leu Glu Phe Ala Leu Cys Ser Leu Phe Val Thr Leu Thr Leu
 185 190 195
 gat tcc tgc cga acg aaa aag cag atc cct tct ctg ctg ctc gca ggt 739
 Asp Ser Cys Arg Thr Lys Lys Gln Ile Pro Ser Leu Leu Leu Ala Gly
 200 205 210
 ttg agc ttc acc att gct ctt gtg gta att cca ggt cag gcc cta ttt 787
 Leu Ser Phe Thr Ile Ala Leu Val Val Ile Pro Gly Gln Ala Leu Phe
 215 220 225
 gcg gcg ctg ctg atc ttc ttg ggt ctg ttg acc atc cgg tac ttc ttc 835
 Ala Ala Leu Leu Ile Phe Leu Gly Leu Leu Thr Ile Arg Tyr Phe Phe
 230 235 240 245
 ttg gga aag gct gct aaa tgacaactga tttctcctgt att 876
 Leu Gly Lys Ala Ala Lys
 250

<210> 1840

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 1840

Val Gln Lys Thr Gln Glu Ile His Ser Ser Leu Glu Val Ser Pro Ser
 1 5 10 15

Lys	Ala	Ala	Leu	Glu	Pro	Asp	Asp	Lys	Gly	Tyr	Arg	Arg	Tyr	Glu	Ile
			20					25					30		
Ala	Gln	Gly	Leu	Lys	Thr	Ser	Leu	Ala	Ala	Gly	Leu	Gly	Met	Tyr	Pro
		35					40					45			
Ile	Gly	Ile	Ala	Phe	Gly	Leu	Leu	Val	Ile	Gln	Tyr	Gly	Tyr	Glu	Trp
	50					55					60				
Trp	Ala	Ala	Pro	Leu	Phe	Ser	Gly	Leu	Ile	Phe	Ala	Gly	Ser	Thr	Glu
	65				70					75					80
Met	Leu	Val	Ile	Ala	Leu	Val	Val	Gly	Ala	Ala	Pro	Leu	Gly	Ala	Ile
				85					90					95	
Ala	Leu	Thr	Thr	Leu	Leu	Val	Asn	Phe	Arg	His	Val	Phe	Tyr	Ala	Phe
			100					105					110		
Ser	Phe	Pro	Leu	His	Val	Val	Lys	Asn	Pro	Ile	Ala	Arg	Phe	Tyr	Ser
		115					120					125			
Val	Phe	Ala	Leu	Ile	Asp	Glu	Ala	Tyr	Ala	Val	Thr	Ala	Ala	Arg	Pro
	130					135					140				
Ala	Gly	Trp	Ser	Ala	Trp	Arg	Leu	Ile	Ser	Met	Gln	Ile	Ala	Phe	His
	145				150					155					160
Ser	Tyr	Trp	Val	Phe	Gly	Gly	Leu	Thr	Gly	Val	Ala	Ile	Ala	Glu	Leu
				165					170					175	
Ile	Pro	Phe	Glu	Ile	Lys	Gly	Leu	Glu	Phe	Ala	Leu	Cys	Ser	Leu	Phe
			180					185					190		
Val	Thr	Leu	Thr	Leu	Asp	Ser	Cys	Arg	Thr	Lys	Lys	Gln	Ile	Pro	Ser
		195					200					205			
Leu	Leu	Leu	Ala	Gly	Leu	Ser	Phe	Thr	Ile	Ala	Leu	Val	Val	Ile	Pro
	210					215					220				
Gly	Gln	Ala	Leu	Phe	Ala	Ala	Leu	Leu	Ile	Phe	Leu	Gly	Leu	Leu	Thr
	225				230					235					240
Ile	Arg	Tyr	Phe	Phe	Leu	Gly	Lys	Ala	Ala	Lys					
				245					250						

<210> 1841

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (391)

<223> RXA00604

<400> 1841

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tgaagcatga atctttttca tctagtgaag gactgatccc atg cgt atg aaa tca 115
Met Arg Met Lys Ser

1

5

atc gca gca att gca atc gct acc gcc gcc ctg gct ggt ggc act gga 163
 Ile Ala Ala Ile Ala Ile Ala Thr Ala Ala Leu Ala Gly Gly Thr Gly
 10 15 20

gtc gct agc gca cag gaa gct ggc tcg act gct ggt tcc tcc aac ctc 211
 Val Ala Ser Ala Gln Glu Ala Gly Ser Thr Ala Gly Ser Ser Asn Leu
 25 30 35

agc tct ggg atc cag ctt cca caa gaa gcc acc gat ctg ttg agc ttc 259
 Ser Ser Gly Ile Gln Leu Pro Gln Glu Ala Thr Asp Leu Leu Ser Phe
 40 45 50

ctg cct gct gct cag gct gcg cag gtt gaa gga gca att cag agc acc 307
 Leu Pro Ala Ala Gln Ala Ala Gln Val Glu Gly Ala Ile Gln Ser Thr
 55 60 65

gct ggt ttc ttt gcc gtt gga ctc ggc tcg acc gcc att ggt tcc act 355
 Ala Gly Phe Phe Ala Val Gly Leu Gly Ser Thr Ala Ile Gly Ser Thr
 70 75 80 85

gca gtg acc ttg gga att gcg gat ctg ctg tct agc taatttcctc 401
 Ala Val Thr Leu Gly Ile Ala Asp Leu Leu Ser Ser
 90 95

tcaatagctt caa 414

<210> 1842

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 1842

Met Arg Met Lys Ser Ile Ala Ala Ile Ala Ile Ala Thr Ala Ala Leu
 1 5 10 15

Ala Gly Gly Thr Gly Val Ala Ser Ala Gln Glu Ala Gly Ser Thr Ala
 20 25 30

Gly Ser Ser Asn Leu Ser Ser Gly Ile Gln Leu Pro Gln Glu Ala Thr
 35 40 45

Asp Leu Leu Ser Phe Leu Pro Ala Ala Gln Ala Ala Gln Val Glu Gly
 50 55 60

Ala Ile Gln Ser Thr Ala Gly Phe Phe Ala Val Gly Leu Gly Ser Thr
 65 70 75 80

Ala Ile Gly Ser Thr Ala Val Thr Leu Gly Ile Ala Asp Leu Leu Ser
 85 90 95

Ser

<210> 1843

<211> 987

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> RXA00610

<400> 1843

caagcactcc caggggaacg ttcattcgaa aaactcgacg ccttatacga gcttctagag 60

cctcggaacc aattgctcga gatcgagtc taactagagt atg gaa ccg aaa aaa 115
 Met Glu Pro Lys Lys
 1 5

cct gtc aca tat aaa gaa ctt gcc cac gaa tat tca aga aga acg ttt 163
 Pro Val Thr Tyr Lys Glu Leu Ala His Glu Tyr Ser Arg Arg Thr Phe
 10 15 20

aac aaa ctc ttc acc aaa att act ggc ttc gtc tat cta aaa aac gat 211
 Asn Lys Leu Phe Thr Lys Ile Thr Gly Phe Val Tyr Leu Lys Asn Asp
 25 30 35

cta atc aac gat ccc aac tta gtg acc caa gca ctg ctc aaa aga tgc 259
 Leu Ile Asn Asp Pro Asn Leu Val Thr Gln Ala Leu Leu Lys Arg Cys
 40 45 50

cca gaa gga gta ctt cgc gga tat gca gca tta aag caa cgt ggc tat 307
 Pro Glu Gly Val Leu Arg Gly Tyr Ala Ala Leu Lys Gln Arg Gly Tyr
 55 60 65

cag ctt tta gac gat cag tgg atg cca atc atc agt gtt tcc gga gat 355
 Gln Leu Leu Asp Asp Gln Trp Met Pro Ile Ile Ser Val Ser Gly Asp
 70 75 80 85

cta aac agg agg gac tgc tca cga ggt gaa att ctc agg cgg att gaa 403
 Leu Asn Arg Arg Asp Cys Ser Arg Gly Glu Ile Leu Arg Arg Ile Glu
 90 95 100

cca gaa aac acc ctg ctc agt ggc aac att agg ttc gtt aat gat gtt 451
 Pro Glu Asn Thr Leu Leu Ser Gly Asn Ile Arg Phe Val Asn Asp Val
 105 110 115

caa gcg atc caa gac gtc ttc gac ctg cat tct ctc aac gac ttt gaa 499
 Gln Ala Ile Gln Asp Val Phe Asp Leu His Ser Leu Asn Asp Phe Glu
 120 125 130

gac caa gta gct ctc atc gat cat ctc atc agg cag cgc ccc gaa tta 547
 Asp Gln Val Ala Leu Ile Asp His Leu Ile Arg Gln Arg Pro Glu Leu
 135 140 145

ttc caa gaa ctc ata caa gag cca aaa ctt aag aaa cac act caa tac 595
 Phe Gln Glu Leu Ile Gln Glu Pro Lys Leu Lys Lys His Thr Gln Tyr
 150 155 160 165

gcc aat cct ttt gct gaa tct ccg caa gaa tca cga ctt cgg gtc aga 643
 Ala Asn Pro Phe Ala Glu Ser Pro Gln Glu Ser Arg Leu Arg Val Arg
 170 175 180

ctt cat tca ctg ggt tac cac ggc ttc atc cca cag att cat gtt gaa 691
 Leu His Ser Leu Gly Tyr His Gly Phe Ile Pro Gln Ile His Val Glu
 185 190 195

tac gac ggt caa tcc tat ttt cta gat ctc gca gat ccg ctg tgg cag 739
 Tyr Asp Gly Gln Ser Tyr Phe Leu Asp Leu Ala Asp Pro Leu Trp Gln
 200 205 210

gtt gcc ctc gaa tac aac ggc gga tgg cac tac acc tct gag cag cga 787
 Val Ala Leu Glu Tyr Asn Gly Gly Trp His Tyr Thr Ser Glu Gln Arg
 215 220 225

gag aaa gat tct cat cgg aag aat gct ctg aaa agt gcg gga tgg gat 835
 Glu Lys Asp Ser His Arg Lys Asn Ala Leu Lys Ser Ala Gly Trp Asp
 230 235 240 245

gtc cta gaa gtg aca tca aaa act ctg cag aat ccg aat tcc tgg aac 883
 Val Leu Glu Val Thr Ser Lys Thr Leu Gln Asn Pro Asn Ser Trp Asn
 250 255 260

aac ctg ata caa cag atc aat agc tct ctc cgc cga aag cag gct cag 931
 Asn Leu Ile Gln Gln Ile Asn Ser Ser Leu Arg Arg Lys Gln Ala Gln
 265 270 275

cga cgc cga agg tta ccc atg caa acg gtg ggc taacggcatc actgaaaaag 984
 Arg Arg Arg Arg Leu Pro Met Gln Thr Val Gly
 280 285

acc 987

<210> 1844

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 1844

Met Glu Pro Lys Lys Pro Val Thr Tyr Lys Glu Leu Ala His Glu Tyr
 1 5 10 15

Ser Arg Arg Thr Phe Asn Lys Leu Phe Thr Lys Ile Thr Gly Phe Val
 20 25 30

Tyr Leu Lys Asn Asp Leu Ile Asn Asp Pro Asn Leu Val Thr Gln Ala
 35 40 45

Leu Leu Lys Arg Cys Pro Glu Gly Val Leu Arg Gly Tyr Ala Ala Leu
 50 55 60

Lys Gln Arg Gly Tyr Gln Leu Leu Asp Asp Gln Trp Met Pro Ile Ile
 65 70 75 80

Ser Val Ser Gly Asp Leu Asn Arg Arg Asp Cys Ser Arg Gly Glu Ile
 85 90 95

Leu Arg Arg Ile Glu Pro Glu Asn Thr Leu Leu Ser Gly Asn Ile Arg
 100 105 110

Phe Val Asn Asp Val Gln Ala Ile Gln Asp Val Phe Asp Leu His Ser
 115 120 125

Leu Asn Asp Phe Glu Asp Gln Val Ala Leu Ile Asp His Leu Ile Arg
 130 135 140

Gln Arg Pro Glu Leu Phe Gln Glu Leu Ile Gln Glu Pro Lys Leu Lys

Ala Gly Ala Gln Ala Gly Phe Leu Thr Ser Gly Thr Glu Glu Leu Thr	
70 75 80 85	
agc gga aca caa gag ctt atc gac ggc gca gcc cca ctc gaa gaa ggc	403
Ser Gly Thr Gln Glu Leu Ile Asp Gly Ala Ala Pro Leu Glu Glu Gly	
90 95 100	
gtc tca gcc gcg gct gac ggt gca gcg caa ctc cac gat ggc ctc atc	451
Val Ser Ala Ala Ala Asp Gly Ala Ala Gln Leu His Asp Gly Leu Ile	
105 110 115	
caa ctc cag gcc ggc act gga caa atg gga acc ggc gcc acc gaa att	499
Gln Leu Gln Ala Gly Thr Gly Gln Met Gly Thr Gly Ala Thr Glu Ile	
120 125 130	
gcc gac ggc gtc caa aac gca gtc gaa caa ctt ggc ggt ctt gtc gtt	547
Ala Asp Gly Val Gln Asn Ala Val Glu Gln Leu Gly Gly Leu Val Val	
135 140 145	
gta cag cag caa ctc tta ggc gcc ctc aac gaa gca gac aaa caa ctc	595
Val Gln Gln Gln Leu Leu Gly Ala Leu Asn Glu Ala Asp Lys Gln Leu	
150 155 160 165	
gcc tcg agc aaa atc ccc gaa gcc gaa gac ctg cgc aaa caa atc acc	643
Ala Ser Ser Lys Ile Pro Glu Ala Glu Asp Leu Arg Lys Gln Ile Thr	
170 175 180	
gaa gtc cga gga cac ctc gaa aac ttc ggc atc tcc gta gaa atg acc	691
Glu Val Arg Gly His Leu Glu Asn Phe Gly Ile Ser Val Glu Met Thr	
185 190 195	
gac caa ctc gat caa cta cgt tcc ggc acc cgc gac ctg gct aac caa	739
Asp Gln Leu Asp Gln Leu Arg Ser Gly Thr Arg Asp Leu Ala Asn Gln	
200 205 210	
ctc gca gtc ccc ggc tac gga ttc cac gat ggt att tac agc gcc acc	787
Leu Ala Val Pro Gly Tyr Gly Phe His Asp Gly Ile Tyr Ser Ala Thr	
215 220 225	
aat gga gca gcc gaa tta tct gca ggt ttg caa gag cta gaa gca ggc	835
Asn Gly Ala Ala Glu Leu Ser Ala Gly Leu Gln Glu Leu Glu Ala Gly	
230 235 240 245	
gtt ggg act gcc gtc gaa ggc ttc acc gca ctc gat gaa ggt gca aac	883
Val Gly Thr Ala Val Glu Gly Phe Thr Ala Leu Asp Glu Gly Ala Asn	
250 255 260	
cga tta gac tcc atg gcc acc ctc aac gaa gaa aaa acc tcc gca gtc	931
Arg Leu Asp Ser Met Ala Thr Leu Asn Glu Glu Lys Thr Ser Ala Val	
265 270 275	
caa cga gcc ctc ccg gta ccc caa gta ccc gcc ggc aca atc gaa ggc	979
Gln Arg Ala Leu Pro Val Pro Gln Val Pro Ala Gly Thr Ile Glu Gly	
280 285 290	
acc gca gac gaa gaa cgc acc agc gca cta gcg ccc atg tac gcc ttc	1027
Thr Ala Asp Glu Glu Arg Thr Ser Ala Leu Ala Pro Met Tyr Ala Phe	
295 300 305	
tta att tca gca ttg gtc atg ctg gcc ggt gca gca ctt gga tgg gca	1075
Leu Ile Ser Ala Leu Val Met Leu Ala Gly Ala Ala Leu Gly Trp Ala	

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310          315          320          325
aca cta aaa aac aag tgg ctg atg gcc ttt gct gtc att ggt gtc act 1123
Thr Leu Lys Asn Lys Trp Leu Met Ala Phe Ala Val Ile Gly Val Thr
          330          335          340

gca atc ggt ggc att atc ttg ttc acc gta gct ttg ggc ata tcc att 1171
Ala Ile Gly Gly Ile Ile Leu Phe Thr Val Ala Leu Gly Ile Ser Ile
          345          350          355

gga gct ttg ttt gga gcc tta gga att ttg ctt ctt gcc act gtt gtt 1219
Gly Ala Leu Phe Gly Ala Leu Gly Ile Leu Leu Leu Ala Thr Val Val
          360          365          370

gcc ggt att ctc tcc cgg att ttg ctt gac gtg ttg gga act acc ggg 1267
Ala Gly Ile Leu Ser Arg Ile Leu Leu Asp Val Leu Gly Thr Thr Gly
          375          380          385

gct att gtg gtt tct gtt ctg gga tgg gta gcc caa gct gca gta att 1315
Ala Ile Val Val Ser Val Leu Gly Trp Val Ala Gln Ala Ala Val Ile
          390          395          400          405

ggc cat gta tgg agt gtt acc gct gta tcc gat atc gca ctt gtt tgg 1363
Gly His Val Trp Ser Val Thr Ala Val Ser Asp Ile Ala Leu Val Trp
          410          415          420

cga gtc gtc gca ggc atg atg cca ctg cat tat cca acc ttt gca gtg 1411
Arg Val Val Ala Gly Met Met Pro Leu His Tyr Pro Thr Phe Ala Val
          425          430          435

acc tcc att ggt aat ggc gga tca gct gca gct atc tgg atg tct gtt 1459
Thr Ser Ile Gly Asn Gly Gly Ser Ala Ala Ala Ile Trp Met Ser Val
          440          445          450

gct gtc ttg ttg gca atg gga gcg atc gga gct gtt gcg ctt cgg aag 1507
Ala Val Leu Leu Ala Met Gly Ala Ile Gly Ala Val Ala Leu Arg Lys
          455          460          465

cca aag gcg gtt gcg gtt gag gtt gaa gaa gct gtt gat gct gat gca 1555
Pro Lys Ala Val Ala Val Glu Val Glu Glu Ala Val Asp Ala Asp Ala
          470          475          480          485

gac caa gca gcc tcg gaa tcc tgatggtttt ggtctgattc gac 1599
Asp Gln Ala Ala Ser Glu Ser
          490

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<210> 1846

<211> 492

<212> PRT

<213> Corynebacterium glutamicum

<400> 1846

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Met Ser Ala Ala Ala Ser Arg Ser Arg Asn Ile Leu Thr Ala Leu Leu
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Leu Leu Val Pro Leu Ile Ala Gly Thr Ile Tyr Ala Ser Ala Met Gly
  20          25          30

Leu Asp Val Ser Arg Ala Trp Ser Ser Ala Asp Glu Val Thr Gly Ala
  35          40          45

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Pro Ala Ala Ser Val Ala Thr Asn Asn Gln Glu Leu Ile Glu Ala Arg
50 55 60

Arg Ala Ala Gly Glu Ala Gly Ala Gln Ala Gly Phe Leu Thr Ser Gly
65 70 75 80

Thr Glu Glu Leu Thr Ser Gly Thr Gln Glu Leu Ile Asp Gly Ala Ala
85 90 95

Pro Leu Glu Glu Gly Val Ser Ala Ala Ala Asp Gly Ala Ala Gln Leu
100 105 110

His Asp Gly Leu Ile Gln Leu Gln Ala Gly Thr Gly Gln Met Gly Thr
115 120 125

Gly Ala Thr Glu Ile Ala Asp Gly Val Gln Asn Ala Val Glu Gln Leu
130 135 140

Gly Gly Leu Val Val Val Gln Gln Gln Leu Leu Gly Ala Leu Asn Glu
145 150 155 160

Ala Asp Lys Gln Leu Ala Ser Ser Lys Ile Pro Glu Ala Glu Asp Leu
165 170 175

Arg Lys Gln Ile Thr Glu Val Arg Gly His Leu Glu Asn Phe Gly Ile
180 185 190

Ser Val Glu Met Thr Asp Gln Leu Asp Gln Leu Arg Ser Gly Thr Arg
195 200 205

Asp Leu Ala Asn Gln Leu Ala Val Pro Gly Tyr Gly Phe His Asp Gly
210 215 220

Ile Tyr Ser Ala Thr Asn Gly Ala Ala Glu Leu Ser Ala Gly Leu Gln
225 230 235 240

Glu Leu Glu Ala Gly Val Gly Thr Ala Val Glu Gly Phe Thr Ala Leu
245 250 255

Asp Glu Gly Ala Asn Arg Leu Asp Ser Met Ala Thr Leu Asn Glu Glu
260 265 270

Lys Thr Ser Ala Val Gln Arg Ala Leu Pro Val Pro Gln Val Pro Ala
275 280 285

Gly Thr Ile Glu Gly Thr Ala Asp Glu Glu Arg Thr Ser Ala Leu Ala
290 295 300

Pro Met Tyr Ala Phe Leu Ile Ser Ala Leu Val Met Leu Ala Gly Ala
305 310 315 320

Ala Leu Gly Trp Ala Thr Leu Lys Asn Lys Trp Leu Met Ala Phe Ala
325 330 335

Val Ile Gly Val Thr Ala Ile Gly Gly Ile Ile Leu Phe Thr Val Ala
340 345 350

Leu Gly Ile Ser Ile Gly Ala Leu Phe Gly Ala Leu Gly Ile Leu Leu
355 360 365

Leu Ala Thr Val Val Ala Gly Ile Leu Ser Arg Ile Leu Leu Asp Val
 370 375 380
 Leu Gly Thr Thr Gly Ala Ile Val Val Ser Val Leu Gly Trp Val Ala
 385 390 395 400
 Gln Ala Ala Val Ile Gly His Val Trp Ser Val Thr Ala Val Ser Asp
 405 410 415
 Ile Ala Leu Val Trp Arg Val Val Ala Gly Met Met Pro Leu His Tyr
 420 425 430
 Pro Thr Phe Ala Val Thr Ser Ile Gly Asn Gly Gly Ser Ala Ala Ala
 435 440 445
 Ile Trp Met Ser Val Ala Val Leu Leu Ala Met Gly Ala Ile Gly Ala
 450 455 460
 Val Ala Leu Arg Lys Pro Lys Ala Val Ala Val Glu Val Glu Glu Ala
 465 470 475 480
 Val Asp Ala Asp Ala Asp Gln Ala Ala Ser Glu Ser
 485 490

<210> 1847

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(553)

<223> RXA00613

<400> 1847

tggcgataacc agctccgagt agggctgcac ttgaaaaagt gagtgtttta gcgatagttg 60
 acaccttatt caccctacct ggggagtact ctgggcaaac atg agt gaa cta aaa 115
 Met Ser Glu Leu Lys
 1 5
 gac aaa atc cgc gca gat ctg acc acc gct atg aag gcc cgc gac aag 163
 Asp Lys Ile Arg Ala Asp Leu Thr Thr Ala Met Lys Ala Arg Asp Lys
 10 15 20
 gac acc act ggt acc ttg cgc atg ctg ctt tcc gca ttg acc cag gaa 211
 Asp Thr Thr Gly Thr Leu Arg Met Leu Leu Ser Ala Leu Thr Gln Glu
 25 30 35
 gaa aca tcg gga acc aag cac gaa ctc aat gat gaa gaa gtg ttg aag 259
 Glu Thr Ser Gly Thr Lys His Glu Leu Asn Asp Glu Glu Val Leu Lys
 40 45 50
 gtg att gct cgt gag att aag aag cgt cgc gag tcc gct gag gtg tac 307
 Val Ile Ala Arg Glu Ile Lys Lys Arg Arg Glu Ser Ala Glu Val Tyr
 55 60 65
 acc gaa aat ggt cgt cag gaa ttg gct gac gtt gag ctt aaa gag gct 355
 Thr Glu Asn Gly Arg Gln Glu Leu Ala Asp Val Glu Leu Lys Glu Ala
 70 75 80 85

gcc att ttg gag ggc tac cag cct gag cag ctt gat gat gat cag ctg 403
 Ala Ile Leu Glu Gly Tyr Gln Pro Glu Gln Leu Asp Asp Asp Gln Leu
 90 95 100

aac gcg ctg atc gat gag gct atc gct gaa gtc ggc ggc gag gcc gat 451
 Asn Ala Leu Ile Asp Glu Ala Ile Ala Glu Val Gly Gly Glu Ala Asp
 105 110 115

atg aag aag atg ggc cag atc atg aag gct gct acc gct aag gct gct 499
 Met Lys Lys Met Gly Gln Ile Met Lys Ala Ala Thr Ala Lys Ala Ala
 120 125 130

ggc cgt gca gat gga aaa cga ctc tcc acc gca gtg aag agc cgt ttg 547
 Gly Arg Ala Asp Gly Lys Arg Leu Ser Thr Ala Val Lys Ser Arg Leu
 135 140 145

agc aac taggtatttc tagcggaaga act 576
 Ser Asn
 150

<210> 1848

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 1848

Met Ser Glu Leu Lys Asp Lys Ile Arg Ala Asp Leu Thr Thr Ala Met
 1 5 10 15

Lys Ala Arg Asp Lys Asp Thr Thr Gly Thr Leu Arg Met Leu Leu Ser
 20 25 30

Ala Leu Thr Gln Glu Glu Thr Ser Gly Thr Lys His Glu Leu Asn Asp
 35 40 45

Glu Glu Val Leu Lys Val Ile Ala Arg Glu Ile Lys Lys Arg Arg Glu
 50 55 60

Ser Ala Glu Val Tyr Thr Glu Asn Gly Arg Gln Glu Leu Ala Asp Val
 65 70 75 80

Glu Leu Lys Glu Ala Ala Ile Leu Glu Gly Tyr Gln Pro Glu Gln Leu
 85 90 95

Asp Asp Asp Gln Leu Asn Ala Leu Ile Asp Glu Ala Ile Ala Glu Val
 100 105 110

Gly Gly Glu Ala Asp Met Lys Lys Met Gly Gln Ile Met Lys Ala Ala
 115 120 125

Thr Ala Lys Ala Ala Gly Arg Ala Asp Gly Lys Arg Leu Ser Thr Ala
 130 135 140

Val Lys Ser Arg Leu Ser Asn
 145 150

<210> 1849

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> RXA00614

<400> 1849

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ttagttcact catgtttgcc cagagtactc cccaggtagg gtg aat aag gtg tca 115
                               Val Asn Lys Val Ser
                               1 5
act atc gct aaa aca ctc act ttt tca agt gca gcc cta ctc gga gct 163
Thr Ile Ala Lys Thr Leu Thr Phe Ser Ser Ala Ala Leu Leu Gly Ala
                10                15                20
ggt atc gcc acc gct gca tgg gga tac tca gag ctc aaa aaa ttc gag 211
Gly Ile Ala Thr Ala Ala Trp Gly Tyr Ser Glu Leu Lys Lys Phe Glu
                25                30                35
ctc aaa aca gta gaa ctg cca att ttg aag cct gga acg ctc cgt gga 259
Leu Lys Thr Val Glu Leu Pro Ile Leu Lys Pro Gly Thr Leu Arg Gly
                40                45                50
aag aag gaa ttc cgc ctt ctc cac atc tct gat ctc cac atg atc cca 307
Lys Lys Glu Phe Arg Leu Leu His Ile Ser Asp Leu His Met Ile Pro
                55                60                65
ggc caa gaa acc aaa aaa gca tgg gtc tcc gca ctc gat tca cta agc 355
Gly Gln Glu Thr Lys Lys Ala Trp Val Ser Ala Leu Asp Ser Leu Ser
                70                75                80                85
ccc gat ttg gtg atc aac acc ggt gac aac ctt agc gat gaa aaa gca 403
Pro Asp Leu Val Ile Asn Thr Gly Asp Asn Leu Ser Asp Glu Lys Ala
                90                95                100
gtc ccc gac gtc ctc cgc gca ctc ggc cca ctg atg aac cgc ccc ggc 451
Val Pro Asp Val Leu Arg Ala Leu Gly Pro Leu Met Asn Arg Pro Gly
                105                110                115
gcg ttc gtc ttc gga acc aac gat tac tgg gca ccc cgc ccc gtc aat 499
Ala Phe Val Phe Gly Thr Asn Asp Tyr Trp Ala Pro Arg Pro Val Asn
                120                125                130
cct ttc ggc tac ctc ttc ggt aaa aaa cgc gaa gtg agc cac atc gac 547
Pro Phe Gly Tyr Leu Phe Gly Lys Lys Arg Glu Val Ser His Ile Asp
                135                140                145
ctc ccc tgg cga gcc atg cga gct gct ttc atc gaa cac gga tgg caa 595
Leu Pro Trp Arg Ala Met Arg Ala Ala Phe Ile Glu His Gly Trp Gln
                150                155                160                165
gac gcc aac caa aag cga ctc gaa ttc caa gta ggt tcc gtc cgc ctc 643
Asp Ala Asn Gln Lys Arg Leu Glu Phe Gln Val Gly Ser Val Arg Leu
                170                175                180
gcc atc tca ggt gtt gat gac ccc cac cat gac ctc gac gac tac aca 691
Ala Ile Ser Gly Val Asp Asp Pro His His Asp Leu Asp Asp Tyr Thr
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185	190	195	
gag atc gca ggg gca cca aac gtg	gac gct gat ctg tcc ata gcg ttg		739
Glu Ile Ala Gly Ala Pro Asn Val	Asp Ala Asp Leu Ser Ile Ala Leu		
200	205 210		
ctt cac gca cca gaa cct cga gtc	ctc gct cag ttc gaa gcc gac ggc		787
Leu His Ala Pro Glu Pro Arg Val	Leu Ala Gln Phe Glu Ala Asp Gly		
215	220 225		
tac cag ctt tcc ctc tcc ggc cac	acc cac ggc ggt cag ctt tgt ctt		835
Tyr Gln Leu Ser Leu Ser Gly His	Thr His Gly Gly Gln Leu Cys Leu		
230	235 240 245		
ccg ggc agc aag cca att gtc acc	aac tgt gga atc gac cgc aaa cgc		883
Pro Gly Ser Lys Pro Ile Val Thr	Asn Cys Gly Ile Asp Arg Lys Arg		
250	255 260		
gcc acc ggc ctc aac aaa ttt ggc	gac atg tgg atg cac gtt tcc aac		931
Ala Thr Gly Leu Asn Lys Phe Gly	Asp Met Trp Met His Val Ser Asn		
265	270 275		
ggc ctc ggc acc tca aaa ttc gtc	cca ttc cgc atc ttc tgc cga ccc		979
Gly Leu Gly Thr Ser Lys Phe Val	Pro Phe Arg Ile Phe Cys Arg Pro		
280	285 290		
agc gcc acc cta ata aag atc act	gaa cag gca ctt tgacctgaaa		1025
Ser Ala Thr Leu Ile Lys Ile Thr	Glu Gln Ala Leu		
295	300 305		
aacccacagg act			1038
<210> 1850			
<211> 305			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1850			
Val Asn Lys Val Ser Thr Ile Ala	Lys Thr Leu Thr Phe Ser Ser Ala		
1	5 10 15		
Ala Leu Leu Gly Ala Gly Ile Ala	Thr Ala Ala Trp Gly Tyr Ser Glu		
20	25 30		
Leu Lys Lys Phe Glu Leu Lys Thr	Val Glu Leu Pro Ile Leu Lys Pro		
35	40 45		
Gly Thr Leu Arg Gly Lys Lys Glu	Phe Arg Leu Leu His Ile Ser Asp		
50	55 60		
Leu His Met Ile Pro Gly Gln Glu	Thr Lys Lys Ala Trp Val Ser Ala		
65	70 75 80		
Leu Asp Ser Leu Ser Pro Asp Leu	Val Ile Asn Thr Gly Asp Asn Leu		
85	90 95		
Ser Asp Glu Lys Ala Val Pro Asp	Val Leu Arg Ala Leu Gly Pro Leu		
100	105 110		
Met Asn Arg Pro Gly Ala Phe Val	Phe Gly Thr Asn Asp Tyr Trp Ala		

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<400> 1851
acgactggga cgacgactaa ctaacccctg aggcactttc tatttcattgg ctaaatacaac 60

tccttttgatt gcacgctac gctggcgaat tgtcctgtgg atg aca gcg gtt gtt 115
Met Thr Ala Val Val
1 5

ttc ttg acc cta gcc agc gtt gtg atc att acc cgt tcg gtg ctg ctt 163
Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr Arg Ser Val Leu Leu
10 15 20

tca gag gta acc aac acc gcg aac tcg gca gtt gag cag gaa att gag 211

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Ser	Glu	Val	Thr	Asn	Thr	Ala	Asn	Ser	Ala	Val	Glu	Gln	Glu	Ile	Glu		
			25					30					35				
gag	ttt	cgt	cgc	ttt	gca	gcc	gaa	gga	att	gat	cca	aca	act	gcg	cag	259	
Glu	Phe	Arg	Arg	Phe	Ala	Ala	Glu	Gly	Ile	Asp	Pro	Thr	Thr	Ala	Gln		
		40					45				50						
cct	ttt	gag	tca	ggg	cat	cgc	ctg	atg	gag	gtt	tac	ctg	tcg	agg	cag	307	
Pro	Phe	Glu	Ser	Gly	His	Arg	Leu	Met	Glu	Val	Tyr	Leu	Ser	Arg	Gln		
		55				60					65						
att	ccg	gat	gaa	aat	gaa	gcc	att	gtc	ggc	att	ttc	ccc	gga	gag	ctc	355	
Ile	Pro	Asp	Glu	Asn	Glu	Ala	Ile	Val	Gly	Ile	Phe	Pro	Gly	Glu	Leu		
	70				75				80						85		
att	cag	gtt	gat	tac	tcc	cag	ctc	agt	ggc	gcc	cat	ccg	ctt	cct	ttg	403	
Ile	Gln	Val	Asp	Tyr	Ser	Gln	Leu	Ser	Gly	Ala	His	Pro	Leu	Pro	Leu		
			90					95						100			
gaa	cac	tcc	gat	ccg	ttg	att	tcg	gaa	atc	cga	cag	acc	acg	ctg	aat	451	
Glu	His	Ser	Asp	Pro	Leu	Ile	Ser	Glu	Ile	Arg	Gln	Thr	Thr	Leu	Asn		
			105					110						115			
tct	gga	gtt	ttc	agc	gat	ctt	gaa	cgc	gga	acc	act	cac	tgg	gga	aag	499	
Ser	Gly	Val	Phe	Ser	Asp	Leu	Glu	Arg	Gly	Thr	Thr	His	Trp	Gly	Lys		
		120					125					130					
gtg	aat	ttc	caa	act	gct	tcc	ggg	gag	gcc	gat	ggg	gag	ttc	gtt	gtc	547	
Val	Asn	Phe	Gln	Thr	Ala	Ser	Gly	Glu	Ala	Asp	Gly	Glu	Phe	Val	Val		
	135					140					145						
gca	ttc	ttc	gct	gat	aat	ctt	aaa	gac	cag	gtc	aac	ggc	cag	atc	cag	595	
Ala	Phe	Phe	Ala	Asp	Asn	Leu	Lys	Asp	Gln	Val	Asn	Gly	Gln	Ile	Gln		
	150				155					160					165		
att	ctt	att	ttg	atc	ggc	aca	ggg	ggg	ttg	att	gcc	tca	att	ctg	att	643	
Ile	Leu	Ile	Leu	Ile	Gly	Thr	Gly	Gly	Leu	Ile	Ala	Ser	Ile	Leu	Ile		
				170				175						180			
gct	tgg	ttg	att	gcg	ggc	cag	atc	att	gcc	ccg	atc	cgc	aaa	ttg	agt	691	
Ala	Trp	Leu	Ile	Ala	Gly	Gln	Ile	Ile	Ala	Pro	Ile	Arg	Lys	Leu	Ser		
			185				190						195				
tcc	gtg	tcc	gca	aag	atc	agt	aat	tcg	gat	ctc	acc	tgg	cgc	gtc	cct	739	
Ser	Val	Ser	Ala	Lys	Ile	Ser	Asn	Ser	Asp	Leu	Thr	Trp	Arg	Val	Pro		
		200					205					210					
gtg	gag	ggg	cgt	gat	gag	att	gcg	cag	ctg	gcc	agg	act	ttt	aat	gcc	787	
Val	Glu	Gly	Arg	Asp	Glu	Ile	Ala	Gln	Leu	Ala	Arg	Thr	Phe	Asn	Ala		
	215					220				225							
atg	ttg	gat	cgc	atc	gaa	atc	gcg	tat	aac	gat	cag	cgc	cag	ttc	gtt	835	
Met	Leu	Asp	Arg	Ile	Glu	Ile	Ala	Tyr	Asn	Asp	Gln	Arg	Gln	Phe	Val		
	230				235				240						245		
gat	gat	gcc	ggc	cac	gag	ctg	cgc	acc	ccg	atc	aca	gtg	gtg	cgt	ggc	883	
Asp	Asp	Ala	Gly	His	Glu	Leu	Arg	Thr	Pro	Ile	Thr	Val	Val	Arg	Gly		
			250					255						260			
cag	tta	gag	ctt	ctc	gcc	acc	acc	ccg	ccg	gag	gaa	caa	gcg	cgg	tcg	931	
Gln	Leu	Glu	Leu	Leu	Ala	Thr	Thr	Pro	Pro	Glu	Glu	Gln	Ala	Arg	Ser		

265	270	275	
att gag ctg gcc acc act gag ttg gat cga atg tcg cga atg gtc aat			979
Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met Ser Arg Met Val Asn			
280	285	290	
gat ctg ctc acc ctc gca gtc gcc gat tct ggc acc ttc atc cac gcc			1027
Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly Thr Phe Ile His Ala			
295	300	305	
cac ccc acg gat gtc acg gat tta aca atc gat atc gaa gac aaa gcc			1075
His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp Ile Glu Asp Lys Ala			
310	315	320	325
cgc acc atc agc gac cga att ttg ctt gtc gac gcc gcc gag ggc ctc			1123
Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp Ala Ala Glu Gly Leu			
	330	335	340
gtc agc ctc gac gag cag cgg gtc acc gag gca gtg ctg gag ttg ttc			1171
Val Ser Leu Asp Glu Gln Arg Val Thr Glu Ala Val Leu Glu Leu Phe			
	345	350	355
ggc aat gcg ttg			1183
Gly Asn Ala Leu			
360			

<210> 1852

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 1852

Met Thr Ala Val Val Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr			
1	5	10	15
Arg Ser Val Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val			
	20	25	30
Glu Gln Glu Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp			
	35	40	45
Pro Thr Thr Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met Glu Val			
	50	55	60
Tyr Leu Ser Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile			
	65	70	75
Phe Pro Gly Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala			
	85	90	95
His Pro Leu Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg			
	100	105	110
Gln Thr Thr Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg Gly Thr			
	115	120	125
Thr His Trp Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu Ala Asp			
	130	135	140
Gly Glu Phe Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp Gln Val			

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145              150              155              160
Asn Gly Gln Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly Leu Ile
      165              170              175
Ala Ser Ile Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile Ala Pro
      180              185              190
Ile Arg Lys Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser Asp Leu
      195              200              205
Thr Trp Arg Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln Leu Ala
      210              215              220
Arg Thr Phe Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr Asn Asp
      225              230              235              240
Gln Arg Gln Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile
      245              250              255
Thr Val Val Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro Pro Glu
      260              265              270
Glu Gln Ala Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met
      275              280              285
Ser Arg Met Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly
      290              295              300
Thr Phe Ile His Ala His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp
      305              310              315              320
Ile Glu Asp Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp
      325              330              335
Ala Ala Glu Gly Leu Val Ser Leu Asp Glu Gln Arg Val Thr Glu Ala
      340              345              350
Val Leu Glu Leu Phe Gly Asn Ala Leu
      355              360

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<210> 1853

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA00628

<400> 1853

ggttgaaagt ggcgtcgaaa agcgccttaa aatgaccggc tcacctgcat tattttatgc 60

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aacctcaatt tgggtgcacg ccaagtagta gtctgtgcat atg gct tct gta ttc    115
                                     Met Ala Ser Val Phe
                                     1              5

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acg aaa att att aat ggc gag ctc ccc ggc cga ttt gtg tat cgt tcc    163
Thr Lys Ile Ile Asn Gly Glu Leu Pro Gly Arg Phe Val Tyr Arg Ser

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10	15	20	
gag aat gtc gtg gct ttt cta tcc atc gaa ccc ctc acc tac ggc cac			211
Glu Asn Val Val Ala Phe Leu Ser Ile Glu Pro Leu Thr Tyr Gly His			
25	30	35	
acc cta gtc gta ccc gtt gca gaa gtt gac cgc tgg acc gac ctt cct			259
Thr Leu Val Val Pro Val Ala Glu Val Asp Arg Trp Thr Asp Leu Pro			
40	45	50	
cag aac atc tgg agc gaa gta aac gag gcc tcc cag ctc atc gga aat			307
Gln Asn Ile Trp Ser Glu Val Asn Glu Ala Ser Gln Leu Ile Gly Asn			
55	60	65	
gca atc cgc aca gca ttc gac gcc cct cga tgt ggt tac atc atc gca			355
Ala Ile Arg Thr Ala Phe Asp Ala Pro Arg Cys Gly Tyr Ile Ile Ala			
70	75	80	85
gga ttc gat gtt ccc cac act cac atc cac ctc ttc ccc acc gac aaa			403
Gly Phe Asp Val Pro His Thr His Ile His Leu Phe Pro Thr Asp Lys			
90	95	100	
atg gcc gat tac gat ttc cgc aac gcc atg gcc gca gac gcc acc gac			451
Met Ala Asp Tyr Asp Phe Arg Asn Ala Met Ala Ala Asp Ala Thr Asp			
105	110	115	
cct gca aaa atg gat gaa gct gca gag aag atc cgc gaa gcg ctg gac			499
Pro Ala Lys Met Asp Glu Ala Ala Glu Lys Ile Arg Glu Ala Leu Asp			
120	125	130	
ggt ctg gtc tagttcttgt agttctaatt gct			531
Gly Leu Val			
135			

<210> 1854

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 1854

Met Ala Ser Val Phe Thr Lys Ile Ile Asn Gly Glu Leu Pro Gly Arg			
1	5	10	15
Phe Val Tyr Arg Ser Glu Asn Val Val Ala Phe Leu Ser Ile Glu Pro			
20	25	30	
Leu Thr Tyr Gly His Thr Leu Val Val Pro Val Ala Glu Val Asp Arg			
35	40	45	
Trp Thr Asp Leu Pro Gln Asn Ile Trp Ser Glu Val Asn Glu Ala Ser			
50	55	60	
Gln Leu Ile Gly Asn Ala Ile Arg Thr Ala Phe Asp Ala Pro Arg Cys			
65	70	75	80
Gly Tyr Ile Ile Ala Gly Phe Asp Val Pro His Thr His Ile His Leu			
85	90	95	
Phe Pro Thr Asp Lys Met Ala Asp Tyr Asp Phe Arg Asn Ala Met Ala			
100	105	110	

Ala Asp Ala Thr Asp Pro Ala Lys Met Asp Glu Ala Ala Glu Lys Ile
 115 120 125

Arg Glu Ala Leu Asp Gly Leu Val
 130 135

<210> 1855

<211> 1578

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1555)

<223> RXA00631

<400> 1855

cctacctgcg ccgcaagggtg gacacccagg atccgcagct aattcagact gtctcgtagcg 60

ttggatatgt tctgcgcacc ccacgtagct aaattctcct atg gaa aat cct tat 115
 Met Glu Asn Pro Tyr
 1 5

gtt gct gcg ctc gat gac gaa aac caa gaa gtc ggc gta aaa aaa gaa 163
 Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val Gly Val Lys Lys Glu
 10 15 20

gca gaa aaa gaa cct gaa ata ggt ccc atc aga gct gcc gga cga gcc 211
 Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg Ala Ala Gly Arg Ala
 25 30 35

ata ccg ctg cgc acc cgc atc att ttg atc gtg gtg ggt atc gcc ggg 259
 Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val Val Gly Ile Ala Gly
 40 45 50

ctt ggt ttg ctg gtc aac gcg att gct gtc tcc agc ctc atg cgt gaa 307
 Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser Ser Leu Met Arg Glu
 55 60 65

gtt tcc tat acc cgc atg gat caa gag cta gag acc tcg atg ggg acg 355
 Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu Thr Ser Met Gly Thr
 70 75 80 85

tgg gcg cat aac gtt gag ctg ttt aat ttc gat ggc gtc cgc caa ggg 403
 Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp Gly Val Arg Gln Gly
 90 95 100

cca ccc agc gat tat tat gtg gcc aag gtt ttt cct gat gga tcc agc 451
 Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe Pro Asp Gly Ser Ser
 105 110 115

atc atc ttc aac gat gca caa tcg gca ccc gat cta gct gaa acc acc 499
 Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp Leu Ala Glu Thr Thr
 120 125 130

atc ggt act ggt cca cac act gtg gat gct gct agc ggt tct gcc tcc 547
 Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala Ser Gly Ser Ala Ser
 135 140 145

aac act ccg tgg cgt gtg atg gcg gaa aag aac ggt gac att atc acc	595
Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn Gly Asp Ile Ile Thr	
150 155 160 165	
gtg gtg ggt aaa agc atg ggg cgt gaa aca aac ctg ctg tac cga ttg	643
Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn Leu Leu Tyr Arg Leu	
170 175 180	
gtg atg gtg cag atg atc atc ggc gcg ctg att ctg gtt gct att ttg	691
Val Met Val Gln Met Ile Ile Gly Ala Leu Ile Leu Val Ala Ile Leu	
185 190 195	
att act tca ctc ttc cta gtc aga cgc tgc ttg cgg ccg ttg aga gaa	739
Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu Arg Pro Leu Arg Glu	
200 205 210	
gtt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt	787
Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly Asp Leu Asp Arg Arg	
215 220 225	
gtc ccg cag tgg cca atg acc aca gaa gtc gga cag ctg tgc aat gcc	835
Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly Gln Leu Ser Asn Ala	
230 235 240 245	
ctc aat atc atg ttg gag cag ctc caa gcc tca att ctg acc gcc cag	883
Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser Ile Leu Thr Ala Gln	
250 255 260	
caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag	931
Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu	
265 270 275	
ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca	979
Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser	
280 285 290	
tca ggt gca aca gat gat gcc aac tgg gtc atg tcc aag atc ggt ggc	1027
Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly	
295 300 305	
gaa gcc caa cgc atg agt gtg ctt gtg gaa gac ctc ctg tca ctg acg	1075
Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp Leu Leu Ser Leu Thr	
310 315 320 325	
cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa	1123
Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu	
330 335 340	
ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc	1171
Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg	
345 350 355	
aca gtc aat gta tcc aac aaa gct gag tcc att ccg gtt gtc aaa ggc	1219
Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly	
360 365 370	
gac cca act cgc ctc cac caa gtg ctt acc aac ctg gtt gcc aac gga	1267
Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly	
375 380 385	
cta aac cac ggc gga ccg gac gcg gaa gtc agc att gag atc aac acc	1315

Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr
 390 395 400 405
 gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg 1363
 Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met
 410 415 420
 tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat 1411
 Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp
 425 430 435
 tcc tcc cgc tca cgc gca tcc ggc gga tcg ggc ctc ggc ctt gcg atc 1459
 Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
 440 445 450
 acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc 1507
 Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr Val Thr Val Asp Ser
 455 460 465
 gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg ccg gcg gtt tct 1555
 Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr Leu Pro Ala Val Ser
 470 475 480 485
 taaaggcatc aagggccgga aaa 1578

<210> 1856

<211> 485

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1856

Met Glu Asn Pro Tyr Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val
 1 5 10 15
 Gly Val Lys Lys Glu Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg
 20 25 30
 Ala Ala Gly Arg Ala Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val
 35 40 45
 Val Gly Ile Ala Gly Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser
 50 55 60
 Ser Leu Met Arg Glu Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu
 65 70 75 80
 Thr Ser Met Gly Thr Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp
 85 90 95
 Gly Val Arg Gln Gly Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe
 100 105 110
 Pro Asp Gly Ser Ser Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp
 115 120 125
 Leu Ala Glu Thr Thr Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala
 130 135 140
 Ser Gly Ser Ala Ser Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn
 145 150 155 160

Gly Asp Ile Ile Thr Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn
165 170 175

Leu Leu Tyr Arg Leu Val Met Val Gln Met Ile Ile Gly Ala Leu Ile
180 185 190

Leu Val Ala Ile Leu Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu
195 200 205

Arg Pro Leu Arg Glu Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly
210 215 220

Asp Leu Asp Arg Arg Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly
225 230 235 240

Gln Leu Ser Asn Ala Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser
245 250 255

Ile Leu Thr Ala Gln Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly
260 265 270

Asp Ala Ser His Glu Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe
275 280 285

Thr Glu Leu Tyr Ser Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met
290 295 300

Ser Lys Ile Gly Gly Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp
305 310 315 320

Leu Leu Ser Leu Thr Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg
325 330 335

Val Asp Val Leu Glu Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala
340 345 350

Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile
355 360 365

Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn
370 375 380

Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser
385 390 395 400

Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp
405 410 415

Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg
420 425 430

Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly
435 440 445

Leu Gly Leu Ala Ile Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr
450 455 460

Val Thr Val Asp Ser Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr
465 470 475 480

Leu Pro Ala Val Ser
485

<210> 1857

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXA00637

<400> 1857

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ccgatggcac tttccgtacc tggaaggtag ttgcccgcgg cagaaacaat tagggaaacc 60

tcttgacctt cacgcgacgt caaggattta actaacagtc atg aca gat cga acc 115
                                         Met Thr Asp Arg Thr
                                         1                               5

att ggc gag gct gct gaa cta ctc ggt gtc acc acc cgc aca ctg cgg 163
Ile Gly Glu Ala Ala Glu Leu Leu Gly Val Thr Thr Arg Thr Leu Arg
                        10                               15                               20

cat tgg gac agc atc ggg ttg ctt caa ccg agc tgg cga acc aca acg 211
His Trp Asp Ser Ile Gly Leu Leu Gln Pro Ser Trp Arg Thr Thr Thr
                        25                               30                               35

gat tat cgc ctt tac aca gaa gac gat gtc gag cgc gcc ctg cag att 259
Asp Tyr Arg Leu Tyr Thr Glu Asp Asp Val Glu Arg Ala Leu Gln Ile
                        40                               45                               50

ctt att tac agg gcc gcc gga atc ggg ttg aag gat att gcg gag gtg 307
Leu Ile Tyr Arg Ala Ala Gly Ile Gly Leu Lys Asp Ile Ala Glu Val
                        55                               60                               65

ctt gat cag ccg gat tcg gcc aat cag cac ctg cgc cgc cag cgg gaa 355
Leu Asp Gln Pro Asp Ser Ala Asn Gln His Leu Arg Arg Gln Arg Glu
                        70                               75                               80                               85

ctc cta gtg gaa cag atc ggt cag ctg cat cgg atg gtc cgg gca gta 403
Leu Leu Val Glu Gln Ile Gly Gln Leu His Arg Met Val Arg Ala Val
                        90                               95                               100

gat gaa atc ctt gga aag gat gcg att agc gtg aag gaa aag att gag 451
Asp Glu Ile Leu Gly Lys Asp Ala Ile Ser Val Lys Glu Lys Ile Glu
                        105                               110                               115

atc ttc ggc gag gat ctg ccc aag tac caa gag gag gct ttc cag cgc 499
Ile Phe Gly Glu Asp Leu Pro Lys Tyr Gln Glu Glu Ala Phe Gln Arg
                        120                               125                               130

tgg ggc gac acc ccg gag tgg aaa gaa tcc caa aag atc cag gag aag 547
Trp Gly Asp Thr Pro Glu Trp Lys Glu Ser Gln Lys Ile Gln Glu Lys
                        135                               140                               145

atg acc aag gag gat ttt cag agg gcg aaa gat gaa cat gag ggg ttc 595
Met Thr Lys Glu Asp Phe Gln Arg Ala Lys Asp Glu His Glu Gly Phe
150                               155                               160                               165

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gtc gaa aag ctt atc gac gcc tcc ctg cgc ggc atc gcg ccc ggc tct 643
 Val Glu Lys Leu Ile Asp Ala Ser Leu Arg Gly Ile Ala Pro Gly Ser
 170 175 180

gca gag ggc aat gag cta gcg ctt gcg cac cgc gca agc atc ggt cag 691
 Ala Glu Gly Asn Glu Leu Ala Leu Ala His Arg Ala Ser Ile Gly Gln
 185 190 195

tgg tac acc gtg agt gca aac aag caa gta att ttg gct cgg atg tac 739
 Trp Tyr Thr Val Ser Ala Asn Lys Gln Val Ile Leu Ala Arg Met Tyr
 200 205 210

gtg gaa gac gag cgt ttt aac gaa act tac aaa gga cac gcc tca tat 787
 Val Glu Asp Glu Arg Phe Asn Glu Thr Tyr Lys Gly His Ala Ser Tyr
 215 220 225

ctt tta aca ctt att gaa gca ttg gcg cag gta gaa ggc gtg gac ttg 835
 Leu Leu Thr Leu Ile Glu Ala Leu Ala Gln Val Glu Gly Val Asp Leu
 230 235 240 245

gag aat gtg gag tgg gaa taatcccaat ttcaactctt tca 876
 Glu Asn Val Glu Trp Glu
 250

<210> 1858

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 1858

Met Thr Asp Arg Thr Ile Gly Glu Ala Ala Glu Leu Leu Gly Val Thr
 1 5 10 15

Thr Arg Thr Leu Arg His Trp Asp Ser Ile Gly Leu Leu Gln Pro Ser
 20 25 30

Trp Arg Thr Thr Thr Asp Tyr Arg Leu Tyr Thr Glu Asp Asp Val Glu
 35 40 45

Arg Ala Leu Gln Ile Leu Ile Tyr Arg Ala Ala Gly Ile Gly Leu Lys
 50 55 60

Asp Ile Ala Glu Val Leu Asp Gln Pro Asp Ser Ala Asn Gln His Leu
 65 70 75 80

Arg Arg Gln Arg Glu Leu Leu Val Glu Gln Ile Gly Gln Leu His Arg
 85 90 95

Met Val Arg Ala Val Asp Glu Ile Leu Gly Lys Asp Ala Ile Ser Val
 100 105 110

Lys Glu Lys Ile Glu Ile Phe Gly Glu Asp Leu Pro Lys Tyr Gln Glu
 115 120 125

Glu Ala Phe Gln Arg Trp Gly Asp Thr Pro Glu Trp Lys Glu Ser Gln
 130 135 140

Lys Ile Gln Glu Lys Met Thr Lys Glu Asp Phe Gln Arg Ala Lys Asp
 145 150 155 160

Glu His Glu Gly Phe Val Glu Lys Leu Ile Asp Ala Ser Leu Arg Gly
 165 170 175

Ile Ala Pro Gly Ser Ala Glu Gly Asn Glu Leu Ala Leu Ala His Arg
 180 185 190

Ala Ser Ile Gly Gln Trp Tyr Thr Val Ser Ala Asn Lys Gln Val Ile
 195 200 205

Leu Ala Arg Met Tyr Val Glu Asp Glu Arg Phe Asn Glu Thr Tyr Lys
 210 215 220

Gly His Ala Ser Tyr Leu Leu Thr Leu Ile Glu Ala Leu Ala Gln Val
 225 230 235 240

Glu Gly Val Asp Leu Glu Asn Val Glu Trp Glu
 245 250

<210> 1859

<211> 541

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(541)

<223> RXA00646

<400> 1859

aatgcaatcg gaacgggttaa cgccaagtga tctggtggga tgtaggtacc gtcagggtcca 60

gcgcataaat ttcccagaaa tctctccttt acctgcaaca atg cag cgc agg gcc 115
 Met Gln Arg Arg Ala
 1 5

cgc cgt gag gtt ggg ttg acg gaa gtt ttg gat cgt ctc cca gag cag 163
 Arg Arg Glu Val Gly Leu Thr Glu Val Leu Asp Arg Leu Pro Glu Gln
 10 15 20

ccc aaa aag cgg ggc cga att cct ttc acc agg gca gat cta gac aat 211
 Pro Lys Lys Arg Gly Arg Ile Pro Phe Thr Arg Ala Asp Leu Asp Asn
 25 30 35

gac gct gaa ttg gcg gag ttt gaa acc ctc gaa gca att gca gcc ggc 259
 Asp Ala Glu Leu Ala Glu Phe Glu Thr Leu Glu Ala Ile Ala Ala Gly
 40 45 50

gac acc ttg att acc ggc gca gtg ttc acg ggc acc ctc gaa ggg gtg 307
 Asp Thr Leu Ile Thr Gly Ala Val Phe Thr Gly Thr Leu Glu Gly Val
 55 60 65

gca tgg gaa gtg caa gtg gat gtc ttg gtg cgc aac cct gat gga agc 355
 Ala Trp Glu Val Gln Val Asp Val Leu Val Arg Asn Pro Asp Gly Ser
 70 75 80 85

tac atg ccc gtg atg gtg agc aat cac cgt gtc gcc cgt ccg gat ccg 403
 Tyr Met Pro Val Met Val Ser Asn His Arg Val Ala Arg Pro Asp Pro
 90 95 100

cac aaa act atg cag ggc att gcc gtc acc cgc ctc ggt ttg ggt cag 451

His Lys Thr Met Gln Gly Ile Ala Val Thr Arg Leu Gly Leu Gly Gln
 105 110 115

cgc cta gag ctc aag gca acg ctg cgc cac cac acg atc gat ggc tat 499
 Pro Leu Glu Leu Lys Ala Thr Leu Arg His His Thr Ile Asp Gly Tyr
 120 125 130

cgc ctc acc ctc gcg ttg atg ggt ttg gag gaa gct gga gca 541
 Arg Leu Thr Leu Ala Leu Met Gly Leu Glu Glu Ala Gly Ala
 135 140 145

<210> 1860

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 1860

Met Gln Arg Arg Ala Arg Arg Glu Val Gly Leu Thr Glu Val Leu Asp
 1 5 10 15

Arg Leu Pro Glu Gln Pro Lys Lys Arg Gly Arg Ile Pro Phe Thr Arg
 20 25 30

Ala Asp Leu Asp Asn Asp Ala Glu Leu Ala Glu Phe Glu Thr Leu Glu
 35 40 45

Ala Ile Ala Ala Gly Asp Thr Leu Ile Thr Gly Ala Val Phe Thr Gly
 50 55 60

Thr Leu Glu Gly Val Ala Trp Glu Val Gln Val Asp Val Leu Val Arg
 65 70 75 80

Asn Pro Asp Gly Ser Tyr Met Pro Val Met Val Ser Asn His Arg Val
 85 90 95

Ala Arg Pro Asp Pro His Lys Thr Met Gln Gly Ile Ala Val Thr Arg
 100 105 110

Leu Gly Leu Gly Gln Pro Leu Glu Leu Lys Ala Thr Leu Arg His His
 115 120 125

Thr Ile Asp Gly Tyr Arg Leu Thr Leu Ala Leu Met Gly Leu Glu Glu
 130 135 140

Ala Gly Ala
 145

<210> 1861

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00649

<400> 1861

gtatttgatc tgtggtgtgg ctgattcggg aggactcgat gacattatgt gtatggtaca 60


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cattttgtgc aagatgcaat agctggcaaa ctggagagcc atg agc acc gac ccc 115
                                         Met Ser Thr Asp Pro
                                         1                               5

atc gcg gcc ttg gaa tac gaa tcc acc atc ttc gcc cgt cac cgg aat 163
Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe Ala Arg His Arg Asn
                        10                15                20

caa tac acc ggc caa gca ggt acg aat gct ggc gtc ctc gat tcc agc 211
Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly Val Leu Asp Ser Ser
                        25                30                35

ggc tac aac cta ctc acg ctg ctc cag tta cgt ggc ccc tcc acc atc 259
Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg Gly Pro Ser Thr Ile
                        40                45                50

ggc gaa ctc agc gcc atc acc ggc cta gac gca tct acc ctt aac cgt 307
Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala Ser Thr Leu Asn Arg
                        55                60                65

cag aca aaa gcc cta cta acc aaa gga ttt gtc gaa cgc atc cca gat 355
Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val Glu Arg Ile Pro Asp
                        70                75                80                85

ccc gac ggt gga atc gct cgg aaa ttc cac ccc acc gac ctc ggc aat 403
Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro Thr Asp Leu Gly Asn
                        90                95                100

gaa ctg ctc aac gag gaa cgc aca tcc agc caa gaa aaa tat gcc gag 451
Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln Glu Lys Tyr Ala Glu
                        105                110                115

tta ctt tca gac tgg ccc gaa gag gat cta cgc acc ttc gtc aaa ctt 499
Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg Thr Phe Val Lys Leu
                        120                125                130

ctt gaa aaa cta aat aaa gcc gtg gag aca cgc gtc gga aag cat tgg 547
Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg Val Gly Lys His Trp
                        135                140                145

ccg cgc ccc tgactcagcc caagccagag ccc 579
Pro Arg Pro
150

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<210> 1862

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 1862

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Met Ser Thr Asp Pro Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe
  1                               5                10                15

Ala Arg His Arg Asn Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly
      20                25                30

Val Leu Asp Ser Ser Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg
      35                40                45

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Gly Pro Ser Thr Ile Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala
 50 55 60
 Ser Thr Leu Asn Arg Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val
 65 70 75 80
 Glu Arg Ile Pro Asp Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro
 85 90 95
 Thr Asp Leu Gly Asn Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln
 100 105 110
 Glu Lys Tyr Ala Glu Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg
 115 120 125
 Thr Phe Val Lys Leu Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg
 130 135 140
 Val Gly Lys His Trp Pro Arg Pro
 145 150

<210> 1863

<211> 672

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(649)

<223> RXA00652

<400> 1863

gcgatagctc atcgcgcccg gttgattccc cttcttcaca agggtttcaa catcgagctc 60

attgcgtccg gtttccgaca cacgatctag gcttgactgc atg cgt cgt aca tta 115
 Met Arg Arg Thr Leu
 1 5

cct act atc ctc gct gct tcc atc atg ctc acc gct tgt acc ccg gcg 163
 Pro Thr Ile Leu Ala Ala Ser Ile Met Leu Thr Ala Cys Thr Pro Ala
 10 15 20

gaa cct gaa gca acc cca gag acc acc acc gag gca gcc ccg gaa gta 211
 Glu Pro Glu Ala Thr Pro Glu Thr Thr Thr Glu Ala Ala Pro Glu Val
 25 30 35

att act gac ggc ctt ccc atc gac gcg atg ccc gcg gtc gaa cgc acc 259
 Ile Thr Asp Gly Leu Pro Ile Asp Ala Met Pro Ala Val Glu Arg Thr
 40 45 50

gca caa acc gca tgc ccc tac ctg ggc acc gac tgg gtc gcc gat acc 307
 Ala Gln Thr Ala Cys Pro Tyr Leu Gly Thr Asp Trp Val Ala Asp Thr
 55 60 65

aac ggc cag cgc gtc acg ggt tac ggc aca gac gaa cgc ttt tcg acg 355
 Asn Gly Gln Arg Val Thr Gly Tyr Gly Thr Asp Glu Arg Phe Ser Thr
 70 75 80 85

ccc tcc tgc gtt ttt tac tcc tac ccc gaa gaa cca caa ctc acg gtg 403
 Pro Ser Cys Val Phe Tyr Ser Tyr Pro Glu Glu Pro Gln Leu Thr Val

	90	95	100	
att gtc cgc gat atg gcc acc acg gat gac gct atc gcg gta gtg gat				451
Ile Val Arg Asp Met Ala Thr Thr Asp Asp Ala Ile Ala Val Val Asp				
	105	110	115	
tgg gca gcc ccc atc gat tcc act gag ccc gct gag gaa ccc gca ggg				499
Trp Ala Ala Pro Ile Asp Ser Thr Glu Pro Ala Glu Glu Pro Ala Gly				
	120	125	130	
tgg tcc ggt ggc cgc cga ggt gga aac gat act tca ggc gca ctc tac				547
Trp Ser Gly Gly Arg Arg Gly Gly Asn Asp Thr Ser Gly Ala Leu Tyr				
	135	140	145	
gcg gtt caa aac ggc ccc acc gcg gtc atc gtg ttc acc aat cag gat				595
Ala Val Gln Asn Gly Pro Thr Ala Val Ile Val Phe Thr Asn Gln Asp				
	150	155	160	165
caa tcc ctc aaa gcg cag tta atc gct gag gaa gta atc cag aat ctt				643
Gln Ser Leu Lys Ala Gln Leu Ile Ala Glu Glu Val Ile Gln Asn Leu				
	170	175	180	
ggt ctc taactattag aaggccacat cgt				672
Gly Leu				

<210> 1864

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 1864

Met Arg Arg Thr Leu Pro Thr Ile Leu Ala Ala Ser Ile Met Leu Thr				
1	5	10	15	
Ala Cys Thr Pro Ala Glu Pro Glu Ala Thr Pro Glu Thr Thr Thr Glu				
	20	25	30	
Ala Ala Pro Glu Val Ile Thr Asp Gly Leu Pro Ile Asp Ala Met Pro				
	35	40	45	
Ala Val Glu Arg Thr Ala Gln Thr Ala Cys Pro Tyr Leu Gly Thr Asp				
	50	55	60	
Trp Val Ala Asp Thr Asn Gly Gln Arg Val Thr Gly Tyr Gly Thr Asp				
	65	70	75	80
Glu Arg Phe Ser Thr Pro Ser Cys Val Phe Tyr Ser Tyr Pro Glu Glu				
	85	90	95	
Pro Gln Leu Thr Val Ile Val Arg Asp Met Ala Thr Thr Asp Asp Ala				
	100	105	110	
Ile Ala Val Val Asp Trp Ala Ala Pro Ile Asp Ser Thr Glu Pro Ala				
	115	120	125	
Glu Glu Pro Ala Gly Trp Ser Gly Gly Arg Arg Gly Gly Asn Asp Thr				
	130	135	140	
Ser Gly Ala Leu Tyr Ala Val Gln Asn Gly Pro Thr Ala Val Ile Val				

gaa tct ttc ctc gct ggt cgc gtg agc aat gtg cct ctg ccc gct tat	595
Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val Pro Leu Pro Ala Tyr	
150 155 160 165	
ggt tct atg ccc act gag cag cta aaa tat ttg agc acc acg cag gcg	643
Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu Ser Thr Thr Gln Ala	
170 175 180	
gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc	691
Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu	
185 190 195	
acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac	739
Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn	
200 205 210	
gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg	787
Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val	
215 220 225	
atg tct atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga	835
Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly	
230 235 240 245	
cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg	883
Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp	
250 255 260	
acg ctc ctc caa aca atc atc atg atg gtc att ttg gaa cgc aaa tac	931
Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr	
265 270 275	
cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc	979
Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile	
280 285 290	
tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc	1027
Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg	
295 300 305	
aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt	1075
Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu	
310 315 320 325	
cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac	1123
His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn	
330 335 340	
gaa gca aaa cag gcc cgc aaa gaa atc gcg aac aag agg cgc gaa acg	1171
Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr	
345 350 355	
caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc	1219
Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg	
360 365 370	
gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac	1267
Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn	
375 380 385	

gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag 1315
 Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln
 390 395 400 405

gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag 1363
 Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu
 410 415 420

gac tgatgttgatgacaccaatcga gat 1389
 Asp

<210> 1866

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 1866

Val Leu Asp Ile Leu Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp
 1 5 10 15

His Leu Leu Leu His Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp
 20 25 30

Phe Phe Ser Leu Phe Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala
 35 40 45

Pro Phe Thr Trp Gln Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile
 50 55 60

Arg Pro His Arg Ala Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp
 65 70 75 80

Glu Ala Ser Ile Arg Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys
 85 90 95

Glu Tyr Gly Ile Asn Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln
 100 105 110

Ile Pro Ile Val Leu Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg
 115 120 125

Pro Glu Gly Gly Leu Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu
 130 135 140

Thr Pro Glu Glu Val Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val
 145 150 155 160

Pro Leu Pro Ala Tyr Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu
 165 170 175

Ser Thr Thr Gln Ala Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile
 180 185 190

Thr Ala Ala Ile Leu Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg
 195 200 205

Ser Phe Gln Thr Asn Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu
 210 215 220

Lys Phe Met Ile Val Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser
 225 230 235 240
 Leu Gly Leu Thr Gly Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val
 245 250 255
 Ser Asn Asn Leu Trp Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile
 260 265 270
 Leu Glu Arg Lys Tyr Pro Leu Thr Asp Asp Phe Lys Val His His Leu
 275 280 285
 Glu Gln Arg Asp Ile Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe
 290 295 300
 Leu Trp Thr Arg Arg Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp
 305 310 315 320
 Asn Ala Ser Thr Leu His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg
 325 330 335
 Thr Ala Glu Ile Asn Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn
 340 345 350
 Lys Arg Arg Glu Thr Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg
 355 360 365
 Leu Lys Gln Arg Arg Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile
 370 375 380
 Asp Ala Ser Pro Asn Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys
 385 390 395 400
 Leu Ser Ser Pro Gln Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg
 405 410 415
 Glu Pro Ser Gln Glu Asp
 420

<210> 1867

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXA00656

<400> 1867

ccttttaata acaatacaat gaataattgg aataggtcga caccttttga gcggagccgg 60

ttaaaattgg cagcattcac cgaaagaaaa ggagaaccac atg ctt gcc cta ggt 115
 Met Leu Ala Leu Gly
 1 5

tgg att aca tgg atc att att ggt ggt cta gct ggt tgg att gcc tcc 163
 Trp Ile Thr Trp Ile Ile Ile Gly Gly Leu Ala Gly Trp Ile Ala Ser
 10 15 20

aag att aaa ggc act gat gct cag caa gga att ttg ctg aac ata gtc 211
Lys Ile Lys Gly Thr Asp Ala Gln Gln Gly Ile Leu Leu Asn Ile Val
25 30 35

gtc ggt att atc ggt ggt ttg tta ggc ggc tgg ctg ctt gga atc ttc 259
Val Gly Ile Ile Gly Gly Leu Leu Gly Gly Trp Leu Leu Gly Ile Phe
40 45 50

gga gtg gat gtt gcc ggt ggc ggc ttg atc ttc agc ttc atc aca tgt 307
Gly Val Asp Val Ala Gly Gly Gly Leu Ile Phe Ser Phe Ile Thr Cys
55 60 65

ctg att ggt gct gtc att ttg ctg acg atc gtg cag ttc ttc act cgg 355
Leu Ile Gly Ala Val Ile Leu Leu Thr Ile Val Gln Phe Phe Thr Arg
70 75 80 85

aag aag taatctgctt taaatccgta ggg 384
Lys Lys

<210> 1868
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 1868
Met Leu Ala Leu Gly Trp Ile Thr Trp Ile Ile Ile Gly Gly Leu Ala
1 5 10 15

Gly Trp Ile Ala Ser Lys Ile Lys Gly Thr Asp Ala Gln Gln Gly Ile
20 25 30

Leu Leu Asn Ile Val Val Gly Ile Ile Gly Gly Leu Leu Gly Gly Trp
35 40 45

Leu Leu Gly Ile Phe Gly Val Asp Val Ala Gly Gly Gly Leu Ile Phe
50 55 60

Ser Phe Ile Thr Cys Leu Ile Gly Ala Val Ile Leu Leu Thr Ile Val
65 70 75 80

Gln Phe Phe Thr Arg Lys Lys
85

<210> 1869
<211> 986
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (61)..(963)
<223> RXA00657

<400> 1869
gatcatgagt ttccacgaac tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac 60

atg agc act gaa gac att gtc gtc gta gca gta gat ggc tcg gac gcc 108
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala

1	5	10	15	
tca aaa caa gct gtt cgg tgg gct gca aat acc gcc aac aaa cgt ggc				156
Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly	20	25	30	
att cca ctt cgc ttg gct tcc agc tac acc atg cct cag ttc ctc tac				204
Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr	35	40	45	
gca gag gga atg gtt cca cca caa gag ctt ttc gat gac ctc cag gcc				252
Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala	50	55	60	
gaa gcc ctg gaa aag att aac gaa gcc cgt gac atc gcc cat gag gta				300
Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val	65	70	75	80
gcg cca gaa atc aag atc ggg cac acc atc gct gaa ggc agt ccc atc				348
Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile	85	90	95	
gac atg ctg ttg gaa atg tct ccc gat gcc aca atg atc gtc atg ggt				396
Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly	100	105	110	
tcc cgc gga ctc ggc gga ctc tcc gga atg gtc atg ggc tcc gtc tcc				444
Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser	115	120	125	
ggg gca gtg gtc agc cac gca aag tgt cca gtc gtt gtt gtc cgt gaa				492
Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu	130	135	140	
gac agc gca gtc aac gaa gac agc aag tac ggc cca gtc gtc gtc ggt				540
Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly	145	150	155	160
gtg gat ggc tcc gaa gtc tcc caa cag gca acc gaa tac gca ttt gcg				588
Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala	165	170	175	
gaa gct gaa gct cgt ggc gcc gaa ctc gtt gca gtt cac acc tgg atg				636
Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met	180	185	190	
gac atg cag gta cag gca tca ctt gca ggt ctt gca gct gct caa cag				684
Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln	195	200	205	
cag tgg gat gaa gtg gaa cgt cag caa acc gac atg ctg atc gaa cgc				732
Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg	210	215	220	
ctc gca cca ctg gtg gaa aag tac cca agt gta acc gtc aag aag atc				780
Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile	225	230	235	240
atc acc cgt gac cgc cca gtt cgc gca ctt gca gaa gca tct gaa aac				828
Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn	245	250	255	

gcg cag ctc cta gtc gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc 876
 Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270

atg ctc ctt ggc tcc acc tcc cgc gca ctg ctg caa tcc gca ccg tgc 924
 Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
 275 280 285

cca atg atg gtg gtt cgc cca cct gag aag att aag aag tagttttcttt 973
 Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
 290 295 300

taagtttcga tgc 986

<210> 1870

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 1870

Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
 1 5 10 15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
 20 25 30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
 35 40 45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
 50 55 60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65 70 75 80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
 85 90 95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
 100 105 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
 115 120 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
 130 135 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
 145 150 155 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
 165 170 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
 180 185 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
 195 200 205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
 210 215 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225 230 235 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
 245 250 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
 275 280 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
 290 295 300

<210> 1871

<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXA00661

<400> 1871

cggatgcaag agaaccgtgg tttcgctgat ttttggcgaa cccggaatta aggccccgag 60

gattacatgc ttttaaattcc tttgaaaagg ggacaagatc atg aat cct ata acc 115
 Met Asn Pro Ile Thr
 1 5

gaa tta tta gac gca aca cta tgg atc ggc gga gtt ccg att ctg tgg 163
 Glu Leu Leu Asp Ala Thr Leu Trp Ile Gly Gly Val Pro Ile Leu Trp
 10 15 20

cgc gaa atc atc ggc aac gtt ttc gga tta ttt agc gcg tgg gca gga 211
 Arg Glu Ile Ile Gly Asn Val Phe Gly Leu Phe Ser Ala Trp Ala Gly
 25 30 35

atg cga cgc atc gtg tgg gca tgg ccc atc ggc atc ata ggc aac gcg 259
 Met Arg Arg Ile Val Trp Ala Trp Pro Ile Gly Ile Ile Gly Asn Ala
 40 45 50

ctg ctg ttc aca gta ttt atg ggc ggc ctt ttc cac act cca caa aac 307
 Leu Leu Phe Thr Val Phe Met Gly Gly Leu Phe His Thr Pro Gln Asn
 55 60 65

ctc gat ctc tac ggc caa gcg ggt cgc cag atc atg ttc atc atc gtc 355
 Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile Met Phe Ile Ile Val
 70 75 80 85

agt ggt tat ggc tgg tac caa tgg tcg gcc gca aaa cgt cgc gca ctc 403
 Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala Lys Arg Arg Ala Leu
 90 95 100

acc cca gaa aat gca gta gca gtg gtt cct cgc tgg gca agc acc aaa 451

Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg Trp Ala Ser Thr Lys
 105 110 115

gaa cgc gcc ggc att gtg att gcg gcg gtt gtg gga aca ctc agc ttt 499
 Glu Arg Ala Gly Ile Val Ile Ala Ala Val Val Gly Thr Leu Ser Phe
 120 125 130

gcc tgg att ttc caa gca ctc ggc tcc tgg ggg cca tgg gcc gac gcg 547
 Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly Pro Trp Ala Asp Ala
 135 140 145

tgg att ttc gtc ggc tca atc ctg gct acc tac gga atg gct cgc gga 595
 Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr Gly Met Ala Arg Gly
 150 155 160 165

tgg aca gag ttc tgg ctg atc tgg atc gcc gtc gac ata gtt ggc gtt 643
 Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val Asp Ile Val Gly Val
 170 175 180

cct cta ctt ttg act gct ggc tac tac cca tcc gcg gtg ctt tac ctg 691
 Pro Leu Leu Leu Thr Ala Gly Tyr Tyr Pro Ser Ala Val Leu Tyr Leu
 185 190 195

gtg tac ggt gcg ttt gtc agc tgg gga ttt gtc gtg tgg ctg cgg gtg 739
 Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val Val Trp Leu Arg Val
 200 205 210

caa aaa gca gac aag gct cgt gcg ctg gaa gct cag gag tct gtg aca 787
 Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala Gln Glu Ser Val Thr
 215 220 225

gtc tgaaaagcgt ttactaaata gaa 813
 Val
 230

<210> 1872

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 1872

Met Asn Pro Ile Thr Glu Leu Leu Asp Ala Thr Leu Trp Ile Gly Gly
 1 5 10 15

Val Pro Ile Leu Trp Arg Glu Ile Ile Gly Asn Val Phe Gly Leu Phe
 20 25 30

Ser Ala Trp Ala Gly Met Arg Arg Ile Val Trp Ala Trp Pro Ile Gly
 35 40 45

Ile Ile Gly Asn Ala Leu Leu Phe Thr Val Phe Met Gly Gly Leu Phe
 50 55 60

His Thr Pro Gln Asn Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile
 65 70 75 80

Met Phe Ile Ile Val Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala
 85 90 95

Lys Arg Arg Ala Leu Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg

100	105	110
Trp Ala Ser Thr Lys Glu Arg Ala Gly Ile Val Ile Ala Ala Val Val		
115	120	125
Gly Thr Leu Ser Phe Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly		
130	135	140
Pro Trp Ala Asp Ala Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr		
145	150	155
Gly Met Ala Arg Gly Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val		
165	170	175
Asp Ile Val Gly Val Pro Leu Leu Thr Ala Gly Tyr Tyr Pro Ser		
180	185	190
Ala Val Leu Tyr Leu Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val		
195	200	205
Val Trp Leu Arg Val Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala		
210	215	220
Gln Glu Ser Val Thr Val		
225	230	

<210> 1873

<211> 685

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(685)

<223> RXA00667

<400> 1873

ggcatcagtgt tttgaaggga aaagcaggtc aaacaagggtg cggctgattt gagcgatcac 60

agcaccgaga tctgtgctga agaattcaat gattgggttg atg att gcg ttg aag	115
Met Ile Ala Leu Lys	
1 5	

tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta	163
Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu	
10 15 20	

ccc atc cgc gac ggc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac	211
Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp	
25 30 35	

gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg	259
Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr	
40 45 50	

cag cgc cac cgc aat ccg gcc gac aac gcc gaa gcg ctt caa gcg cgt	307
Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg	
55 60 65	

ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc	355
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Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro
 70 75 80 85
 gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc 403
 Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro
 90 95 100
 gcc gcc gaa cgg ccg atc cct tac aaa att cat gtc att cac gaa gac 451
 Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp
 105 110 115
 gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct 499
 Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro
 120 125 130
 cgt ggc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg 547
 Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu
 135 140 145
 act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act 595
 Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr
 150 155 160 165
 tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt ggc gct tac 643
 Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr
 170 175 180
 caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag 685
 Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu
 185 190 195

<210> 1874

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 1874

Met Ile Ala Leu Lys Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys
 1 5 10 15
 Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val
 20 25 30
 Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
 35 40 45
 Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
 50 55 60
 Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65 70 75 80
 Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp
 85 90 95
 Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His
 100 105 110
 Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr
 115 120 125

Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val
130 135 140

Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg
145 150 155 160

Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu
165 170 175

Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys
180 185 190

Thr Tyr Glu
195

<210> 1875

<211> 870

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(847)

<223> RXA00676

<400> 1875

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gaatatcaaa atcataaaac agccttatat acttcaacgt atg gcg aag aat tct 115
Met Ala Lys Asn Ser
1 5

cga atc cga tac agc gcg tca atc aag cgt gcc gca gct gca atc ctc 163
Arg Ile Arg Tyr Ser Ala Ser Ile Lys Arg Ala Ala Ala Ala Ile Leu
10 15 20

acc gca gct gct acc tca gtc gcg ttg atc gct gtg cca gca act gct 211
Thr Ala Ala Ala Thr Ser Val Ala Leu Ile Ala Val Pro Ala Thr Ala
25 30 35

tca gca cag gac ctc gca acc ggc agc tcc cag atc cag act gat gct 259
Ser Ala Gln Asp Leu Ala Thr Gly Ser Ser Gln Ile Gln Thr Asp Ala
40 45 50

cgt gaa ggt gcg tgg gca acc cgc aac acc atc caa gac caa ctt gcc 307
Arg Glu Gly Ala Trp Ala Thr Arg Asn Thr Ile Gln Asp Gln Leu Ala
55 60 65

tcc att ggg cca gca gcc ctc cca gtc cgc gca gcg gta gac aat gcc 355
Ser Ile Gly Pro Ala Ala Leu Pro Val Arg Ala Ala Val Asp Asn Ala
70 75 80 85

atc aac ggc atg ttc cca gga ctt gtt gat gaa aag gtt gca gca gag 403
Ile Asn Gly Met Phe Pro Gly Leu Val Asp Glu Lys Val Ala Ala Glu
90 95 100

cag gaa gct gca cgc gca gaa gct gag cgc gaa gca gca gct gca cgt 451
Gln Glu Ala Ala Arg Ala Glu Ala Glu Arg Glu Ala Ala Ala Arg
105 110 115

gaa gca gaa gca gcc cgc gta gcc gca gaa gaa gcc gca cgc ttt gac 499
 Glu Ala Glu Ala Ala Arg Val Ala Ala Glu Glu Ala Ala Arg Phe Asp
 120 125 130

cgc ggc tct tgc cca gca atc gct gat gtc tgc gtg gac att gat ggt 547
 Arg Gly Ser Cys Pro Ala Ile Ala Asp Val Cys Val Asp Ile Asp Gly
 135 140 145

gga cgt acc tgg ctg cag gaa aac ggt cag gtc acc tac ggt gca gtc 595
 Gly Arg Thr Trp Leu Gln Glu Asn Gly Gln Val Thr Tyr Gly Ala Val
 150 155 160 165

cca gtt tcc tcc ggc gga gtt ggc cag gaa acc cct cgc gga acg ttc 643
 Pro Val Ser Ser Gly Gly Val Gly Gln Glu Thr Pro Arg Gly Thr Phe
 170 175 180

tac atc aac cgc aag gtc aag gat gaa atc tct tac gag ttc ggt aac 691
 Tyr Ile Asn Arg Lys Val Lys Asp Glu Ile Ser Tyr Glu Phe Gly Asn
 185 190 195

gcc cca atg ccg tac gcc atg tac ttc acc tac aac ggc cac gca ttc 739
 Ala Pro Met Pro Tyr Ala Met Tyr Phe Thr Tyr Asn Gly His Ala Phe
 200 205 210

cac cag ggc aat gtt gcg act act tcc gct ggt tgt gtt cgc cta aac 787
 His Gln Gly Asn Val Ala Thr Thr Ser Ala Gly Cys Val Arg Leu Asn
 215 220 225

act caa gat gcc atc tac tac ttc aac aac gtt ggc atc ggc gac atg 835
 Thr Gln Asp Ala Ile Tyr Tyr Phe Asn Asn Val Gly Ile Gly Asp Met
 230 235 240 245

gtg tac atc tac taaaactcac cggtgctagc agg 870
 Val Tyr Ile Tyr

<210> 1876

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 1876

Met Ala Lys Asn Ser Arg Ile Arg Tyr Ser Ala Ser Ile Lys Arg Ala
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 20 25 30

Val Pro Ala Thr Ala Ser Ala Gln Asp Leu Ala Thr Gly Ser Ser Gln
 35 40 45

Ile Gln Thr Asp Ala Arg Glu Gly Ala Trp Ala Thr Arg Asn Thr Ile
 50 55 60

Gln Asp Gln Leu Ala Ser Ile Gly Pro Ala Ala Leu Pro Val Arg Ala
 65 70 75 80

Ala Val Asp Asn Ala Ile Asn Gly Met Phe Pro Gly Leu Val Asp Glu
 85 90 95

ttt gag caa tta tgg aaa gcc att gag ccg gaa acc cgc acc cgc gcc 307
 Phe Glu Gln Leu Trp Lys Ala Ile Glu Pro Glu Thr Arg Thr Arg Ala
 55 60 65
 aac gac att cat ctt ccc atc gtc gtg gcg tac gct gaa cgt ctc tgc 355
 Asn Asp Ile His Leu Pro Ile Val Val Ala Tyr Ala Glu Arg Leu Cys
 70 75 80 85
 gac gct tac cca ctg gca gat aga gaa ttg gtt ctc gta gcc gca atc 403
 Asp Ala Tyr Pro Leu Ala Asp Arg Glu Leu Val Leu Val Ala Ala Ile
 90 95 100
 ctc cac gac acg ggc tgg gca cat gtc gat gag agc cga atc atc tcc 451
 Leu His Asp Thr Gly Trp Ala His Val Asp Glu Ser Arg Ile Ile Ser
 105 110 115
 gaa gga ttc tcc gga aac tgg cgc aaa gca gca atc cgc ttc gaa cac 499
 Glu Gly Phe Ser Gly Asn Trp Arg Lys Ala Ala Ile Arg Phe Glu His
 120 125 130
 gaa aca gaa ggc tgc act gtg gcc cgc cga gtg ctt cca tcc ctc gga 547
 Glu Thr Glu Gly Cys Thr Val Ala Arg Arg Val Leu Pro Ser Leu Gly
 135 140 145
 tat act gtc gat ttt gtc gag cat gtc tgc gac atc atc gac gga cac 595
 Tyr Thr Val Asp Phe Val Glu His Val Cys Asp Ile Ile Asp Gly His
 150 155 160 165
 gac acc cgc caa gtg gcc tac tca cta gaa gac gct ctt gtt cgc gat 643
 Asp Thr Arg Gln Val Ala Tyr Ser Leu Glu Asp Ala Leu Val Arg Asp
 170 175 180
 tgc gac cga ctc tgg cgt ttc gac cgc gcc ggg atc acg gct tct agc 691
 Cys Asp Arg Leu Trp Arg Phe Asp Arg Ala Gly Ile Thr Ala Ser Ser
 185 190 195
 tca tgg ttc ggg atg cca gtc tca gat tat gtc gac cgc ctg cac agg 739
 Ser Trp Phe Gly Met Pro Val Ser Asp Tyr Val Asp Arg Leu His Arg
 200 205 210
 gaa atc ctc cca gaa tta atc acc gaa gct gca cac cag atg gct act 787
 Glu Ile Leu Pro Glu Leu Ile Thr Glu Ala Ala His Gln Met Ala Thr
 215 220 225
 gca gac ctc aat cgt gca aag gcc ctg tta aga acg gat gcg atc cga 835
 Ala Asp Leu Asn Arg Ala Lys Ala Leu Leu Arg Thr Asp Ala Ile Arg
 230 235 240 245
 tgaatgctgc aaccaggcgt gct 858

<210> 1878

<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 1878

Met Thr Arg Ser Asn Leu Pro Ala Trp Glu Gln Ala Asp Pro Ser Val
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His Ala Ser Asp Pro Arg Ala Ile Thr Phe Ala Glu Asp Phe Gly Ile

20										25					30															
Arg	Pro	Ile	Pro	Ala	Val	Gly	Pro	Ile	Asp	Thr	Thr	Ala	Ile	Cys	Ala															
		35						40					45																	
Thr	Pro	Ser	Asn	Gly	Phe	Glu	Gln	Leu	Trp	Lys	Ala	Ile	Glu	Pro	Glu															
	50					55					60																			
Thr	Arg	Thr	Arg	Ala	Asn	Asp	Ile	His	Leu	Pro	Ile	Val	Val	Ala	Tyr															
65					70				75						80															
Ala	Glu	Arg	Leu	Cys	Asp	Ala	Tyr	Pro	Leu	Ala	Asp	Arg	Glu	Leu	Val															
				85					90					95																
Leu	Val	Ala	Ala	Ile	Leu	His	Asp	Thr	Gly	Trp	Ala	His	Val	Asp	Glu															
			100					105					110																	
Ser	Arg	Ile	Ile	Ser	Glu	Gly	Phe	Ser	Gly	Asn	Trp	Arg	Lys	Ala	Ala															
		115					120					125																		
Ile	Arg	Phe	Glu	His	Glu	Thr	Glu	Gly	Cys	Thr	Val	Ala	Arg	Arg	Val															
	130					135					140																			
Leu	Pro	Ser	Leu	Gly	Tyr	Thr	Val	Asp	Phe	Val	Glu	His	Val	Cys	Asp															
145					150				155					160																
Ile	Ile	Asp	Gly	His	Asp	Thr	Arg	Gln	Val	Ala	Tyr	Ser	Leu	Glu	Asp															
				165					170					175																
Ala	Leu	Val	Arg	Asp	Cys	Asp	Arg	Leu	Trp	Arg	Phe	Asp	Arg	Ala	Gly															
			180					185					190																	
Ile	Thr	Ala	Ser	Ser	Ser	Trp	Phe	Gly	Met	Pro	Val	Ser	Asp	Tyr	Val															
		195					200					205																		
Asp	Arg	Leu	His	Arg	Glu	Ile	Leu	Pro	Glu	Leu	Ile	Thr	Glu	Ala	Ala															
210						215					220																			
His	Gln	Met	Ala	Thr	Ala	Asp	Leu	Asn	Arg	Ala	Lys	Ala	Leu	Leu	Arg															
225					230				235						240															
Thr	Asp	Ala	Ile	Arg																										
				245																										

<210> 1879
 <211> 1053
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1030)
 <223> RXA00691

<400> 1879
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 Met Val Glu Gly Asn
 1 5

acc atc ggc tgt gct gac gcc ggc gga aat ggc tat caa acg ctt ctt	163
Thr Ile Gly Cys Ala Asp Ala Gly Gly Asn Gly Tyr Gln Thr Leu Leu	
10 15 20	
gat gcc gga ttt gat gtg gaa acc acc gtt cag ttt cca gaa ttc ttg	211
Asp Ala Gly Phe Asp Val Glu Thr Thr Val Gln Phe Pro Glu Phe Leu	
25 30 35	
tgc cga atc aat gat ttc cca ggt cct gat gtg gac gat tgc atg acc	259
Cys Arg Ile Asn Asp Phe Pro Gly Pro Asp Val Asp Asp Cys Met Thr	
40 45 50	
gca tca cct gct gaa gct tat tgg tct tat tgg cat gct ccc ctc ggc	307
Ala Ser Pro Ala Glu Ala Tyr Trp Ser Tyr Trp His Ala Pro Leu Gly	
55 60 65	
gga gat gaa tgg gaa tac agc aac ctt gga gct ttc ctc tac tac ccc	355
Gly Asp Glu Trp Glu Tyr Ser Asn Leu Gly Ala Phe Leu Tyr Tyr Pro	
70 75 80 85	
aaa ccc ggc act gtt gaa gcg tgg tat tgg gga gat act gat cgt ccc	403
Lys Pro Gly Thr Val Glu Ala Trp Tyr Trp Gly Asp Thr Asp Arg Pro	
90 95 100	
ggc gcg atc ccg gtg agt aaa tct cag gcg gag ttg ggg tta gac tcc	451
Gly Ala Ile Pro Val Ser Lys Ser Gln Ala Glu Leu Gly Leu Asp Ser	
105 110 115	
gcg gat ccg gat tac aaa att gat ttt gat cca aat gat ttc atc acc	499
Ala Asp Pro Asp Tyr Lys Ile Asp Phe Asp Pro Asn Asp Phe Ile Thr	
120 125 130	
aca acc cca acc tcc gag tcc cct atc gcc gat tta ggg ggt gac gaa	547
Thr Thr Pro Thr Ser Glu Ser Pro Ile Ala Asp Leu Gly Gly Asp Glu	
135 140 145	
gag ccc act gaa act act gaa gct cct atc gca ggg gct gga gct ggt	595
Glu Pro Thr Glu Thr Thr Glu Ala Pro Ile Ala Gly Ala Gly Ala Gly	
150 155 160 165	
tcg gca aga gga caa gca gct gaa ccc act gtt gag gta aac cct gag	643
Ser Ala Arg Gly Gln Ala Ala Glu Pro Thr Val Glu Val Asn Pro Glu	
170 175 180	
aac cct aat gag gta ttg gtg tat cag gat tct gaa gga aac tcg att	691
Asn Pro Asn Glu Val Leu Val Tyr Gln Asp Ser Glu Gly Asn Ser Ile	
185 190 195	
act aaa ggt cag tac gag aac ttg gtt gct gca gca gcc gct aag acc	739
Thr Lys Gly Gln Tyr Glu Asn Leu Val Ala Ala Ala Ala Lys Thr	
200 205 210	
act gct gct gtc caa gcc cca gct ggg gct ggt gaa gca aat agc caa	787
Thr Ala Ala Val Gln Ala Pro Ala Gly Ala Gly Glu Ala Asn Ser Gln	
215 220 225	
ccg cag gca aca gcg gtg gca gaa gct cct gaa gtt gat ccg atg acc	835
Pro Gln Ala Thr Ala Val Ala Glu Ala Pro Glu Val Asp Pro Met Thr	
230 235 240 245	

acg cag gtt ctt atg gcg cct gcg ggc caa gat gga gac gtc atg gct 883
 Thr Gln Val Leu Met Ala Pro Ala Gly Gln Asp Gly Asp Val Met Ala
 250 255 260

gag ggt tcg acg cag cag acg tac gcc aca ggc acg gtg gat tct tct 931
 Glu Gly Ser Thr Gln Gln Thr Tyr Ala Thr Gly Thr Val Asp Ser Ser
 265 270 275

gct cag gga tgg atc att gga ctc aca ctg gct gtc att tcc ttg gtt 979
 Ala Gln Gly Trp Ile Ile Gly Leu Thr Leu Ala Val Ile Ser Leu Val
 280 285 290

tca gcg tct gct gtg gcg gcg tgg gcg att cgt cgt tca gag gtc cag 1027
 Ser Ala Ser Ala Val Ala Ala Trp Ala Ile Arg Arg Ser Glu Val Gln
 295 300 305

ggt taaagcttcg tgaaatggat tga 1053
 Gly
 310

<210> 1880

<211> 310

<212> PRT

<213> Corynebacterium glutamicum

<400> 1880

Met Val Glu Gly Asn Thr Ile Gly Cys Ala Asp Ala Gly Gly Asn Gly
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 20 25 30

Phe Pro Glu Phe Leu Cys Arg Ile Asn Asp Phe Pro Gly Pro Asp Val
 35 40 45

Asp Asp Cys Met Thr Ala Ser Pro Ala Glu Ala Tyr Trp Ser Tyr Trp
 50 55 60

His Ala Pro Leu Gly Gly Asp Glu Trp Glu Tyr Ser Asn Leu Gly Ala
 65 70 75 80

Phe Leu Tyr Tyr Pro Lys Pro Gly Thr Val Glu Ala Trp Tyr Trp Gly
 85 90 95

Asp Thr Asp Arg Pro Gly Ala Ile Pro Val Ser Lys Ser Gln Ala Glu
 100 105 110

Leu Gly Leu Asp Ser Ala Asp Pro Asp Tyr Lys Ile Asp Phe Asp Pro
 115 120 125

Asn Asp Phe Ile Thr Thr Thr Pro Thr Ser Glu Ser Pro Ile Ala Asp
 130 135 140

Leu Gly Gly Asp Glu Glu Pro Thr Glu Thr Thr Glu Ala Pro Ile Ala
 145 150 155 160

Gly Ala Gly Ala Gly Ser Ala Arg Gly Gln Ala Ala Glu Pro Thr Val
 165 170 175

Glu Val Asn Pro Glu Asn Pro Asn Glu Val Leu Val Tyr Gln Asp Ser

180	185	190
Glu Gly Asn Ser Ile Thr Lys Gly Gln Tyr Glu Asn Leu Val Ala Ala		
195	200	205
Ala Ala Ala Lys Thr Thr Ala Ala Val Gln Ala Pro Ala Gly Ala Gly		
210	215	220
Glu Ala Asn Ser Gln Pro Gln Ala Thr Ala Val Ala Glu Ala Pro Glu		
225	230	235
Val Asp Pro Met Thr Thr Gln Val Leu Met Ala Pro Ala Gly Gln Asp		
245	250	255
Gly Asp Val Met Ala Glu Gly Ser Thr Gln Gln Thr Tyr Ala Thr Gly		
260	265	270
Thr Val Asp Ser Ser Ala Gln Gly Trp Ile Ile Gly Leu Thr Leu Ala		
275	280	285
Val Ile Ser Leu Val Ser Ala Ser Ala Val Ala Ala Trp Ala Ile Arg		
290	295	300
Arg Ser Glu Val Gln Gly		
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<210> 1881

<211> 1257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1234)

<223> RXA00692

<400> 1881

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tctacgtggg aagagaacca ttcgctgggc tgctgcaacc gtg gct tta gca acc 115
                                         Val Ala Leu Ala Thr
                                         1           5

ggg gtt tcc ctg ttg gct cca cag gtc gtt gct gca cag gat gca tca 163
Gly Val Ser Leu Leu Ala Pro Gln Val Val Ala Ala Gln Asp Ala Ser
                10                15                20

tcg gat att caa tta gct acc caa ttc atc gaa aaa gaa ttt gca acg 211
Ser Asp Ile Gln Leu Ala Thr Gln Phe Ile Glu Lys Glu Phe Ala Thr
                25                30                35

aat ggc ctc atc cct ggg cct gta ggt act cca gat att ggg ctc aat 259
Asn Gly Leu Ile Pro Gly Pro Val Gly Thr Pro Asp Ile Gly Leu Asn
                40                45                50

cag gat ctg ttg ctg tcc cta aat gcg ctt gcc cct gat tct cca gag 307
Gln Asp Leu Leu Leu Ser Leu Asn Ala Leu Ala Pro Asp Ser Pro Glu
                55                60                65

atc gac gct gca tat gct gca att gct ccg gag ctc gag ggc tat gtc 355

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Ile Asp Ala Ala Tyr Ala Ala Ile Ala Pro Glu Leu Glu Gly Tyr Val	
70 75 80 85	
tca gtt tct gac tac atc ttc agc gat cgt cta gcc aag acc gta gct	403
Ser Val Ser Asp Tyr Ile Phe Ser Asp Arg Leu Ala Lys Thr Val Ala	
90 95 100	
ttc caa gat gcc ctc ggc gtc aga gat gct gat ttt atc gcg caa ctt	451
Phe Gln Asp Ala Leu Gly Val Arg Asp Ala Asp Phe Ile Ala Gln Leu	
105 110 115	
gtc agc gct gtt caa gaa aac ggt cag atc aaa aac tta gat aat ggt	499
Val Ser Ala Val Gln Glu Asn Gly Gln Ile Lys Asn Leu Asp Asn Gly	
120 125 130	
gaa gcc aca act gca att aat aac ttc agc cag gcc tgg ggc gtt cta	547
Glu Ala Thr Thr Ala Ile Asn Asn Phe Ser Gln Ala Trp Gly Val Leu	
135 140 145	
gct ctg cac cgc gtc ggt gaa acc gaa gca gcc gag cgc gca aca gaa	595
Ala Leu His Arg Val Gly Glu Thr Glu Ala Ala Glu Arg Ala Thr Glu	
150 155 160 165	
ttc ctt aaa act caa gtg tgc tcc gac ggt ggt gtc caa tta gcc tca	643
Phe Leu Lys Thr Gln Val Cys Ser Asp Gly Gly Val Gln Leu Ala Ser	
170 175 180	
gca atc gaa cct aca tgc aaa acc acg gat tcc gat gtc act gca atg	691
Ala Ile Glu Pro Thr Cys Lys Thr Thr Asp Ser Asp Val Thr Ala Met	
185 190 195	
gct gca cag gct ttg act ctg gca aat ggt gcg cag gat cca acc aca	739
Ala Ala Gln Ala Leu Thr Leu Ala Asn Gly Ala Gln Asp Pro Thr Thr	
200 205 210	
caa gcc act ctc gat tac ctc gtc acc acg atg gat gag acc ggt ggt	787
Gln Ala Thr Leu Asp Tyr Leu Val Thr Thr Met Asp Glu Thr Gly Gly	
215 220 225	
gtc aaa aat act tgg acc ggt gtg aat tcc aac tcc acg gga att gtc	835
Val Lys Asn Thr Trp Thr Gly Val Asn Ser Asn Ser Thr Gly Ile Val	
230 235 240 245	
gga tcc gct ttt gct ctt gcg ggc gat gag gaa aac tac ctc aag gct	883
Gly Ser Ala Phe Ala Leu Ala Gly Asp Glu Glu Asn Tyr Leu Lys Ala	
250 255 260	
cgt gaa tac ctg gca tct gtt caa ttt ggc gaa gat gca gac cca tcg	931
Arg Glu Tyr Leu Ala Ser Val Gln Phe Gly Glu Asp Ala Asp Pro Ser	
265 270 275	
att cag ggt ggc ttt gct ttc acc gtg aag gct aag gaa acc aac act	979
Ile Gln Gly Gly Phe Ala Phe Thr Val Lys Ala Lys Glu Thr Asn Thr	
280 285 290	
gcg att agc gat cag att cga cgc gca act ggc caa gca gca tta ggt	1027
Ala Ile Ser Asp Gln Ile Arg Arg Ala Thr Gly Gln Ala Ala Leu Gly	
295 300 305	
ttt gca ggc ggt aac tac gcc aac gat aaa ctg atc acc att gcg aac	1075
Phe Ala Gly Gly Asn Tyr Ala Asn Asp Lys Leu Ile Thr Ile Ala Asn	

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310          315          320          325
cca gta gat cca act cca gat cca gaa att cca act ccc cca gct gat 1123
Pro Val Asp Pro Thr Pro Asp Pro Glu Ile Pro Thr Pro Pro Ala Asp
          330          335          340

tca gag gga tcc acc ggt gga att ggc ggc gct gga att atc atc gcc 1171
Ser Glu Gly Ser Thr Gly Gly Ile Gly Gly Ala Gly Ile Ile Ile Ala
          345          350          355

atc ttg gcc atc ctt gcc gcc atc gct ggt gtc atg gga cca atg atg 1219
Ile Leu Ala Ile Leu Ala Ala Ile Ala Gly Val Met Gly Pro Met Met
          360          365          370

gct aac ctg cag ttt taacatctga gagaagtaca gtg 1257
Ala Asn Leu Gln Phe
          375

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<210> 1882

<211> 378

<212> PRT

<213> Corynebacterium glutamicum

<400> 1882

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      20              25              30

Lys Glu Phe Ala Thr Asn Gly Leu Ile Pro Gly Pro Val Gly Thr Pro
      35              40              45

Asp Ile Gly Leu Asn Gln Asp Leu Leu Leu Ser Leu Asn Ala Leu Ala
      50              55              60

Pro Asp Ser Pro Glu Ile Asp Ala Ala Tyr Ala Ala Ile Ala Pro Glu
      65              70              75              80

Leu Glu Gly Tyr Val Ser Val Ser Asp Tyr Ile Phe Ser Asp Arg Leu
      85              90              95

Ala Lys Thr Val Ala Phe Gln Asp Ala Leu Gly Val Arg Asp Ala Asp
      100             105             110

Phe Ile Ala Gln Leu Val Ser Ala Val Gln Glu Asn Gly Gln Ile Lys
      115             120             125

Asn Leu Asp Asn Gly Glu Ala Thr Thr Ala Ile Asn Asn Phe Ser Gln
      130             135             140

Ala Trp Gly Val Leu Ala Leu His Arg Val Gly Glu Thr Glu Ala Ala
      145             150             155             160

Glu Arg Ala Thr Glu Phe Leu Lys Thr Gln Val Cys Ser Asp Gly Gly
      165             170             175

Val Gln Leu Ala Ser Ala Ile Glu Pro Thr Cys Lys Thr Thr Asp Ser
      180             185             190

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Asp Val Thr Ala Met Ala Ala Gln Ala Leu Thr Leu Ala Asn Gly Ala
 195 200 205
 Gln Asp Pro Thr Thr Gln Ala Thr Leu Asp Tyr Leu Val Thr Thr Met
 210 215 220
 Asp Glu Thr Gly Gly Val Lys Asn Thr Trp Thr Gly Val Asn Ser Asn
 225 230 235 240
 Ser Thr Gly Ile Val Gly Ser Ala Phe Ala Leu Ala Gly Asp Glu Glu
 245 250 255
 Asn Tyr Leu Lys Ala Arg Glu Tyr Leu Ala Ser Val Gln Phe Gly Glu
 260 265 270
 Asp Ala Asp Pro Ser Ile Gln Gly Gly Phe Ala Phe Thr Val Lys Ala
 275 280 285
 Lys Glu Thr Asn Thr Ala Ile Ser Asp Gln Ile Arg Arg Ala Thr Gly
 290 295 300
 Gln Ala Ala Leu Gly Phe Ala Gly Gly Asn Tyr Ala Asn Asp Lys Leu
 305 310 315 320
 Ile Thr Ile Ala Asn Pro Val Asp Pro Thr Pro Asp Pro Glu Ile Pro
 325 330 335
 Thr Pro Pro Ala Asp Ser Glu Gly Ser Thr Gly Gly Ile Gly Gly Ala
 340 345 350
 Gly Ile Ile Ile Ala Ile Leu Ala Ile Leu Ala Ala Ile Ala Gly Val
 355 360 365
 Met Gly Pro Met Met Ala Asn Leu Gln Phe
 370 375

<210> 1883

<211> 606

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(583)

<223> RXA00693

<400> 1883

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gatgtacaaa ttaatctcac cgcatttgct aggccacgcc atg tgg aaa gag gct 115
 Met Trp Lys Glu Ala
 1 5

ttg gaa gaa ttc gga tca ggc ccc atc cac ggc tcg ggt tat ttc gag 163
 Leu Glu Glu Phe Gly Ser Gly Pro Ile His Gly Ser Gly Tyr Phe Glu
 10 15 20

aac tat ctt ccc atc gac tat tcc gaa gca gga ttt cac cac tac ctc 211
 Asn Tyr Leu Pro Ile Asp Tyr Ser Glu Ala Gly Phe His His Tyr Leu
 25 30 35

aag gag cgc act gac gcg gcc gat cct tcg gtt cca cca ccg gaa ggt 259
Lys Glu Arg Thr Asp Ala Ala Asp Pro Ser Val Pro Pro Pro Glu Gly
40 45 50

ttt gtg cac tgc agc tat ttc tgg atc gtt gat gat gac gat gtt ctt 307
Phe Val His Cys Ser Tyr Phe Trp Ile Val Asp Asp Asp Asp Val Leu
55 60 65

gtc gga ttc tta gct tta agg cac gag ctg aac caa cat ctc ctg gaa 355
Val Gly Phe Leu Ala Leu Arg His Glu Leu Asn Gln His Leu Leu Glu
70 75 80 85

gtc gcg ggc cac att ggt tac ggc gtg cgc ccg tct gcg cgt cga aaa 403
Val Ala Gly His Ile Gly Tyr Gly Val Arg Pro Ser Ala Arg Arg Lys
90 95 100

ggt gct gca acc gca gcg ctg aaa ctc ggt gtt cat gaa gct cag gcc 451
Gly Ala Ala Thr Ala Ala Leu Lys Leu Gly Val His Glu Ala Gln Ala
105 110 115

ttg ggc atc gac aag gtt ttg ctg tgc gtc gca gga gat aac gaa gcg 499
Leu Gly Ile Asp Lys Val Leu Leu Cys Val Ala Gly Asp Asn Glu Ala
120 125 130

tcc agg aac gtc atc gaa aag tgc ggt gga gtt tat gaa tcc acg atc 547
Ser Arg Asn Val Ile Glu Lys Cys Gly Gly Val Tyr Glu Ser Thr Ile
135 140 145

cgt gga atg cga cgc tat tgg ata gcc aca gat tct taaaaaatct 593
Arg Gly Met Arg Arg Tyr Trp Ile Ala Thr Asp Ser
150 155 160

tcgcaagaac tta 606

<210> 1884

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 1884

Met Trp Lys Glu Ala Leu Glu Glu Phe Gly Ser Gly Pro Ile His Gly
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Ser Gly Tyr Phe Glu Asn Tyr Leu Pro Ile Asp Tyr Ser Glu Ala Gly
20 25 30

Phe His His Tyr Leu Lys Glu Arg Thr Asp Ala Ala Asp Pro Ser Val
35 40 45

Pro Pro Pro Glu Gly Phe Val His Cys Ser Tyr Phe Trp Ile Val Asp
50 55 60

Asp Asp Asp Val Leu Val Gly Phe Leu Ala Leu Arg His Glu Leu Asn
65 70 75 80

Gln His Leu Leu Glu Val Ala Gly His Ile Gly Tyr Gly Val Arg Pro
85 90 95

Ser Ala Arg Arg Lys Gly Ala Ala Thr Ala Ala Leu Lys Leu Gly Val

100	105	110
His Glu Ala Gln Ala Leu Gly Ile Asp Lys Val Leu Leu Cys Val Ala		
115	120	125
Gly Asp Asn Glu Ala Ser Arg Asn Val Ile Glu Lys Cys Gly Gly Val		
130	135	140
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145	150	155
		160
Ser		

<210> 1885

<211> 498

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(475)

<223> RXA00701

<400> 1885

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                                   Leu Val Gly Glu Pro
                                   1 5
cgg tcc gat tcc tgc ggt gag cag cgc gga tgc gaa cag tcc ggt gtt 163
Arg Ser Asp Ser Cys Gly Glu Gln Arg Gly Cys Glu Gln Ser Gly Val
              10              15              20
gcc gag gat gaa tcc gaa gcc ggg tcc gaa ggc tcg tcc gcc gag gat 211
Ala Glu Asp Glu Ser Glu Ala Gly Ser Glu Gly Ser Ser Ala Glu Asp
              25              30              35
gag gac aaa gaa gac tgc ttc aaa gcc tgc tgc gcc ggc acc gaa tgg 259
Glu Asp Lys Glu Asp Cys Phe Lys Ala Cys Cys Ala Gly Thr Glu Trp
              40              45              50
tcg gac tac ggc aac cat ggc ggt gag gac gcc gag cat ggc tac ggc 307
Ser Asp Tyr Gly Asn His Gly Gly Glu Asp Ala Glu His Gly Tyr Gly
              55              60              65
ttt aac gtc gaa tcc gtt ttc act gat ttc ggc gat gac agc ggc cag 355
Phe Asn Val Glu Ser Val Phe Thr Asp Phe Gly Asp Asp Ser Gly Gln
              70              75              80              85
cac gag ggg aat gac gat cgc gat gta gag ggg cgc ttg ggc ttt gtc 403
His Glu Gly Asn Asp Asp Arg Asp Val Glu Gly Arg Leu Gly Phe Val
              90              95              100
gga cag gaa gga ttc cgg gtt gac gat cag cgg cca gaa gaa aat cac 451
Gly Gln Glu Gly Phe Arg Val Asp Asp Gln Arg Pro Glu Glu Asn His
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gat gct caa aac cgc aag gaa gct taaggtgagg aaggttttgg gct 498

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<210> 1886
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 1886
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Ser Ser Ala Glu Asp Glu Asp Lys Glu Asp Cys Phe Lys Ala Cys Cys
35 40 45
Ala Gly Thr Glu Trp Ser Asp Tyr Gly Asn His Gly Gly Glu Asp Ala
50 55 60
Glu His Gly Tyr Gly Phe Asn Val Glu Ser Val Phe Thr Asp Phe Gly
65 70 75 80
Asp Asp Ser Gly Gln His Glu Gly Asn Asp Asp Arg Asp Val Glu Gly
85 90 95
Arg Leu Gly Phe Val Gly Gln Glu Gly Phe Arg Val Asp Asp Gln Arg
100 105 110
Pro Glu Glu Asn His Asp Ala Gln Asn Arg Lys Glu Ala
115 120 125

<210> 1887
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1072)
<223> RXA00707

<400> 1887
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Met Asn Val Gln Arg
1 5
aaa ctg ctg gcg atc gta ggg gct ttc atg gca ggg tct tta gcc ttg 163
Lys Leu Leu Ala Ile Val Gly Ala Phe Met Ala Gly Ser Leu Ala Leu
10 15 20
gga aca cca act gca cag gcc caa agc att ggc agc agt gcc tca cag 211
Gly Thr Pro Thr Ala Gln Ala Gln Ser Ile Gly Ser Ser Ala Ser Gln
25 30 35
aga act gaa gtc tta cgt ggg ctg acc tca tct gcc gga ata cca gat 259

Arg Thr Glu Val Leu Arg Gly Leu Thr Ser Ser Ala Gly Ile Pro Asp	
40 45 50	
gcc aca gcg ccg gaa ggc ggg gca aaa gtc gtg gtc ttt gga gat tca	307
Ala Thr Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe Gly Asp Ser	
55 60 65	
cat gca tca gga acc aat gca cca ttt gat gtg gat gaa cgc ggc tgc	355
His Ala Ser Gly Thr Asn Ala Pro Phe Asp Val Asp Glu Arg Gly Cys	
70 75 80 85	
ctc aag ggg aac caa tcg tgg cct gat caa ttg caa gca caa caa gga	403
Leu Lys Gly Asn Gln Ser Trp Pro Asp Gln Leu Gln Ala Gln Gln Gly	
90 95 100	
ttg cag cag ggg gag ctc att gac ctt tcc tgc aac ggc gcc tcc atc	451
Leu Gln Gln Gly Glu Leu Ile Asp Leu Ser Cys Asn Gly Ala Ser Ile	
105 110 115	
aac tcg acg ggt ttc cac ttt tcc gat gaa gtt cgg cat gca gaa gca	499
Asn Ser Thr Gly Phe His Phe Ser Asp Glu Val Arg His Ala Glu Ala	
120 125 130	
cta ggg gcc att gga cca aat acc gag aac atc ttc atc caa ttt ggc	547
Leu Gly Ala Ile Gly Pro Asn Thr Glu Asn Ile Phe Ile Gln Phe Gly	
135 140 145	
aag aat gat cag tgg gga cac tca cca atc aat ttg cgc tat tcc gtg	595
Lys Asn Asp Gln Trp Gly His Ser Pro Ile Asn Leu Arg Tyr Ser Val	
150 155 160 165	
atc aac tgc ctt ttt gat gcg gcc aac gga tgc ggt gag aaa gct gta	643
Ile Asn Cys Leu Phe Asp Ala Ala Asn Gly Cys Gly Glu Lys Ala Val	
170 175 180	
gcg gct gga acc atg cag gat ccc tcc tcg gtc acc ggc gaa aac tat	691
Ala Ala Gly Thr Met Gln Asp Pro Ser Ser Val Thr Gly Glu Asn Tyr	
185 190 195	
gct cag cgg atg aaa cct gtc atc gac tac ctc aag tac tac gct cca	739
Ala Gln Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr Tyr Ala Pro	
200 205 210	
aat gcg cag atc acg ttg ctg gga tac cag gaa tac acc cca cga agc	787
Asn Ala Gln Ile Thr Leu Leu Gly Tyr Gln Glu Tyr Thr Pro Arg Ser	
215 220 225	
gga agc gag att tgt gtc cgc gtg gga ggt acg gaa cta agg aaa cca	835
Gly Ser Glu Ile Cys Val Arg Val Gly Gly Thr Glu Leu Arg Lys Pro	
230 235 240 245	
gac gcc acc aac ctg gtg tcc tat atg aac aat ctt gag tcg gcc att	883
Asp Ala Thr Asn Leu Val Ser Tyr Met Asn Asn Leu Glu Ser Ala Ile	
250 255 260	
ttt gaa gcc tct gag att ctt gac gtc cag cat gcc aat ctc cgt gag	931
Phe Glu Ala Ser Glu Ile Leu Asp Val Gln His Ala Asn Leu Arg Glu	
265 270 275	
gcc act gca gga cac agc agc tgc tca gct gaa ccg tgg gtc aac gga	979
Ala Thr Ala Gly His Ser Ser Cys Ser Ala Glu Pro Trp Val Asn Gly	

280 285 290
 gtg ctg gat atg cgg gta aac gct gta gga ggc acc tgg cac cca tct 1027
 Val Leu Asp Met Arg Val Asn Ala Val Gly Gly Thr Trp His Pro Ser
 295 300 305
 cca aag gga gat gaa gtg acc gcg ggc ctc ctc gga acc ttg atg 1072
 Pro Lys Gly Asp Glu Val Thr Ala Gly Leu Leu Gly Thr Leu Met
 310 315 320
 taactatcta gaattcttca tag 1095

 <210> 1888
 <211> 324
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1888
 Met Asn Val Gln Arg Lys Leu Leu Ala Ile Val Gly Ala Phe Met Ala
 1 5 10 15
 Gly Ser Leu Ala Leu Gly Thr Pro Thr Ala Gln Ala Gln Ser Ile Gly
 20 25 30
 Ser Ser Ala Ser Gln Arg Thr Glu Val Leu Arg Gly Leu Thr Ser Ser
 35 40 45
 Ala Gly Ile Pro Asp Ala Thr Ala Pro Glu Gly Gly Ala Lys Val Val
 50 55 60
 Val Phe Gly Asp Ser His Ala Ser Gly Thr Asn Ala Pro Phe Asp Val
 65 70 75 80
 Asp Glu Arg Gly Cys Leu Lys Gly Asn Gln Ser Trp Pro Asp Gln Leu
 85 90 95
 Gln Ala Gln Gln Gly Leu Gln Gln Gly Glu Leu Ile Asp Leu Ser Cys
 100 105 110
 Asn Gly Ala Ser Ile Asn Ser Thr Gly Phe His Phe Ser Asp Glu Val
 115 120 125
 Arg His Ala Glu Ala Leu Gly Ala Ile Gly Pro Asn Thr Glu Asn Ile
 130 135 140
 Phe Ile Gln Phe Gly Lys Asn Asp Gln Trp Gly His Ser Pro Ile Asn
 145 150 155 160
 Leu Arg Tyr Ser Val Ile Asn Cys Leu Phe Asp Ala Ala Asn Gly Cys
 165 170 175
 Gly Glu Lys Ala Val Ala Ala Gly Thr Met Gln Asp Pro Ser Ser Val
 180 185 190
 Thr Gly Glu Asn Tyr Ala Gln Arg Met Lys Pro Val Ile Asp Tyr Leu
 195 200 205
 Lys Tyr Tyr Ala Pro Asn Ala Gln Ile Thr Leu Leu Gly Tyr Gln Glu
 210 215 220

Tyr Thr Pro Arg Ser Gly Ser Glu Ile Cys Val Arg Val Gly Gly Thr
 225 230 235 240
 Glu Leu Arg Lys Pro Asp Ala Thr Asn Leu Val Ser Tyr Met Asn Asn
 245 250 255
 Leu Glu Ser Ala Ile Phe Glu Ala Ser Glu Ile Leu Asp Val Gln His
 260 265 270
 Ala Asn Leu Arg Glu Ala Thr Ala Gly His Ser Ser Cys Ser Ala Glu
 275 280 285
 Pro Trp Val Asn Gly Val Leu Asp Met Arg Val Asn Ala Val Gly Gly
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 Gly Thr Leu Met

<210> 1889
 <211> 1056
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (71)..(1033)
 <223> RXA00713

<400> 1889
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 Met Thr Lys Val Ala Glu Leu Asp Gln Glu Trp Ser Glu
 1 5 10
 gta gat gac gcg gaa tta gac gcg caa agc gct ggc act tct gat agt 157
 Val Asp Asp Ala Glu Leu Asp Ala Gln Ser Ala Gly Thr Ser Asp Ser
 15 20 25
 tcc agc aca gac gac ttc gct gac gca gaa aac act tct gaa aat ctg 205
 Ser Ser Thr Asp Asp Phe Ala Asp Ala Glu Asn Thr Ser Glu Asn Leu
 30 35 40 45
 gga ccc atc ggc cca gaa cca ctc cct gaa cca gat ggg gat gtt ccg 253
 Gly Pro Ile Gly Pro Glu Pro Leu Pro Glu Pro Asp Gly Asp Val Pro
 50 55 60
 gca tcg ggt ttc caa gtg cag ctc gat aat ttt gaa ggt cct ttt gac 301
 Ala Ser Gly Phe Gln Val Gln Leu Asp Asn Phe Glu Gly Pro Phe Asp
 65 70 75
 ctt ctc ctg cag ctg att acc aag aag aaa ctt gat gtc act gaa gtt 349
 Leu Leu Leu Gln Leu Ile Thr Lys Lys Lys Leu Asp Val Thr Glu Val
 80 85 90
 gcc ttg gcc cag gtg acc gac gag ttt att gct tac acc cga aaa ctg 397
 Ala Leu Ala Gln Val Thr Asp Glu Phe Ile Ala Tyr Thr Arg Lys Leu

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gtc gac gat gaa gat gat ctc gaa ttg ctc gaa ata aag gat ctc ctt Val Asp Asp Glu Asp Asp Leu Glu Leu Leu Glu Ile Lys Asp Leu Leu 145 150 155			541
ttc gcc agg ttg ttg cag tat cgc gct tac aag caa gtt gcg gaa atg Phe Ala Arg Leu Leu Gln Tyr Arg Ala Tyr Lys Gln Val Ala Glu Met 160 165 170			589
ttt gcg caa tgg cag cga gat gct cga cgc agg tac ccg cgc gct gtc Phe Ala Gln Trp Gln Arg Asp Ala Arg Arg Arg Tyr Pro Arg Ala Val 175 180 185			637
tca tta gaa act cag ttt gcc aac ctc ttg ccg ccc gtt tcc ttg ggt Ser Leu Glu Thr Gln Phe Ala Asn Leu Leu Pro Pro Val Ser Leu Gly 190 195 200 205			685
cat tcc tta aaa agt ttc agc gag ttg gct gct gtg gtg ttt cgt ccg His Ser Leu Lys Ser Phe Ser Glu Leu Ala Ala Val Val Phe Arg Pro 210 215 220			733
aaa ccc cca gag acg gtg aaa aca gat cac gtg cac caa gtt gcg gtg Lys Pro Pro Glu Thr Val Lys Thr Asp His Val His Gln Val Ala Val 225 230 235			781
tca gtt cca gag caa gcg ggc agg att ctt aac acg ttg aaa ctt gcc Ser Val Pro Glu Gln Ala Gly Arg Ile Leu Asn Thr Leu Lys Leu Ala 240 245 250			829
gga att gat cat tat ttg agc ttt cag ctg ctc aca cgt gat tgt acc Gly Ile Asp His Tyr Leu Ser Phe Gln Leu Leu Thr Arg Asp Cys Thr 255 260 265			877
gcg tca atg gaa gtg att ggc cgc ttc ctt gcc ttg ctg gaa ttg tat Ala Ser Met Glu Val Ile Gly Arg Phe Leu Ala Leu Leu Glu Leu Tyr 270 275 280 285			925
aag gca cgc gct att gaa acc ttg caa gaa gag cca ctc ggc gag ctt Lys Ala Arg Ala Ile Glu Thr Leu Gln Glu Glu Pro Leu Gly Glu Leu 290 295 300			973
aaa gtt tcg tgg act ggc att gat gtc gat cca gca gtc gtc gcg gcg Lys Val Ser Trp Thr Gly Ile Asp Val Asp Pro Ala Val Val Ala Ala 305 310 315			1021
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<210> 1890

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 1890

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Asp Asp Phe Ala Asp Ala Glu Asn Thr Ser Glu Asn Leu Gly Pro Ile
35 40 45
Gly Pro Glu Pro Leu Pro Glu Pro Asp Gly Asp Val Pro Ala Ser Gly
50 55 60
Phe Gln Val Gln Leu Asp Asn Phe Glu Gly Pro Phe Asp Leu Leu Leu
65 70 75 80
Gln Leu Ile Thr Lys Lys Lys Leu Asp Val Thr Glu Val Ala Leu Ala
85 90 95
Gln Val Thr Asp Glu Phe Ile Ala Tyr Thr Arg Lys Leu Gly Glu Thr
100 105 110
Ser Asp Leu Asp Glu Thr Thr Glu Phe Leu Val Val Ala Ala Thr Leu
115 120 125
Leu Asp Leu Lys Thr Ala Arg Leu Leu Pro Arg Gly Glu Val Asp Asp
130 135 140
Glu Asp Asp Leu Glu Leu Leu Glu Ile Lys Asp Leu Leu Phe Ala Arg
145 150 155 160
Leu Leu Gln Tyr Arg Ala Tyr Lys Gln Val Ala Glu Met Phe Ala Gln
165 170 175
Trp Gln Arg Asp Ala Arg Arg Arg Tyr Pro Arg Ala Val Ser Leu Glu
180 185 190
Thr Gln Phe Ala Asn Leu Leu Pro Pro Val Ser Leu Gly His Ser Leu
195 200 205
Lys Ser Phe Ser Glu Leu Ala Ala Val Val Phe Arg Pro Lys Pro Pro
210 215 220
Glu Thr Val Lys Thr Asp His Val His Gln Val Ala Val Ser Val Pro
225 230 235 240
Glu Gln Ala Gly Arg Ile Leu Asn Thr Leu Lys Leu Ala Gly Ile Asp
245 250 255
His Tyr Leu Ser Phe Gln Leu Leu Thr Arg Asp Cys Thr Ala Ser Met
260 265 270
Glu Val Ile Gly Arg Phe Leu Ala Leu Leu Glu Leu Tyr Lys Ala Arg
275 280 285
Ala Ile Glu Thr Leu Gln Glu Glu Pro Leu Gly Glu Leu Lys Val Ser
290 295 300

Trp Thr Gly Ile Asp Val Asp Pro Ala Val Val Ala Ala Ser Asp Trp
 305 310 315 320

Glu

<210> 1891

<211> 684

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(661)

<223> RXA00714

<400> 1891

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 Met Ala Thr Ile Thr
 1 5
 cgc acc gac aga ctg atc ctc gta ccg ctc act gtt gag ctc gaa gac 163
 Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr Val Glu Leu Glu Asp
 10 15 20
 gag gcc cac cag att tac tct gat tct cga atc tgg gaa cac cgc ccc 211
 Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile Trp Glu His Arg Pro
 25 30 35
 cag gcg cgt cac acc aac gtg cgt gtc acg cgc gac atc atc aag cgc 259
 Gln Ala Arg His Thr Asn Val Arg Val Thr Arg Asp Ile Ile Lys Arg
 40 45 50
 acc aat gaa agc tgg ggc aag aaa gac ctt ggc ccc tgg ggt gtt tac 307
 Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly Pro Trp Gly Val Tyr
 55 60 65
 ctc cgt gac cgc cca tcg gaa ttc gtt ggc gtt ggt ggc gtt gaa ctc 355
 Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val Gly Gly Val Glu Leu
 70 75 80 85
 atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta 403
 Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu
 90 95 100
 tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc 451
 Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala
 105 110 115
 acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc 499
 Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr
 120 125 130
 aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc 547
 Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro
 135 140 145
 gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct 595

Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro
 150 155 160 165

gat gtg aga att tat tct gac cgt ccg cta tcg gat gaa att ctt gaa 643
 Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser Asp Glu Ile Leu Glu
 170 175 180

atg ctc aag caa cga cca tagaccagaa aatctcaccc ctt 684
 Met Leu Lys Gln Arg Pro
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<210> 1892

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 1892

Met Ala Thr Ile Thr Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr
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Val Glu Leu Glu Asp Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile
 20 25 30

Trp Glu His Arg Pro Gln Ala Arg His Thr Asn Val Arg Val Thr Arg
 35 40 45

Asp Ile Ile Lys Arg Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly
 50 55 60

Pro Trp Gly Val Tyr Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val
 65 70 75 80

Gly Gly Val Glu Leu Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg
 85 90 95

Leu Arg Pro Asp Leu Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn
 100 105 110

Ala Ala Thr Leu Ala Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr
 115 120 125

Ala Arg Val Thr Thr Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys
 130 135 140

Leu Gly Leu Thr Pro Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp
 145 150 155 160

Asp Pro Asn Glu Pro Asp Val Arg Ile Tyr Ser Asp Arg Pro Leu Ser
 165 170 175

Asp Glu Ile Leu Glu Met Leu Lys Gln Arg Pro
 180 185

<210> 1893

<211> 636

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXA00716

<400> 1893

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                                         Met Glu Ser Ile Leu
                                         1      5

ttg gtg gtc gat acc cca gtt tca gca cgc acg ctg gct ggg gtg ttg 163
Leu Val Val Asp Thr Pro Val Ser Ala Arg Thr Leu Ala Gly Val Leu
                        10                        15                        20

ggc att gac gtg cct gca aca gag gca att ttg aag gaa atg gcc ttt 211
Gly Ile Asp Val Pro Ala Thr Glu Ala Ile Leu Lys Glu Met Ala Phe
                        25                        30                        35

gag ctt tct gaa cgg ggc agc ggc att gat ctg cgg gaa acg gca gaa 259
Glu Leu Ser Glu Arg Gly Ser Gly Ile Asp Leu Arg Glu Thr Ala Glu
                        40                        45                        50

gga tgg cgc tat tac acc cgc ccg gaa aat gcg gac atc gtc gag caa 307
Gly Trp Arg Tyr Tyr Thr Arg Pro Glu Asn Ala Asp Ile Val Glu Gln
                        55                        60                        65

ttc ctc ctc gat gga aac caa acc aga ctg tcc cgt gca gca ttg gaa 355
Phe Leu Leu Asp Gly Asn Gln Thr Arg Leu Ser Arg Ala Ala Leu Glu
                        70                        75                        80                        85

aca ctc gcg gtg gtg gca tat cgg cag ccg gtc aca cgc tcc cag att 403
Thr Leu Ala Val Val Ala Tyr Arg Gln Pro Val Thr Arg Ser Gln Ile
                        90                        95                        100

tca gca gtg cgc gga gta aat gtc gac ggc gtc atg aga acc ttg cag 451
Ser Ala Val Arg Gly Val Asn Val Asp Gly Val Met Arg Thr Leu Gln
                        105                        110                        115

ctt cga ggc cta gtc aaa gaa gtc gat gtg gac gaa tca acg ggc gca 499
Leu Arg Gly Leu Val Lys Glu Val Asp Val Asp Glu Ser Thr Gly Ala
                        120                        125                        130

cac cgc tat ggc aca acg gaa ttg ctg ctt gag ctg ttg ggt att gat 547
His Arg Tyr Gly Thr Thr Glu Leu Leu Leu Glu Leu Leu Gly Ile Asp
                        135                        140                        145

tct ttg gat aaa tta cca gat cta gca ccg ctt ttg ccg gat gtt gac 595
Ser Leu Asp Lys Leu Pro Asp Leu Ala Pro Leu Leu Pro Asp Val Asp
                        150                        155                        160                        165

tcc att gat gaa gac ttc taaagcatca gttaaagccc cga 636
Ser Ile Asp Glu Asp Phe
                        170

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<210> 1894

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1894

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Leu Ala Gly Val Leu Gly Ile Asp Val Pro Ala Thr Glu Ala Ile Leu
          20           25           30

Lys Glu Met Ala Phe Glu Leu Ser Glu Arg Gly Ser Gly Ile Asp Leu
          35           40           45

Arg Glu Thr Ala Glu Gly Trp Arg Tyr Tyr Thr Arg Pro Glu Asn Ala
          50           55           60

Asp Ile Val Glu Gln Phe Leu Leu Asp Gly Asn Gln Thr Arg Leu Ser
          65           70           75           80

Arg Ala Ala Leu Glu Thr Leu Ala Val Val Ala Tyr Arg Gln Pro Val
          85           90           95

Thr Arg Ser Gln Ile Ser Ala Val Arg Gly Val Asn Val Asp Gly Val
          100          105          110

Met Arg Thr Leu Gln Leu Arg Gly Leu Val Lys Glu Val Asp Val Asp
          115          120          125

Glu Ser Thr Gly Ala His Arg Tyr Gly Thr Thr Glu Leu Leu Leu Glu
          130          135          140

Leu Leu Gly Ile Asp Ser Leu Asp Lys Leu Pro Asp Leu Ala Pro Leu
          145          150          155          160

Leu Pro Asp Val Asp Ser Ile Asp Glu Asp Phe
          165          170

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<210> 1895

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXA00719

<400> 1895

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tcatccacct agtggaagcc tccgctgaaa ggagcaacca gtg act gat aaa cac 115
                               Val Thr Asp Lys His
                               1           5

acc atg cct ggt gaa gag gac gac acc gta ttc gtc tac cac acc cac 163
Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe Val Tyr His Thr His
          10           15           20

aaa ggc gaa atg gac gtc gaa ggt gcg ttt gct gac gaa gaa gaa cta 211
Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala Asp Glu Glu Glu Leu
          25           30           35

gca cca cac ggc ggt tgg gct tcc gca gat ttc gac cca gca gaa ttc 259

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Gly	Tyr	Glu	Asp	Ser	Asp	Asp	Asp	Phe	Asp	Ala	Glu	Asp	Phe	Asp	Glu		
	55					60					65						
aca	gag	ttc	tcc	aac	cct	gat	ttc	ggc	gaa	gac	tac	tct	gat	gaa	gac	355	
Thr	Glu	Phe	Ser	Asn	Pro	Asp	Phe	Gly	Glu	Asp	Tyr	Ser	Asp	Glu	Asp		
	70				75					80					85		
tgg	gaa	gaa	atc	gag	acc	gca	ttc	gga	ttc	gac	cca	agc	cac	ctt	gaa	403	
Trp	Glu	Glu	Ile	Glu	Thr	Ala	Phe	Gly	Phe	Asp	Pro	Ser	His	Leu	Glu		
				90				95						100			
gaa	gct	ctc	tgc	acg	gtc	gct	atc	gtc	gga	cgc	cca	aat	gtt	ggt	aaa	451	
Glu	Ala	Leu	Cys	Thr	Val	Ala	Ile	Val	Gly	Arg	Pro	Asn	Val	Gly	Lys		
		105						110					115				
tca	acc	ttg	gtg	aac	cgc	ttt	att	gga	cgt	cga	gaa	gca	gtc	gtg	gaa	499	
Ser	Thr	Leu	Val	Asn	Arg	Phe	Ile	Gly	Arg	Arg	Glu	Ala	Val	Val	Glu		
		120					125					130					
gat	ttc	ccc	ggc	gta	acc	cgt	gac	cgc	atc	tcc	tac	atc	tct	gac	tgg	547	
Asp	Phe	Pro	Gly	Val	Thr	Arg	Asp	Arg	Ile	Ser	Tyr	Ile	Ser	Asp	Trp		
	135					140					145						
ggt	gga	cac	cgt	ttc	tgg	gtt	cag	gac	aca	ggc	gga	tgg	gat	cct	aac	595	
Gly	Gly	His	Arg	Phe	Trp	Val	Gln	Asp	Thr	Gly	Gly	Trp	Asp	Pro	Asn		
	150				155				160						165		
gtc	aag	ggc	atc	cac	gca	tcg	atc	gca	cag	caa	gca	gaa	gtt	gct	atg	643	
Val	Lys	Gly	Ile	His	Ala	Ser	Ile	Ala	Gln	Gln	Ala	Glu	Val	Ala	Met		
				170				175						180			
agc	act	gcc	gat	gtc	atc	gta	ttc	gtc	gtg	gac	acc	aag	gtg	ggc	atc	691	
Ser	Thr	Ala	Asp	Val	Ile	Val	Phe	Val	Val	Asp	Thr	Lys	Val	Gly	Ile		
			185					190					195				
acc	gaa	act	gac	tca	gtg	atg	gca	gca	aaa	ctg	ttg	cgc	tcg	gaa	gtg	739	
Thr	Glu	Thr	Asp	Ser	Val	Met	Ala	Ala	Lys	Leu	Leu	Arg	Ser	Glu	Val		
		200					205					210					
cca	gtg	atc	ttg	gtt	gcg	aac	aaa	ttc	gac	tcc	gac	agc	cag	tgg	gct	787	
Pro	Val	Ile	Leu	Val	Ala	Asn	Lys	Phe	Asp	Ser	Asp	Ser	Gln	Trp	Ala		
	215					220					225						
gac	atg	gct	gag	ttc	tac	agc	ctc	ggc	ctt	ggc	gat	cca	tac	cca	gtt	835	
Asp	Met	Ala	Glu	Phe	Tyr	Ser	Leu	Gly	Leu	Gly	Asp	Pro	Tyr	Pro	Val		
	230				235				240					245			
tca	gcc	cag	cat	gga	cgt	ggt	ggc	gct	gac	gtt	ttg	gac	aaa	gtc	ctt	883	
Ser	Ala	Gln	His	Gly	Arg	Gly	Gly	Ala	Asp	Val	Leu	Asp	Lys	Val	Leu		
				250				255						260			
gaa	ctc	ttc	cca	gaa	gag	cct	cgc	tcc	aag	tcc	atc	gtg	gaa	ggc	cct	931	
Glu	Leu	Phe	Pro	Glu	Glu	Pro	Arg	Ser	Lys	Ser	Ile	Val	Glu	Gly	Pro		
		265					270					275					
cgt	cgt	gtc	gcc	ctt	gtg	ggt	aag	cca	aac	gtg	ggt	aag	tct	tca	ctg	979	
Arg	Arg	Val	Ala	Leu	Val	Gly	Lys	Pro	Asn	Val	Gly	Lys	Ser	Ser	Leu		

280	285	290	
ctc aac aag ttt gct ggc gag acc cgc tct gtc gtg gac aat gtt gca Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val Val Asp Asn Val Ala 295 300 305			1027
gga acc acc gtt gac ccc gtt gac tcc ctg att cag ctg gat caa aaa Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile Gln Leu Asp Gln Lys 310 315 320 325			1075
ctg tgg aaa ttc gtg gat act gct ggt ctt cgc aaa aag gtc aag act Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg Lys Lys Val Lys Thr 330 335 340			1123
gca tct ggc cac gag tac tac gca tca ctg cgt acc cac ggt gcc atc Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg Thr His Gly Ala Ile 345 350 355			1171
gat gca gct gag ctg tgt gtt ttg ctt atc gat tcc tcc gaa ccc atc Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp Ser Ser Glu Pro Ile 360 365 370			1219
acc gag cag gat cag cgc gtg ctc gca atg atc acc gat gcc ggt aag Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile Thr Asp Ala Gly Lys 375 380 385			1267
gca ctg gtt att gcg ttc aac aag tgg gat ctc atg gat gaa gat cgc Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu Met Asp Glu Asp Arg 390 395 400 405			1315
cgc atc gat ttg gat cgc gaa ctt gat ctc cag ttg gca cac gtg cct Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln Leu Ala His Val Pro 410 415 420			1363
tgg gca aag cgc atc aac atc tcc gcc aaa acc ggt cgt gca ctg cag Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr Gly Arg Ala Leu Gln 425 430 435			1411
cgc ctc gag cca gca atg ttg gaa gcg ctc gac aac tgg gat cgc cgt Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp Asn Trp Asp Arg Arg 440 445 450			1459
atc tcc act ggt cag ctg aac acc tgg ctg cgt gaa gca att gct gcg Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala 455 460 465			1507
aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala 470 475 480 485			1555
acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly 490 495 500			1603
ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu 505 510 515			1651
cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg 520 525 530			1699

gag cgc cgc ggc aag ggc gga aac aag cag taaagcttga ttttcctaa 1749
Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
535 540

aag 1752

<210> 1896

<211> 543

<212> PRT

<213> Corynebacterium glutamicum

<400> 1896

Val Thr Asp Lys His Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe
1 5 10 15
Val Tyr His Thr His Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala
20 25 30
Asp Glu Glu Glu Leu Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe
35 40 45
Asp Pro Ala Glu Phe Gly Tyr Glu Asp Ser Asp Asp Phe Asp Ala
50 55 60
Glu Asp Phe Asp Glu Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp
65 70 75 80
Tyr Ser Asp Glu Asp Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp
85 90 95
Pro Ser His Leu Glu Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg
100 105 110
Pro Asn Val Gly Lys Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg
115 120 125
Glu Ala Val Val Glu Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser
130 135 140
Tyr Ile Ser Asp Trp Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly
145 150 155 160
Gly Trp Asp Pro Asn Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln
165 170 175
Ala Glu Val Ala Met Ser Thr Ala Asp Val Ile Val Phe Val Val Asp
180 185 190
Thr Lys Val Gly Ile Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu
195 200 205
Leu Arg Ser Glu Val Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser
210 215 220
Asp Ser Gln Trp Ala Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly
225 230 235 240
Asp Pro Tyr Pro Val Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val
245 250 255

Leu Asp Lys Val Leu Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser
 260 265 270
 Ile Val Glu Gly Pro Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val
 275 280 285
 Gly Lys Ser Ser Leu Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val
 290 295 300
 Val Asp Asn Val Ala Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile
 305 310 315 320
 Gln Leu Asp Gln Lys Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg
 325 330 335
 Lys Lys Val Lys Thr Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg
 340 345 350
 Thr His Gly Ala Ile Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp
 355 360 365
 Ser Ser Glu Pro Ile Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile
 370 375 380
 Thr Asp Ala Gly Lys Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu
 385 390 395 400
 Met Asp Glu Asp Arg Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln
 405 410 415
 Leu Ala His Val Pro Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr
 420 425 430
 Gly Arg Ala Leu Gln Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp
 435 440 445
 Asn Trp Asp Arg Arg Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg
 450 455 460
 Glu Ala Ile Ala Ala Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro
 465 470 475 480
 Arg Val Leu Phe Ala Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val
 485 490 495
 Leu Phe Thr Thr Gly Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu
 500 505 510
 Arg Lys Phe Arg Glu Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile
 515 520 525
 Ala Val Arg Val Arg Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
 530 535 540

<210> 1897

<211> 671

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(648)

<223> RXA00724

<400> 1897

atc ggt gag gaa gtc ctc gcc gga cgc caa gcc tat gtg gtg tgt ccg	48
Ile Gly Glu Glu Val Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro	
1 5 10 15	
cgc att gaa ggc gaa ggc ggc gtg ctg gaa atc cac gcc tat ctt tcc	96
Arg Ile Glu Gly Glu Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser	
20 25 30	
gaa cag gta tat cca gga ttg aat gtt gga atg ctg cac ggt cgc atg	144
Glu Gln Val Tyr Pro Gly Leu Asn Val Gly Met Leu His Gly Arg Met	
35 40 45	
gac acg gat ctc aaa gat tcg gtc atg cag gaa ttc gcc caa ggt gag	192
Asp Thr Asp Leu Lys Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu	
50 55 60	
atc gat att ttg gtc gcc acc acg gtc att gag gtc ggt att gac gtt	240
Ile Asp Ile Leu Val Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val	
65 70 75 80	
gcc aac gcc acc gtc atg ctc atc cgc gag gcg gaa cgc ttc ggc gtt	288
Ala Asn Ala Thr Val Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val	
85 90 95	
tcc cag atc cac cag ctg cgc ggc cgt gtt ggc cgt ggg cag cac gat	336
Ser Gln Ile His Gln Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp	
100 105 110	
tcc ctc tgc ctg ctg cac acc acc ttc gac gag gac tcc cca caa ggc	384
Ser Leu Cys Leu Leu His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly	
115 120 125	
caa cgc ctc gcc gca att tcc acc aca acc gac ggt ttt caa ctc tct	432
Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser	
130 135 140	
gaa ctt gat ttg cag gta cgc caa gaa ggc gac gtg ttg ggc acc cgc	480
Glu Leu Asp Leu Gln Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg	
145 150 155 160	
cag tcc ggc agc gac acc aaa ctc cgt cac ctc tcg ttt atc agc gac	528
Gln Ser Gly Ser Asp Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp	
165 170 175	
caa aaa atc atc gag cgt gcg ctt atc gac gcc acc gag ctg gtt gcc	576
Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala	
180 185 190	
gcc agc cgt tcc agg gcg ctt gag ctg gtc agc gac atc gca atg atc	624
Ala Ser Arg Ser Arg Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile	
195 200 205	
aac cag gaa tac ctg gaa aag agc tgatattgat agggtttaag tca	671
Asn Gln Glu Tyr Leu Glu Lys Ser	
210 215	

<210> 1898

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 1898

Ile Gly Glu Glu Val Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro
1 5 10 15
Arg Ile Glu Gly Glu Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser
20 25 30
Glu Gln Val Tyr Pro Gly Leu Asn Val Gly Met Leu His Gly Arg Met
35 40 45
Asp Thr Asp Leu Lys Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu
50 55 60
Ile Asp Ile Leu Val Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val
65 70 75 80
Ala Asn Ala Thr Val Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val
85 90 95
Ser Gln Ile His Gln Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp
100 105 110
Ser Leu Cys Leu Leu His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly
115 120 125
Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser
130 135 140
Glu Leu Asp Leu Gln Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg
145 150 155 160
Gln Ser Gly Ser Asp Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp
165 170 175
Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala
180 185 190
Ala Ser Arg Ser Arg Ala Leu Glu Leu Val Ser Asp Ile Ala Met Ile
195 200 205
Asn Gln Glu Tyr Leu Glu Lys Ser
210 215

<210> 1899

<211> 164

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(141)

<223> RXA00726

<400> 1899

cac gaa atg ggc ttc gcc cac gaa gtc gcc gac cag gtc gtg ttc atg 48
 His Glu Met Gly Phe Ala His Glu Val Ala Asp Gln Val Val Phe Met
 1 5 10 15

gcc gat gga gtt gtc gtt gaa gcc gga acc ccc gaa caa gtt ctg gac 96
 Ala Asp Gly Val Val Val Glu Ala Gly Thr Pro Glu Gln Val Leu Asp
 20 25 30

aat cca aag gaa cag cgc acc aaa gac ttc ctg tct tct ctg ctc 141
 Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe Leu Ser Ser Leu Leu
 35 40 45

taaccttttc gggctcttaaa aaa 164

<210> 1900

<211> 47

<212> PRT

<213> Corynebacterium glutamicum

<400> 1900

His Glu Met Gly Phe Ala His Glu Val Ala Asp Gln Val Val Phe Met
 1 5 10 15

Ala Asp Gly Val Val Val Glu Ala Gly Thr Pro Glu Gln Val Leu Asp
 20 25 30

Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe Leu Ser Ser Leu Leu
 35 40 45

<210> 1901

<211> 702

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(679)

<223> RXA00740

<400> 1901

gttataaata ttaaagtacg ctaaccatgg gtgcaggggg agacttctac agcagtcacg 60

gtccacacca cgactgctgt atatattaag gacgtaactc atg ttg aag aat aaa 115
 Met Leu Lys Asn Lys
 1 5

act ctt gcg ctg ctg gct gtc agt acg ctg atg ttt ggc tta tct gct 163
 Thr Leu Ala Leu Leu Ala Val Ser Thr Leu Met Phe Gly Leu Ser Ala
 10 15 20

tgc tct agt gat gct gac ggc ccg gac agt agc ggt gct agt agt agc 211
 Cys Ser Ser Asp Ala Asp Gly Pro Asp Ser Ser Gly Ala Ser Ser Ser
 25 30 35

agt act ggc tca tct tct gca tcg gct gac aca aca gat tct gca gct 259
 Ser Thr Gly Ser Ser Ser Ala Ser Ala Asp Thr Thr Asp Ser Ala Ala
 40 45 50

gtt gat aag gat gct caa tta gac acc ttt atg cgt tct gct gtg gct 307
 Val Asp Lys Asp Ala Gln Leu Asp Thr Phe Met Arg Ser Ala Val Ala
 55 60 65

gat gga tca tct gct gct gtg gct gtg gac aac gct gta ggt aag ggc 355
 Asp Gly Ser Ser Ala Ala Val Ala Val Asp Asn Ala Val Gly Lys Gly
 70 75 80 85

ttt gat aaa gct gat gcg cag gcg gct gcg gag cgc ttg ggt gat ggt 403
 Phe Asp Lys Ala Asp Ala Gln Ala Ala Glu Arg Leu Gly Asp Gly
 90 95 100

ttc caa ttc gct gcg gat tac cag gct gtt ggc tat ttg gaa tct tgg 451
 Phe Gln Phe Ala Ala Asp Tyr Gln Ala Val Gly Tyr Leu Glu Ser Trp
 105 110 115

tac ttt ggt ggc gcg cga agc gag aag ctt gac gag gtg cgt agt gat 499
 Tyr Phe Gly Gly Ala Arg Ser Glu Lys Leu Asp Glu Val Arg Ser Asp
 120 125 130

gtc atc gct cat ttg tct gaa ttg gga ttt aca gat tta gag gct gaa 547
 Val Ile Ala His Leu Ser Glu Leu Gly Phe Thr Asp Leu Glu Ala Glu
 135 140 145

tcc tcg gca tct cgt att aca tta ggt gat tac tgt gat ggg gtc cct 595
 Ser Ser Ala Ser Arg Ile Thr Leu Gly Asp Tyr Cys Asp Gly Val Pro
 150 155 160 165

gag tat tgt gag ttg ttt ttt gat ggc gaa tct cct gac ttg tat gac 643
 Glu Tyr Cys Glu Leu Phe Phe Asp Gly Glu Ser Pro Asp Leu Tyr Asp
 170 175 180

atg ggt acg gag ctt gac tcg tat aag ccc act gaa taaagctatt 689
 Met Gly Thr Glu Leu Asp Ser Tyr Lys Pro Thr Glu
 185 190

tcacttaaag cac 702

<210> 1902
 <211> 193
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1902
 Met Leu Lys Asn Lys Thr Leu Ala Leu Leu Ala Val Ser Thr Leu Met
 1 5 10 15
 Phe Gly Leu Ser Ala Cys Ser Ser Asp Ala Asp Gly Pro Asp Ser Ser
 20 25 30
 Gly Ala Ser Ser Ser Thr Gly Ser Ser Ser Ala Ser Ala Asp Thr
 35 40 45
 Thr Asp Ser Ala Ala Val Asp Lys Asp Ala Gln Leu Asp Thr Phe Met
 50 55 60
 Arg Ser Ala Val Ala Asp Gly Ser Ser Ala Ala Val Ala Val Asp Asn
 65 70 75 80
 Ala Val Gly Lys Gly Phe Asp Lys Ala Asp Ala Gln Ala Ala Ala Glu

85	90	95
Arg Leu Gly Asp Gly Phe Gln Phe Ala Ala Asp Tyr Gln Ala Val Gly		
100	105	110
Tyr Leu Glu Ser Trp Tyr Phe Gly Gly Ala Arg Ser Glu Lys Leu Asp		
115	120	125
Glu Val Arg Ser Asp Val Ile Ala His Leu Ser Glu Leu Gly Phe Thr		
130	135	140
Asp Leu Glu Ala Glu Ser Ser Ala Ser Arg Ile Thr Leu Gly Asp Tyr		
145	150	155
Cys Asp Gly Val Pro Glu Tyr Cys Glu Leu Phe Phe Asp Gly Glu Ser		
165	170	175
Pro Asp Leu Tyr Asp Met Gly Thr Glu Leu Asp Ser Tyr Lys Pro Thr		
180	185	190

Glu

<210> 1903

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA00741

<400> 1903

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tggtgatcac taggtccacc tcgtcttgca tggtgggtcac ctcagtccag aacgcattga 60
ttgacaccga tcaaattgttt gatggattat gatatttagc atg act gat tct ctg 115
                                     Met Thr Asp Ser Leu
                                     1 5

ctt gta tcc atc aga aaa ggc tta ata gaa gag cgt cca tta acg gag 163
Leu Val Ser Ile Arg Lys Gly Leu Ile Glu Glu Arg Pro Leu Thr Glu
                                     10 15 20

ctt ctt cgg gcg tgt atc ttc ctt gga agt gat act aac tcg gac tct 211
Leu Leu Arg Ala Cys Ile Phe Leu Gly Ser Asp Thr Asn Ser Asp Ser
                                     25 30 35

tta caa gag tgg gcg aaa aat gaa tta aat ggt tat ggc tcc att gat 259
Leu Gln Glu Trp Ala Lys Asn Glu Leu Asn Gly Tyr Gly Ser Ile Asp
                                     40 45 50

ggt att ccg gaa tat cgc aaa ttg aaa gga cct cct gta ttc gcg aaa 307
Gly Ile Pro Glu Tyr Arg Lys Leu Lys Gly Pro Pro Val Phe Ala Lys
                                     55 60 65

att caa gct ggt aat tca ata atg tct aat atg gta ctg ggg cca cat 355
Ile Gln Ala Gly Asn Ser Ile Met Ser Asn Met Val Leu Gly Pro His
                                     70 75 80 85

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aat gtt cct gaa aga gct cgt aag tat ttc cct gaa gag ctg cat ttt Asn Val Pro Glu Arg Ala Arg Lys Tyr Phe Pro Glu Glu Leu His Phe 90 95 100	403
gat cag ccg att caa acg cta att gaa tgg tcg act agg cag gat ggg Asp Gln Pro Ile Gln Thr Leu Ile Glu Trp Ser Thr Arg Gln Asp Gly 105 110 115	451
att aat tta tcg ccc ccg aat tta ctt cgg gtc cgc gat ctt cat aat Ile Asn Leu Ser Pro Pro Asn Leu Leu Arg Val Arg Asp Leu His Asn 120 125 130	499
gat cag tac gcg cca tta aat caa att ttg aat tta aat gtt tac tta Asp Gln Tyr Ala Pro Leu Asn Gln Ile Leu Asn Leu Asn Val Tyr Leu 135 140 145	547
gat aac tct tat ttt tcg gga att gtg gac cgc atc cga act cta atg Asp Asn Ser Tyr Phe Ser Gly Ile Val Asp Arg Ile Arg Thr Leu Met 150 155 160 165	595
act tcc atg att gcc gac ctc aca cac gca act cct ctg gat gaa cta Thr Ser Met Ile Ala Asp Leu Thr His Ala Thr Pro Leu Asp Glu Leu 170 175 180	643
cca agc agc gaa aag gtt aat gcc acg gtc atg aag cac att gaa aat Pro Ser Ser Glu Lys Val Asn Ala Thr Val Met Lys His Ile Glu Asn 185 190 195	691
aac tac gaa act aca atc act caa gcc aat gga gct gta gcc att ggt Asn Tyr Glu Thr Thr Ile Thr Gln Ala Asn Gly Ala Val Ala Ile Gly 200 205 210	739
aac agc gct aaa gct gtg cag aag gga ttg tcc gtg gat gac cta ctg Asn Ser Ala Lys Ala Val Gln Lys Gly Leu Ser Val Asp Asp Leu Leu 215 220 225	787
aag att atg cag acc att aat cct gaa aag ttc gac tta ggg gaa gct Lys Ile Met Gln Thr Ile Asn Pro Glu Lys Phe Asp Leu Gly Glu Ala 230 235 240 245	835
aga gct gaa gcc gaa gaa agc att caa tcc atc gcg gat gag ttg aag Arg Ala Glu Ala Glu Glu Ser Ile Gln Ser Ile Ala Asp Glu Leu Lys 250 255 260	883
aag gag tct ccg aat aaa ggt ttt atc cag aat gct ttt gaa aag ttg Lys Glu Ser Pro Asn Lys Gly Phe Ile Gln Asn Ala Phe Glu Lys Leu 265 270 275	931
aag gaa ctc agc ata aaa gcc ggc gat aaa gcc ttc act aca atg tta Lys Glu Leu Ser Ile Lys Ala Gly Asp Lys Ala Phe Thr Thr Met Leu 280 285 290	979
aat ctt gta ggt aaa cag ata atc gaa aac atc cca caa ctg gtt tca Asn Leu Val Gly Lys Gln Ile Ile Glu Asn Ile Pro Gln Leu Val Ser 295 300 305	1027
ggt ggc tagagaaatt caaggccgtc agc Gly Gly 310	1056

<210> 1904
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 1904

Met Thr Asp Ser Leu Leu Val Ser Ile Arg Lys Gly Leu Ile Glu Glu
1 5 10 15
Arg Pro Leu Thr Glu Leu Leu Arg Ala Cys Ile Phe Leu Gly Ser Asp
20 25 30
Thr Asn Ser Asp Ser Leu Gln Glu Trp Ala Lys Asn Glu Leu Asn Gly
35 40 45
Tyr Gly Ser Ile Asp Gly Ile Pro Glu Tyr Arg Lys Leu Lys Gly Pro
50 55 60
Pro Val Phe Ala Lys Ile Gln Ala Gly Asn Ser Ile Met Ser Asn Met
65 70 75 80
Val Leu Gly Pro His Asn Val Pro Glu Arg Ala Arg Lys Tyr Phe Pro
85 90 95
Glu Glu Leu His Phe Asp Gln Pro Ile Gln Thr Leu Ile Glu Trp Ser
100 105 110
Thr Arg Gln Asp Gly Ile Asn Leu Ser Pro Pro Asn Leu Leu Arg Val
115 120 125
Arg Asp Leu His Asn Asp Gln Tyr Ala Pro Leu Asn Gln Ile Leu Asn
130 135 140
Leu Asn Val Tyr Leu Asp Asn Ser Tyr Phe Ser Gly Ile Val Asp Arg
145 150 155 160
Ile Arg Thr Leu Met Thr Ser Met Ile Ala Asp Leu Thr His Ala Thr
165 170 175
Pro Leu Asp Glu Leu Pro Ser Ser Glu Lys Val Asn Ala Thr Val Met
180 185 190
Lys His Ile Glu Asn Asn Tyr Glu Thr Thr Ile Thr Gln Ala Asn Gly
195 200 205
Ala Val Ala Ile Gly Asn Ser Ala Lys Ala Val Gln Lys Gly Leu Ser
210 215 220
Val Asp Asp Leu Leu Lys Ile Met Gln Thr Ile Asn Pro Glu Lys Phe
225 230 235 240
Asp Leu Gly Glu Ala Arg Ala Glu Ala Glu Glu Ser Ile Gln Ser Ile
245 250 255
Ala Asp Glu Leu Lys Lys Glu Ser Pro Asn Lys Gly Phe Ile Gln Asn
260 265 270
Ala Phe Glu Lys Leu Lys Glu Leu Ser Ile Lys Ala Gly Asp Lys Ala
275 280 285
Phe Thr Thr Met Leu Asn Leu Val Gly Lys Gln Ile Ile Glu Asn Ile

290

295

300

Pro Gln Leu Val Ser Gly Gly
305 310

<210> 1905

<211> 1773

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1750)

<223> RXA00742

<400> 1905

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agagggggttt tttagtgaac atgataaaac cactttttaca gatggacaca tagatattag 60
taatgatgct tctggagcta agcgtagctt tgggggtcgg gtg aat gtt cag att 115
                               Val Asn Val Gln Ile
                               1 5

aaa ggg cga aag gtt aat gcc aag gct gcc gac tta aat agc tat ccg 163
Lys Gly Arg Lys Val Asn Ala Lys Ala Ala Asp Leu Asn Ser Tyr Pro
                               10 15 20

gtc tca gta gtt gat cta cga ggc ttc gtg aca ctg gct ggt ctc tta 211
Val Ser Val Val Asp Leu Arg Gly Phe Val Thr Leu Ala Gly Leu Leu
                               25 30 35

ttt ttt gtg gtt gat att gat aag aaa tca aat aag aaa tat cca aag 259
Phe Phe Val Val Asp Ile Asp Lys Lys Ser Asn Lys Lys Tyr Pro Lys
                               40 45 50

tat gtt ctt ttg aaa ccg ttt tat att cat gat cta ctg agt aaa gcg 307
Tyr Val Leu Leu Lys Pro Phe Tyr Ile His Asp Leu Leu Ser Lys Ala
                               55 60 65

aag ccg ggc caa aag aca att agc gtc cgc tta aaa ccg tta cca tct 355
Lys Pro Gly Gln Lys Thr Ile Ser Val Arg Leu Lys Arg Leu Pro Ser
                               70 75 80 85

gat gaa gat cga atg gaa gcc ata atc gca tta gcg ctc gca tcg agg 403
Asp Glu Asp Arg Met Glu Ala Ile Ile Ala Leu Ala Leu Ala Ser Arg
                               90 95 100

caa gaa aag ata gtc gag aac ccc agt aac tat ctc tat gaa aat atg 451
Gln Glu Lys Ile Val Glu Asn Pro Ser Asn Tyr Leu Tyr Glu Asn Met
                               105 110 115

gaa tca att act gtt aaa tcg gct gaa ccc ctt aat agg gat aag ctg 499
Glu Ser Ile Thr Val Lys Ser Ala Glu Pro Leu Asn Arg Asp Lys Leu
                               120 125 130

gct gta tat gat ggt agt tcg cca gac cat tcg atc att att cgt act 547
Ala Val Tyr Asp Gly Ser Ser Pro Asp His Ser Ile Ile Ile Arg Thr
                               135 140 145

ggg gat gga att gaa cag ttc gtc aat gcc acc gta gaa ata ata ccc 595
Gly Asp Gly Ile Glu Gln Phe Val Asn Ala Thr Val Glu Ile Ile Pro

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150	155	160	165	
ccg aat atg cag ttt cat caa gcc aat tat aat gtt tcg tgt aat ggg				643
Pro Asn Met Gln Phe His Gln Ala Asn Tyr Asn Val Ser Cys Asn Gly				
	170	175	180	
gtc gtc tat gac aat gtt ttg cat cga aac att gat gat gag cac att				691
Val Val Tyr Asp Asn Val Leu His Arg Asn Ile Asp Asp Glu His Ile				
	185	190	195	
gaa ttg aaa atc gga aag ggg att act ctc cgc cta caa aag ctc gcc				739
Glu Leu Lys Ile Gly Lys Gly Ile Thr Leu Arg Leu Gln Lys Leu Ala				
	200	205	210	
att gat gct ccg ggg agc gtt acg gtt gag ttt caa gat agt ctt cct				787
Ile Asp Ala Pro Gly Ser Val Thr Val Glu Phe Gln Asp Ser Leu Pro				
	215	220	225	
gaa cgg tta aaa gac att gag ttc ttc cta gga gtg ctt cag gcg aat				835
Glu Arg Leu Lys Asp Ile Glu Phe Phe Leu Gly Val Leu Gln Ala Asn				
	230	235	240	245
acg ttt ttt att aat gaa gaa cct gtt gtg ttg aag att aac tcg aac				883
Thr Phe Phe Ile Asn Glu Glu Pro Val Val Leu Lys Ile Asn Ser Asn				
	250	255	260	
cgg act gtg gct gac ctt aag gat gaa gcg ggt gtt ctt cgt cag ttg				931
Arg Thr Val Ala Asp Leu Lys Asp Glu Ala Gly Val Leu Arg Gln Leu				
	265	270	275	
gta gaa ata gct aac cat ttc aat att gat ccg tcc ctt att cga att				979
Val Glu Ile Ala Asn His Phe Asn Ile Asp Pro Ser Leu Ile Arg Ile				
	280	285	290	
ggt gag att aca gaa aaa cag ttc tgg cag ttg gat att gtg tat cga				1027
Gly Glu Ile Thr Glu Lys Gln Phe Trp Gln Leu Asp Ile Val Tyr Arg				
	295	300	305	
aca gcc gtt aag gga gaa tac gta aag aat tta gag gtt aaa gat gag				1075
Thr Ala Val Lys Gly Glu Tyr Val Lys Asn Leu Glu Val Lys Asp Glu				
	310	315	320	325
act aga ctt ata ttg cag cct ttt ggt cgt tgg aat ctt gcg ttg ata				1123
Thr Arg Leu Ile Leu Gln Pro Phe Gly Arg Trp Asn Leu Ala Leu Ile				
	330	335	340	
gct cac cct ggt gat gtt gca ggg gag tgg act tat cat gaa gta att				1171
Ala His Pro Gly Asp Val Ala Gly Glu Trp Thr Tyr His Glu Val Ile				
	345	350	355	
tcc aag cgt cat cat ttt gct atg aca cct tca acg gat cgg agc gac				1219
Ser Lys Arg His His Phe Ala Met Thr Pro Ser Thr Asp Arg Ser Asp				
	360	365	370	
tcc tca atc gag cga gtg acg ccg tac gag ctc att gat aat cga tgg				1267
Ser Ser Ile Glu Arg Val Thr Pro Tyr Glu Leu Ile Asp Asn Arg Trp				
	375	380	385	
ctt cca tca gta ttg aat ctg cat ttg gat aag ctt gtt gat ttc tat				1315
Leu Pro Ser Val Leu Asn Leu His Leu Asp Lys Leu Val Asp Phe Tyr				
	390	395	400	405

tca gcg ctt gaa gaa act gtt gat gtt gat aat ctc gcc aca tgg atg 1363
 Ser Ala Leu Glu Glu Thr Val Asp Val Asp Asn Leu Ala Thr Trp Met
 410 415 420

gtg ctt cgc cta att aag gca gct gat tct gag cag agc agg aaa act 1411
 Val Leu Arg Leu Ile Lys Ala Ala Asp Ser Glu Gln Ser Arg Lys Thr
 425 430 435

gca ttt ctt ata gca gct caa gct ctc aat gat tgg ctc gtg gaa cga 1459
 Ala Phe Leu Ile Ala Ala Gln Ala Leu Asn Asp Trp Leu Val Glu Arg
 440 445 450

gat cga gaa gag tcg cca att tac agg ctt aat ggt tgg caa att ttg 1507
 Asp Arg Glu Glu Ser Pro Ile Tyr Arg Leu Asn Gly Trp Gln Ile Leu
 455 460 465

tat cgc caa act gga tta ctg gat tca caa aga aca gaa att cga tct 1555
 Tyr Arg Gln Thr Gly Leu Leu Asp Ser Gln Arg Thr Glu Ile Arg Ser
 470 475 480 485

ttt agg cat aat ctt gat caa aca atg cac cca gac aac tat agc gag 1603
 Phe Arg His Asn Leu Asp Gln Thr Met His Pro Asp Asn Tyr Ser Glu
 490 495 500

att atg att ggt tgc gct ttg ctt ctt gac gat aga gaa gag gcg aat 1651
 Ile Met Ile Gly Cys Ala Leu Leu Leu Asp Asp Arg Glu Glu Ala Asn
 505 510 515

ttt ttg ctt act cag ctt tcg gtt gat cga cgc gca gtt ttt aat gaa 1699
 Phe Leu Leu Thr Gln Leu Ser Val Asp Arg Arg Ala Val Phe Asn Glu
 520 525 530

tgg ccg ata gct caa ttg atg acg ggt gcc cta aaa gaa gag att gaa 1747
 Trp Pro Ile Ala Gln Leu Met Thr Gly Ala Leu Lys Glu Glu Ile Glu
 535 540 545

aaa tgagttctga gatcttgatt taa 1773
 Lys
 550

<210> 1906

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 1906

Val Asn Val Gln Ile Lys Gly Arg Lys Val Asn Ala Lys Ala Ala Asp
 1 5 10 15

Leu Asn Ser Tyr Pro Val Ser Val Val Asp Leu Arg Gly Phe Val Thr
 20 25 30

Leu Ala Gly Leu Leu Phe Phe Val Val Asp Ile Asp Lys Lys Ser Asn
 35 40 45

Lys Lys Tyr Pro Lys Tyr Val Leu Leu Lys Pro Phe Tyr Ile His Asp
 50 55 60

Leu Leu Ser Lys Ala Lys Pro Gly Gln Lys Thr Ile Ser Val Arg Leu

65	70	75	80
Lys Arg Leu Pro Ser Asp Glu Asp Arg Met Glu Ala Ile Ile Ala Leu	85	90	95
Ala Leu Ala Ser Arg Gln Glu Lys Ile Val Glu Asn Pro Ser Asn Tyr	100	105	110
Leu Tyr Glu Asn Met Glu Ser Ile Thr Val Lys Ser Ala Glu Pro Leu	115	120	125
Asn Arg Asp Lys Leu Ala Val Tyr Asp Gly Ser Ser Pro Asp His Ser	130	135	140
Ile Ile Ile Arg Thr Gly Asp Gly Ile Glu Gln Phe Val Asn Ala Thr	145	150	155
Val Glu Ile Ile Pro Pro Asn Met Gln Phe His Gln Ala Asn Tyr Asn	165	170	175
Val Ser Cys Asn Gly Val Val Tyr Asp Asn Val Leu His Arg Asn Ile	180	185	190
Asp Asp Glu His Ile Glu Leu Lys Ile Gly Lys Gly Ile Thr Leu Arg	195	200	205
Leu Gln Lys Leu Ala Ile Asp Ala Pro Gly Ser Val Thr Val Glu Phe	210	215	220
Gln Asp Ser Leu Pro Glu Arg Leu Lys Asp Ile Glu Phe Phe Leu Gly	225	230	235
Val Leu Gln Ala Asn Thr Phe Phe Ile Asn Glu Glu Pro Val Val Leu	245	250	255
Lys Ile Asn Ser Asn Arg Thr Val Ala Asp Leu Lys Asp Glu Ala Gly	260	265	270
Val Leu Arg Gln Leu Val Glu Ile Ala Asn His Phe Asn Ile Asp Pro	275	280	285
Ser Leu Ile Arg Ile Gly Glu Ile Thr Glu Lys Gln Phe Trp Gln Leu	290	295	300
Asp Ile Val Tyr Arg Thr Ala Val Lys Gly Glu Tyr Val Lys Asn Leu	305	310	315
Glu Val Lys Asp Glu Thr Arg Leu Ile Leu Gln Pro Phe Gly Arg Trp	325	330	335
Asn Leu Ala Leu Ile Ala His Pro Gly Asp Val Ala Gly Glu Trp Thr	340	345	350
Tyr His Glu Val Ile Ser Lys Arg His His Phe Ala Met Thr Pro Ser	355	360	365
Thr Asp Arg Ser Asp Ser Ser Ile Glu Arg Val Thr Pro Tyr Glu Leu	370	375	380
Ile Asp Asn Arg Trp Leu Pro Ser Val Leu Asn Leu His Leu Asp Lys	385	390	395
			400

ttg agg gtg tcc atc gag gtt ccc gac gga aag ata acg gta gag cct 307
 Leu Arg Val Ser Ile Glu Val Pro Asp Gly Lys Ile Thr Val Glu Pro
 55 60 65
 gaa gca atc tat ttg att cct gag aat aag gtt tat tta acg gaa tct 355
 Glu Ala Ile Tyr Leu Ile Pro Glu Asn Lys Val Tyr Leu Thr Glu Ser
 70 75 80 85
 gat gca atg gtg gat tat ttt aac aac cat gcg att ttt act ctg gtg 403
 Asp Ala Met Val Asp Tyr Phe Asn Asn His Ala Ile Phe Thr Leu Val
 90 95 100
 cca tat gca cga cag gcc gtg tct gat tta ggg cag cgt gca ttc cac 451
 Pro Tyr Ala Arg Gln Ala Val Ser Asp Leu Gly Gln Arg Ala Phe His
 105 110 115
 acg cag atc ctc atg cct gcg tta ggt cct ggt gat ttg gtt ttt agt 499
 Thr Gln Ile Leu Met Pro Ala Leu Gly Pro Gly Asp Leu Val Phe Ser
 120 125 130
 aaa tcg acg gcc tca cga gaa tgg tagagaatta cctgatagtt gca 546
 Lys Ser Thr Ala Ser Arg Glu Trp
 135 140

<210> 1908

<211> 141

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1908

Val Gln His Leu Val Leu Ala Asp Val Lys Tyr Arg Glu Leu Ser Ala
 1 5 10 15
 Leu Ser Val Lys Ile Glu Glu Pro Ser Asp Arg Pro Glu Phe Lys Leu
 20 25 30
 Gly Val Thr Val Asn Asp Lys Ser Lys Asp Glu Glu Gly Val Pro Arg
 35 40 45
 Ile Ile Glu Val Ser Leu Arg Val Ser Ile Glu Val Pro Asp Gly Lys
 50 55 60
 Ile Thr Val Glu Pro Glu Ala Ile Tyr Leu Ile Pro Glu Asn Lys Val
 65 70 75 80
 Tyr Leu Thr Glu Ser Asp Ala Met Val Asp Tyr Phe Asn Asn His Ala
 85 90 95
 Ile Phe Thr Leu Val Pro Tyr Ala Arg Gln Ala Val Ser Asp Leu Gly
 100 105 110
 Gln Arg Ala Phe His Thr Gln Ile Leu Met Pro Ala Leu Gly Pro Gly
 115 120 125
 Asp Leu Val Phe Ser Lys Ser Thr Ala Ser Arg Glu Trp
 130 135 140

<210> 1909

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> RXA00745

<400> 1909

tttgacgtgg gatggccaca ccggtgacgg ggtcaatgtg cagaatctgt gcagtgggtga 60

gttcagcatt gttttccgca tcagataacg ccggtgggcga gtg gct tat ctg tac 115
Val Ala Tyr Leu Tyr
1 5

gga tct gcc gat ggg atg ctt aat aca gat ggt ttt aat atg ttt ccg 163
Gly Ser Ala Asp Gly Met Leu Asn Thr Asp Gly Phe Asn Met Phe Pro
10 15 20

cgt gcg tcg tac acc att ctt ggc cct atg gat gct gac gcg gtc ggt 211
Arg Ala Ser Tyr Thr Ile Leu Gly Pro Met Asp Ala Asp Ala Val Gly
25 30 35

gtg tac caa cag cta ctg aac agc acg att ccc atg gat ttg gca cgt 259
Val Tyr Gln Gln Leu Leu Asn Ser Thr Ile Pro Met Asp Leu Ala Arg
40 45 50

ctt gta acc acg cat aat tcc ggt gca agt tat ctt cgc cgc ggt gct 307
Leu Val Thr Thr His Asn Ser Gly Ala Ser Tyr Leu Arg Arg Gly Ala
55 60 65

acc aac gta gtt ttt gaa acg aat ctt gcc ctc ggt gtg aat ccg tat 355
Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu Gly Val Asn Pro Tyr
70 75 80 85

atg aag aaa cgc cga gca aca gaa gca caa cgt ggt aag aag cgt ttt 403
Met Lys Lys Arg Arg Ala Thr Glu Ala Gln Arg Gly Lys Lys Arg Phe
90 95 100

aaa cga gac agt cat tac ggc ggt ggc act gtg acc aca ggt act gct 451
Lys Arg Asp Ser His Tyr Gly Gly Gly Thr Val Thr Thr Gly Thr Ala
105 110 115

gat ttg gat gtg gtg gcg atg cag gcg cgg gca gag cac cgg gaa gaa 499
Asp Leu Asp Val Val Ala Met Gln Ala Arg Ala Glu His Arg Glu Glu
120 125 130

agg ttg gga gaa aaa tct acc cgc aag aaa gag gag ctt gct gca gta 547
Arg Leu Gly Glu Lys Ser Thr Arg Lys Lys Glu Glu Leu Ala Ala Val
135 140 145

gag gcg aaa gag tta gct gcg aag aag ggt ccg cag act gtg gaa gaa 595
Glu Ala Lys Glu Leu Ala Ala Lys Lys Gly Pro Gln Thr Val Glu Glu
150 155 160 165

ggt ctt gct gcg gtg gag aag aaa cac ctg gcg aag cgg taggcgacgt 644
Gly Leu Ala Ala Val Glu Lys Lys His Leu Ala Lys Arg
170 175

ggttggcggt ggg 657

<210> 1910

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 1910

Val Ala Tyr Leu Tyr Gly Ser Ala Asp Gly Met Leu Asn Thr Asp Gly
 1 5 10 15

Phe Asn Met Phe Pro Arg Ala Ser Tyr Thr Ile Leu Gly Pro Met Asp
 20 25 30

Ala Asp Ala Val Gly Val Tyr Gln Gln Leu Leu Asn Ser Thr Ile Pro
 35 40 45

Met Asp Leu Ala Arg Leu Val Thr Thr His Asn Ser Gly Ala Ser Tyr
 50 55 60

Leu Arg Arg Gly Ala Thr Asn Val Val Phe Glu Thr Asn Leu Ala Leu
 65 70 75 80

Gly Val Asn Pro Tyr Met Lys Lys Arg Arg Ala Thr Glu Ala Gln Arg
 85 90 95

Gly Lys Lys Arg Phe Lys Arg Asp Ser His Tyr Gly Gly Gly Thr Val
 100 105 110

Thr Thr Gly Thr Ala Asp Leu Asp Val Val Ala Met Gln Ala Arg Ala
 115 120 125

Glu His Arg Glu Glu Arg Leu Gly Glu Lys Ser Thr Arg Lys Lys Glu
 130 135 140

Glu Leu Ala Ala Val Glu Ala Lys Glu Leu Ala Ala Lys Lys Gly Pro
 145 150 155 160

Gln Thr Val Glu Glu Gly Leu Ala Ala Val Glu Lys Lys His Leu Ala
 165 170 175

Lys Arg

<210> 1911

<211> 1314

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1291)

<223> RXA00746

<400> 1911

aaactacgtt ggtagcaccg cggcgaagat aacttgcacc ggaattatgc gtgggttaca 60

gacgtgccaa atccatggga atcgtgctgt tcagtagctg ttg gta cac acc gac 115
 Leu Val His Thr Asp
 1 5

cgc gtc agc atc cat agg gcc aag aat ggt gta cga cgc acg cgg aaa	163
Arg Val Ser Ile His Arg Ala Lys Asn Gly Val Arg Arg Thr Arg Lys	
10 15 20	
cat att aaa acc atc tgt att aag cat ccc atc ggc aga tcc gta cag	211
His Ile Lys Thr Ile Cys Ile Lys His Pro Ile Gly Arg Ser Val Gln	
25 30 35	
ata agc cac tcg ccc acc gcg tta tct gat gcg gaa aac aat gct gaa	259
Ile Ser His Ser Pro Thr Ala Leu Ser Asp Ala Glu Asn Asn Ala Glu	
40 45 50	
ctc acc act gca cag att ctg cac att gac ccc gtc acc ggt gtg gcc	307
Leu Thr Thr Ala Gln Ile Leu His Ile Asp Pro Val Thr Gly Val Ala	
55 60 65	
atc cca cgt caa aac att ctg ctg ggt gag gat ttt cag act atg gcc	355
Ile Pro Arg Gln Asn Ile Leu Leu Gly Glu Asp Phe Gln Thr Met Ala	
70 75 80 85	
agc tct ttt agt caa atc cgc cat gga tgg ggt atc acc cag ctc atc	403
Ser Ser Phe Ser Gln Ile Arg His Gly Trp Gly Ile Thr Gln Leu Ile	
90 95 100	
gga caa gac ccc aac aga aac caa cca atc cgc tct gct gat acg tgg	451
Gly Gln Asp Pro Asn Arg Asn Gln Pro Ile Arg Ser Ala Asp Thr Trp	
105 110 115	
aca gtg act gga tcg act gga ctc acc ggc ttt aat act gct acg cat	499
Thr Val Thr Gly Ser Thr Gly Leu Thr Gly Phe Asn Thr Ala Thr His	
120 125 130	
aat aca gat gac aca gac gcc act gcc gca tat acc atg ccg gca agc	547
Asn Thr Asp Asp Thr Asp Ala Thr Ala Ala Tyr Thr Met Pro Ala Ser	
135 140 145	
gat cct gcc gta gga cta tgc gca ctg gaa tcc aac aaa gac gca ccg	595
Asp Pro Ala Val Gly Leu Cys Ala Leu Glu Ser Asn Lys Asp Ala Pro	
150 155 160 165	
gtg gat gaa ttt cgc gat ctc agc ctc agt gct tta cgt acc gct acg	643
Val Asp Glu Phe Arg Asp Leu Ser Leu Ser Ala Leu Arg Thr Ala Thr	
170 175 180	
gtc atg tca agc tct ggc tcc gcc gtg att act atg cat gat cct atg	691
Val Met Ser Ser Ser Gly Ser Ala Val Ile Thr Met His Asp Pro Met	
185 190 195	
gtc atg agc acc act ggc gca ttg gaa gca cgt gca tac gtt gac ggc	739
Val Met Ser Thr Thr Gly Ala Leu Glu Ala Arg Ala Tyr Val Asp Gly	
200 205 210	
gaa gtc atc aac cag cac gat ctt gac tca ctg cgt gac cag cta ggt	787
Glu Val Ile Asn Gln His Asp Leu Asp Ser Leu Arg Asp Gln Leu Gly	
215 220 225	
att act aca gac agc gca gat acc acc cct gcc cta cct gct gat ccc	835
Ile Thr Thr Asp Ser Ala Asp Thr Thr Pro Ala Leu Pro Ala Asp Pro	
230 235 240 245	
ttg gca gca ttg ggc ttg agc aca cca act aca tca gct ctt gtc cca	883

Phe Gln Thr Met Ala Ser Ser Phe Ser Gln Ile Arg His Gly Trp Gly
85 90 95

Ile Thr Gln Leu Ile Gly Gln Asp Pro Asn Arg Asn Gln Pro Ile Arg
100 105 110

Ser Ala Asp Thr Trp Thr Val Thr Gly Ser Thr Gly Leu Thr Gly Phe
115 120 125

Asn Thr Ala Thr His Asn Thr Asp Asp Thr Asp Ala Thr Ala Ala Tyr
130 135 140

Thr Met Pro Ala Ser Asp Pro Ala Val Gly Leu Cys Ala Leu Glu Ser
145 150 155 160

Asn Lys Asp Ala Pro Val Asp Glu Phe Arg Asp Leu Ser Leu Ser Ala
165 170 175

Leu Arg Thr Ala Thr Val Met Ser Ser Ser Gly Ser Ala Val Ile Thr
180 185 190

Met His Asp Pro Met Val Met Ser Thr Thr Gly Ala Leu Glu Ala Arg
195 200 205

Ala Tyr Val Asp Gly Glu Val Ile Asn Gln His Asp Leu Asp Ser Leu
210 215 220

Arg Asp Gln Leu Gly Ile Thr Thr Asp Ser Ala Asp Thr Thr Pro Ala
225 230 235 240

Leu Pro Ala Asp Pro Leu Ala Ala Leu Gly Leu Ser Thr Pro Thr Thr
245 250 255

Ser Ala Leu Val Pro Gly Leu Ala Glu Leu Asp Cys Leu Asn Thr Asp
260 265 270

Gln Ala Arg Thr Trp His Asp Arg Asp Asn Ser Ile Gly Thr Gly Lys
275 280 285

Pro Ala Ile Leu Ala Val Ile Asn Ala Glu Leu Ala Asp Asp Tyr Thr
290 295 300

Leu Gln Ile Leu Lys Asn Ser Thr Ala Thr Pro Thr Asp Ser Thr Asp
305 310 315 320

Ser Ser Asp Thr Ala Glu Arg Phe Val Ala Gln Leu Pro Ala Glu Thr
325 330 335

Ala Phe Val Leu Ile Asp Pro Asp Ile Gly Ala Val Thr Asp Leu Phe
340 345 350

Phe Ile Asn Ser Ile Asn Gln Asp Leu Pro Ala Pro Thr Thr Gln Ile
355 360 365

Asn Ser Val Ala Val Asp Gln Arg Asp Pro Asn Ile Ile Tyr Ala Thr
370 375 380

Phe Ala Asn Asp Asp Arg Val Tyr Gln Leu Met Leu Gly
385 390 395

tca cgc cac aca atg cac gtc atc aac gtt cga gat cat aca gtg 688
 Ser Arg His Thr Met His Val Ile Asn Val Arg Asp His Thr Val
 185 190 195

tgaactaccg cgccgctaga gat 711

<210> 1914

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 1914

Met Thr Phe Leu His Arg Ser Ala Ser Phe His Pro Arg Thr His Asp
 1 5 10 15

His Leu Ser Glu Leu Gly Leu Asp Pro Tyr Lys Leu Ser Gln Asp Ile
 20 25 30

Pro Thr Val Ile Tyr Glu Val Gln Pro His Ser Val Phe Ile Leu Lys
 35 40 45

Phe Asn Thr Ala Asp Val Arg Val Tyr Gln Glu His Ser Asp Leu Phe
 50 55 60

Val Arg His Ala Val Leu Val Asp Pro Glu Gln Arg Lys His Glu His
 65 70 75 80

Asp Gln Leu Leu Lys Glu Ile Leu Asp Leu Asp Ala Pro Arg Val Asn
 85 90 95

Asp Asp Ile Ser Gly Arg Thr Thr Val Phe Leu His Asp Lys Thr Val
 100 105 110

Val Thr His Ser Gly Gly Pro Ile Ala Ile Ile Pro His Asn Pro Asp
 115 120 125

Val Ala Ser Ala Ala Ala Ser Ala Asn Lys His Lys Gln Ser Val Met
 130 135 140

Thr Thr Ser Arg His Pro Tyr Ala Gln Met Ser Leu Ser Asp Met Leu
 145 150 155 160

Lys Gln Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Tyr Cys Ala Val
 165 170 175

Asp Asp Pro Asp Ser Ser Arg His Thr Met His Val Ile Asn Val Arg
 180 185 190

Asp His Thr Val
 195

<210> 1915

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA00748

<400> 1915

aagccttatt ctccctcttaa ctaccatgag gtaaccatct aaagtagatg gttgcaacaa 60
cttttcatta catcaacatg tttaaaaaag gacactgatt atg act tac ttc gca 115
Met Thr Tyr Phe Ala
1 5
ctc gtt gct cgc aat tac gct gag aca ggt gtc tct gtt gaa ttc cat 163
Leu Val Ala Arg Asn Tyr Ala Glu Thr Gly Val Ser Val Glu Phe His
10 15 20
gag gtc gat gat gac gca gat aac tca aat ggc ccc aac aac aca agc 211
Glu Val Asp Asp Asp Ala Asp Asn Ser Asn Gly Pro Asn Asn Thr Ser
25 30 35
aat tta cct cta aaa ctt ctt cga gat cac tct ttt gat gcc act gtt 259
Asn Leu Pro Leu Lys Leu Leu Arg Asp His Ser Phe Asp Ala Thr Val
40 45 50
gtc tat ggt gac ctg gtg ctt cac acc tca gca cat ctc aga gat acg 307
Val Tyr Gly Asp Leu Val Leu His Thr Ser Ala His Leu Arg Asp Thr
55 60 65
gct atc gcc aac tca gac aac cgt ccg cga gta gtg acc aca gct caa 355
Ala Ile Ala Asn Ser Asp Asn Arg Pro Arg Val Val Thr Thr Ala Gln
70 75 80 85
aaa ttc ttt gat tac atc cgc tta gcc acc aga cac ggt gct atc cac 403
Lys Phe Phe Asp Tyr Ile Arg Leu Ala Thr Arg His Gly Ala Ile His
90 95 100
gac atg atc aat aac gcg cca gat acc ggc act gac atc gtt gtt att 451
Asp Met Ile Asn Asn Ala Pro Asp Thr Gly Thr Asp Ile Val Val Ile
105 110 115
acg gcc act aat gat gct ctt att agt gat gaa tca gaa tac tat gac 499
Thr Ala Thr Asn Asp Ala Leu Ile Ser Asp Glu Ser Glu Tyr Tyr Asp
120 125 130
gag ctt ttt cat att ctc gaa tcc gca cag ggt gtg att ctt aaa 544
Glu Leu Phe His Ile Leu Ser Ala Gln Gly Val Ile Leu Lys
135 140 145
tgattgatta attgatatga tta 567

<210> 1916

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 1916

Met Thr Tyr Phe Ala Leu Val Ala Arg Asn Tyr Ala Glu Thr Gly Val
1 5 10 15
Ser Val Glu Phe His Glu Val Asp Asp Ala Asp Asn Ser Asn Gly
20 25 30
Pro Asn Asn Thr Ser Asn Leu Pro Leu Lys Leu Leu Arg Asp His Ser

ctg agg tcg gtc tct gga gaa gaa att ctc cca gat aat gtt gaa gtg 403
 Leu Arg Ser Val Ser Gly Glu Glu Ile Leu Pro Asp Asn Val Glu Val
 90 95 100

 gtt cag acg gac aac gta ggc gac gaa gat cca aat gtc att tct cca 451
 Val Gln Thr Asp Asn Val Gly Asp Glu Asp Pro Asn Val Ile Ser Pro
 105 110 115

 gca gcc tgg cag ggt tct gat tat att gag ggg tgt tta acg aat act 499
 Ala Ala Trp Gln Gly Ser Asp Tyr Ile Glu Gly Cys Leu Thr Asn Thr
 120 125 130

 ctc tac gga att gaa gtc cta aag gtt tgt act ggt gga acc tac tac 547
 Leu Tyr Gly Ile Glu Val Leu Lys Val Cys Thr Gly Gly Thr Tyr Tyr
 135 140 145

 tcc aat gta gga atc gct act tct gtc agc aat cct cgc agt tac gta 595
 Ser Asn Val Gly Ile Ala Thr Ser Val Ser Asn Pro Arg Ser Tyr Val
 150 155 160 165

 aag tat aac agt gct cca gga ttg gca gtg acg aca agc aat cca cgt 643
 Lys Tyr Asn Ser Ala Pro Gly Leu Ala Val Thr Thr Ser Asn Pro Arg
 170 175 180

 gga ggt ata gag ggt ggt ctt gcg gcc ttc tat ggt gat gtt aac ctt 691
 Gly Gly Ile Glu Gly Gly Leu Ala Ala Phe Tyr Gly Asp Val Asn Leu
 185 190 195

 gtt gct ttt cca aat att cca tgg gtg gga cca att agt tct tct gca 739
 Val Ala Phe Pro Asn Ile Pro Trp Val Gly Pro Ile Ser Ser Ser Ala
 200 205 210

 gga act cac cgc gtt gtc gct aga tca ttt ccg aat tca gtg gtg ctt 787
 Gly Thr His Arg Val Val Ala Arg Ser Phe Pro Asn Ser Val Val Leu
 215 220 225

 aac gtc tac tac taatcggtttt ttagtttgaa aca 822
 Asn Val Tyr Tyr
 230

<210> 1918

<211> 233

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1918

Met Leu Arg Lys Thr Val Thr Gly Gly Ile Val Ala Leu Ile Ala Thr
 1 5 10 15

 Ala Thr Leu Met Asn Ser Val Ser Ser Ala Glu Glu Val Ser Gly Asp
 20 25 30

 Val Ser Ala Val Asp Leu Ala Phe Ala Glu Phe Glu Arg Thr Thr Ala
 35 40 45

 Glu Asp Val Ala Asn Gly Val Pro Glu Ala Ile Ala Asn Ala Glu Lys
 50 55 60

 Ile Ser Asn Phe Thr Pro Ser Glu Leu Glu Gly Phe Lys Ser Leu Leu
 65 70 75 80

Ala	Ser	Asp	Ala	Val 85	Leu	Arg	Ser	Val	Ser 90	Gly	Glu	Glu	Ile	Leu 95	Pro
Asp	Asn	Val	Glu 100	Val	Val	Gln	Thr	Asp 105	Asn	Val	Gly	Asp	Glu 110	Asp	Pro
Asn	Val	Ile 115	Ser	Pro	Ala	Ala	Trp 120	Gln	Gly	Ser	Asp	Tyr 125	Ile	Glu	Gly
Cys	Leu 130	Thr	Asn	Thr	Leu	Tyr 135	Gly	Ile	Glu	Val	Leu 140	Lys	Val	Cys	Thr
Gly 145	Gly	Thr	Tyr	Tyr 150	Ser	Asn	Val	Gly	Ile 155	Ala	Thr	Ser	Val	Ser	Asn 160
Pro	Arg	Ser	Tyr	Val 165	Lys	Tyr	Asn	Ser	Ala 170	Pro	Gly	Leu	Ala	Val 175	Thr
Thr	Ser	Asn	Pro 180	Arg	Gly	Gly	Ile	Glu 185	Gly	Gly	Leu	Ala	Ala 190	Phe	Tyr
Gly	Asp	Val 195	Asn	Leu	Val	Ala	Phe 200	Pro	Asn	Ile	Pro	Trp 205	Val	Gly	Pro
Ile 210	Ser	Ser	Ser	Ala	Gly	Thr 215	His	Arg	Val	Val	Ala 220	Arg	Ser	Phe	Pro
Asn 225	Ser	Val	Val	Leu	Asn 230	Val	Tyr	Tyr							

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<210> 1919
<211> 951
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(928)  
<223> RXA00751
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<400> 1919
cgcagcaacc ccgtccatga gggcagggaa cgccacacat cctgtaccta tactgtgagg 60

tggcatagag tatctctaatttagaaagtg gtgtagaagt atg ttg gta cgt tca 115
Met Leu Val Arg Ser
1 5

cgc acg ttg gtt acc gct gca ctg tca tgt tca ctg ttg ttc gga gca 163
Arg Thr Leu Val Thr Ala Ala Leu Ser Cys Ser Leu Leu Phe Gly Ala
10 15 20

acg gta aat ggc acg ggt gtt gcg att gca tat gaa aat gtg tct atg 211
Thr Val Asn Gly Thr Gly Val Ala Ile Ala Tyr Glu Asn Val Ser Met
25 30 35

gct gct cag tat gaa cca cgg tat gaa tcc tta gaa acg cgt ctc ggt 259
Ala Ala Gln Tyr Glu Pro Arg Tyr Glu Ser Leu Glu Thr Arg Leu Gly
40 45 50

tct agt gga gtc ttt ccc aag tcg gtt gaa cag tct gtt gaa aac ctt 307
 Ser Ser Gly Val Phe Pro Lys Ser Val Glu Gln Ser Val Glu Asn Leu
 55 60 65

gct gaa tta cca gag gag act cga ttt tta ctt gag ggt gat tcg ttt 355
 Ala Glu Leu Pro Glu Glu Thr Arg Phe Leu Leu Glu Gly Asp Ser Phe
 70 75 80 85

tca att att att gat gat ggt ctg ctc gct tct cga ttg gac cca aat 403
 Ser Ile Ile Ile Asp Asp Gly Leu Leu Ala Ser Arg Leu Asp Pro Asn
 90 95 100

aca ggg gag att cga cat act ctt ggg gct tcg ggg atc agc tac acc 451
 Thr Gly Glu Ile Arg His Thr Leu Gly Ala Ser Gly Ile Ser Tyr Thr
 105 110 115

cct ggt gaa atg aaa cga tct tat aca gat cga gtg act gtc aag gtg 499
 Pro Gly Glu Met Lys Arg Ser Tyr Thr Asp Arg Val Thr Val Lys Val
 120 125 130

gtc tac cct gat ggg tca ttt gat aga gtg aca ccc cat tca gtg gtt 547
 Val Tyr Pro Asp Gly Ser Phe Asp Arg Val Thr Pro His Ser Val Val
 135 140 145

tat gtg gct gac agt att tac tac ggc att gaa agc acg ggt tat cct 595
 Tyr Val Ala Asp Ser Ile Tyr Tyr Gly Ile Glu Ser Thr Gly Tyr Pro
 150 155 160 165

aaa gtc cgc aat ggt cag act gtc aag atc cca ttg agg gtg acg gat 643
 Lys Val Arg Asn Gly Gln Thr Val Lys Ile Pro Leu Arg Val Thr Asp
 170 175 180

ggg ggt aca gga gcg gtt ggt ggg gtc cca cag gga tcg aag gtg gtc 691
 Gly Gly Thr Gly Ala Val Gly Gly Val Pro Gln Gly Ser Lys Val Val
 185 190 195

cga gat cgt tac ggc tca att gag aat gcg gag ttg atg ggt gca atc 739
 Arg Asp Arg Tyr Gly Ser Ile Glu Asn Ala Glu Leu Met Gly Ala Ile
 200 205 210

att ctc ata gat gag aag act ggc gat ctc acc ttc acg gcg cct gat 787
 Ile Leu Ile Asp Glu Lys Thr Gly Asp Leu Thr Phe Thr Ala Pro Asp
 215 220 225

gat cga acc ggt caa ctg tgg ttt cgt aca gaa gtg act ttc ccg gat 835
 Asp Arg Thr Gly Gln Leu Trp Phe Arg Thr Glu Val Thr Phe Pro Asp
 230 235 240 245

ggg tcg gac tca gag gtt caa tat gtg atc gag gtg acg gat cag cct 883
 Gly Ser Asp Ser Glu Val Gln Tyr Val Ile Glu Val Thr Asp Gln Pro
 250 255 260

gaa cct gtg gat gtc att cgt cct gcc gga tcg tct ctg agt tct 928
 Glu Pro Val Asp Val Ile Arg Pro Ala Gly Ser Ser Leu Ser Ser
 265 270 275

tgatttatgc ctgagactta agc 951

<210> 1920

<211> 276

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1920

Met Leu Val Arg Ser Arg Thr Leu Val Thr Ala Ala Leu Ser Cys Ser
1 5 10 15
Leu Leu Phe Gly Ala Thr Val Asn Gly Thr Gly Val Ala Ile Ala Tyr
20 25 30
Glu Asn Val Ser Met Ala Ala Gln Tyr Glu Pro Arg Tyr Glu Ser Leu
35 40 45
Glu Thr Arg Leu Gly Ser Ser Gly Val Phe Pro Lys Ser Val Glu Gln
50 55 60
Ser Val Glu Asn Leu Ala Glu Leu Pro Glu Glu Thr Arg Phe Leu Leu
65 70 75 80
Glu Gly Asp Ser Phe Ser Ile Ile Ile Asp Asp Gly Leu Leu Ala Ser
85 90 95
Arg Leu Asp Pro Asn Thr Gly Glu Ile Arg His Thr Leu Gly Ala Ser
100 105 110
Gly Ile Ser Tyr Thr Pro Gly Glu Met Lys Arg Ser Tyr Thr Asp Arg
115 120 125
Val Thr Val Lys Val Val Tyr Pro Asp Gly Ser Phe Asp Arg Val Thr
130 135 140
Pro His Ser Val Val Tyr Val Ala Asp Ser Ile Tyr Tyr Gly Ile Glu
145 150 155 160
Ser Thr Gly Tyr Pro Lys Val Arg Asn Gly Gln Thr Val Lys Ile Pro
165 170 175
Leu Arg Val Thr Asp Gly Gly Thr Gly Ala Val Gly Gly Val Pro Gln
180 185 190
Gly Ser Lys Val Val Arg Asp Arg Tyr Gly Ser Ile Glu Asn Ala Glu
195 200 205
Leu Met Gly Ala Ile Ile Leu Ile Asp Glu Lys Thr Gly Asp Leu Thr
210 215 220
Phe Thr Ala Pro Asp Asp Arg Thr Gly Gln Leu Trp Phe Arg Thr Glu
225 230 235 240
Val Thr Phe Pro Asp Gly Ser Asp Ser Glu Val Gln Tyr Val Ile Glu
245 250 255
Val Thr Asp Gln Pro Glu Pro Val Asp Val Ile Arg Pro Ala Gly Ser
260 265 270
Ser Leu Ser Ser
275

<210> 1921

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXA00752

<400> 1921

aagggtcagcc gtatttcggt cagtcagcaa ctaactacgc ttatcttccg tgtacgatag 60

accgtagtta acataaggaa tggaatagga gaattgcggc atg tat tcc gac aag 115
 Met Tyr Ser Asp Lys
 1 5

ctg att ctc ttg ttc ctt tct gag cag gat tca agc tat gaa tgc tgc 163
 Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser Ser Tyr Glu Cys Cys
 10 15 20

gta ggt tta tta gat ggc tca gat gga ctt gat tat att gaa aag ctt 211
 Val Gly Leu Leu Asp Gly Ser Asp Gly Leu Asp Tyr Ile Glu Lys Leu
 25 30 35

ctg aag ggt agg aag ctg aag aac cat ttt ctt gaa tgg gaa gat att 259
 Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu Glu Trp Glu Asp Ile
 40 45 50

aac aag gct gat gtt gct cgt gaa gaa ata tat aaa ggg caa ttg gtg 307
 Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr Lys Gly Gln Leu Val
 55 60 65

cat ctg gtg ttt gtg acg gct ctt tcc acg cct ggt gaa att tct ttt 355
 His Leu Val Phe Val Thr Ala Leu Ser Thr Pro Gly Glu Ile Ser Phe
 70 75 80 85

gtt ttt cca ggt caa tct ctt atg agt gca aca ctc gaa gaa gac ttt 403
 Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr Leu Glu Glu Asp Phe
 90 95 100

gct gcg ctt gtg ctc gaa gag gag cgc aca tca ttt aga cct gaa ctg 451
 Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser Phe Arg Pro Glu Leu
 105 110 115

tct cac ctg tgg tca ctc ccc gta ggg tgg gta gct ccg ggg ctt gag 499
 Ser His Leu Trp Ser Leu Pro Val Gly Trp Val Ala Pro Gly Leu Glu
 120 125 130

ggt ttc gtg gag cgt aat tcc gag gca gct tgaaccaccg ctttctgagc 549
 Gly Phe Val Glu Arg Asn Ser Glu Ala Ala
 135 140

cgg 552

<210> 1922

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 1922

Met Tyr Ser Asp Lys Leu Ile Leu Leu Phe Leu Ser Glu Gln Asp Ser

1	5	10	15
Ser Tyr Glu Cys Cys Val Gly Leu Leu Asp Gly Ser Asp Gly Leu Asp	20	25	30
Tyr Ile Glu Lys Leu Leu Lys Gly Arg Lys Leu Lys Asn His Phe Leu	35	40	45
Glu Trp Glu Asp Ile Asn Lys Ala Asp Val Ala Arg Glu Glu Ile Tyr	50	55	60
Lys Gly Gln Leu Val His Leu Val Phe Val Thr Ala Leu Ser Thr Pro	65	70	75
Gly Glu Ile Ser Phe Val Phe Pro Gly Gln Ser Leu Met Ser Ala Thr	85	90	95
Leu Glu Glu Asp Phe Ala Ala Leu Val Leu Glu Glu Glu Arg Thr Ser	100	105	110
Phe Arg Pro Glu Leu Ser His Leu Trp Ser Leu Pro Val Gly Trp Val	115	120	125
Ala Pro Gly Leu Glu Gly Phe Val Glu Arg Asn Ser Glu Ala Ala	130	135	140

<210> 1923

<211> 1377

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1354)

<223> RXA00757

<400> 1923

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tgacctcgag caacttttta ttccgctcga tcaaaacaac	gtg agt ttc ggc gtc	115
	Val Ser Phe Gly Val	
	1 5	

gtt aag cgc ccc gat gcg tgc tac gcg ctt ttt gcc atc ctg atc aag	163
Val Lys Arg Pro Asp Ala Cys Tyr Ala Leu Phe Ala Ile Leu Ile Lys	
	10 15 20

cgc aac cag gcg acc gcg gtt tct gcg cca atg gcg cgg cag cgt cag	211
Arg Asn Gln Ala Thr Ala Val Ser Ala Pro Met Ala Arg Gln Arg Gln	
	25 30 35

tgg gtt gtc cac gcc cgg cgt gga cac ttc gag cgt gta acc cgc tcc	259
Trp Val Val His Ala Arg Arg Gly His Phe Glu Arg Val Thr Arg Ser	
	40 45 50

gaa gtt gag ctc tcc gcg ctg ctc ggc ggc gtc gaa aag ctc tcc gat	307
Glu Val Glu Leu Ser Ala Leu Leu Gly Gly Val Glu Lys Leu Ser Asp	
	55 60 65

ttc ttg gct gaa tac ttc cag ctg gtc gag atc ggg gcg gga atc cga	355
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Phe 70	Leu	Ala	Glu	Tyr	Phe 75	Gln	Leu	Val	Glu	Ile 80	Gly	Ala	Gly	Ile	Arg 85	
atc	tac	ctt	gat	ggc	gac	ggc	gga	ttt	tgg	acc	tgc	ttt	ggt	cac	ttt	403
Ile	Tyr	Leu	Asp	Gly 90	Asp	Gly	Gly	Phe	Trp 95	Thr	Cys	Phe	Gly	His 100	Phe	
cag	gcc	ctc	gag	gtc	gaa	ttt	gtg	gga	tgc	ggc	gag	cgg	ctc	gat	gag	451
Gln	Ala	Leu	Glu	Val 105	Glu	Phe	Val	Gly 110	Cys	Gly	Glu	Arg	Leu	Asp	Glu	
cgc	aga	cag	aat	ttc	agt	ggt	tgg	aaa	agc	cat	aaa	gac	aag	gat	aac	499
Arg	Arg	Gln	Asn	Phe 120	Ser	Gly	Trp	Lys 125	Ser	His	Lys	Asp 130	Lys	Asp	Asn	
ctg	ccg	gca	aaa	atc	atc	ggg	cta	tta	cac	tgt	gaa	gcc	atg	cgt	agg	547
Leu	Pro	Ala	Lys	Ile 135	Ile	Gly 140	Leu	Leu	His	Cys	Glu 145	Ala	Met	Arg	Arg	
cgt	atc	ccc	tct	gtc	ctt	ggt	gtt	tct	ctt	ctg	gct	gcc	ttt	ttg	gtg	595
Arg	Ile	Pro	Ser	Val 150	Leu	Gly 155	Val	Ser	Leu	Leu 160	Ala	Ala	Phe	Leu	Val 165	
gcg	tgc	acc	ccc	tcc	ccc	aat	ccg	aat	gcg	gcg	ttg	gcc	cag	atg	tat	643
Ala	Cys	Thr	Pro	Ser 170	Pro	Asn	Pro	Asn	Ala 175	Ala	Leu	Ala	Gln	Met 180	Tyr	
cag	gat	gcg	ctt	ttt	gat	tcc	cag	gcg	atg	tca	gag	gcc	gag	cct	gag	691
Gln	Asp	Ala	Leu	Phe 185	Asp	Ser	Gln	Ala 190	Met	Ser	Glu	Ala	Glu	Pro	Glu	
ctt	gcc	act	ttg	cgc	agt	cag	cac	gca	gat	gaa	tta	ttg	gcc	gag	att	739
Leu	Ala	Thr 200	Leu	Arg	Ser	Gln 205	His	Ala	Asp	Glu	Leu	Leu	Ala	Glu	Ile 210	
cgg	cgt	att	tgt	ggc	ttt	gat	gaa	ggc	cag	gtt	ccg	gaa	tcg	tgc	cag	787
Arg	Arg	Ile	Cys	Gly 215	Phe	Asp 220	Glu	Gly	Gln	Val	Pro 225	Glu	Ser	Cys	Gln	
gta	acg	gtt	cct	gcg	atc	gct	att	ctg	ccc	acc	gat	gat	cca	gag	aag	835
Val	Thr	Val	Pro	Ala 230	Ile	Ala 235	Ile	Leu	Pro	Thr 240	Asp	Asp	Pro	Glu	Lys 245	
tat	gtc	aac	gac	agt	cag	gcg	ttg	atc	ctt	gat	aat	ttg	gat	gac	att	883
Tyr	Val	Asn	Asp	Ser 250	Gln	Ala	Leu	Ile 255	Leu	Asp	Asn	Leu	Asp	Asp	Ile 260	
ccg	gaa	gat	tcc	gtg	gct	tta	gtg	gtt	gag	caa	tac	atc	gcg	cag	gcg	931
Pro	Glu	Asp	Ser 265	Val	Ala	Leu	Val 270	Val	Glu	Gln	Tyr	Ile	Ala	Gln	Ala 275	
gaa	ttt	gct	gaa	gga	tct	gag	gtg	tcc	gtt	cct	gtt	gat	ttg	gag	ctc	979
Glu	Phe 280	Ala	Glu	Gly	Ser	Glu 285	Val	Ser	Val	Pro	Val 290	Asp	Leu	Glu	Leu	
acc	gag	gca	gaa	tta	gct	gct	gcg	aag	gac	ttg	gcg	gac	cgc	gag	ttt	1027
Thr	Glu	Ala	Glu	Leu	Ala	Ala 300	Ala	Lys	Asp	Leu	Ala 305	Asp	Arg	Glu	Phe	
tcc	gcc	gcg	tgg	tct	ttg	ggc	gtg	gct	ttg	gct	cag	ctt	ccg	gaa	acc	1075
Ser	Ala	Ala	Trp	Ser	Leu	Gly	Val	Ala	Leu	Ala	Gln	Leu	Pro	Glu	Thr	

310 315 320 325
 gac cgc gag gag gtg gaa acg gcg atc agc aac cac cat gac cgc gcg 1123
 Asp Arg Glu Glu Val Glu Thr Ala Ile Ser Asn His His Asp Arg Ala
 330 335 340
 tcg cag ctg caa att att acc tcc ggc act acc cca gcg cca ggt tac 1171
 Ser Gln Leu Gln Ile Ile Thr Ser Gly Thr Thr Pro Ala Pro Gly Tyr
 345 350 355
 gtg agc gag ctg ccc gac ccc acc gac gag act tca gcg cga agc aac 1219
 Val Ser Glu Leu Pro Asp Pro Thr Asp Glu Thr Ser Ala Arg Ser Asn
 360 365 370
 att gaa acc gtc gaa aac aac gtc acc cag gcc tgg cat gca gct gca 1267
 Ile Glu Thr Val Glu Asn Asn Val Thr Gln Ala Trp His Ala Ala Ala
 375 380 385
 agc gcc gca acc acc gac gcc tgg cgt gtc ttc tgc gcg cac atc gcc 1315
 Ser Ala Ala Thr Thr Asp Ala Trp Arg Val Phe Cys Ala His Ile Ala
 390 395 400 405
 ggc gat acc gca cgc gaa tta acg ctt atc gac gtc tcc tagcagtttc 1364
 Gly Asp Thr Ala Arg Glu Leu Thr Leu Ile Asp Val Ser
 410 415
 actgcccaatt ttt 1377

 <210> 1924
 <211> 418
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1924
 Val Ser Phe Gly Val Val Lys Arg Pro Asp Ala Cys Tyr Ala Leu Phe
 1 5 10 15
 Ala Ile Leu Ile Lys Arg Asn Gln Ala Thr Ala Val Ser Ala Pro Met
 20 25 30
 Ala Arg Gln Arg Gln Trp Val Val His Ala Arg Arg Gly His Phe Glu
 35 40 45
 Arg Val Thr Arg Ser Glu Val Glu Leu Ser Ala Leu Leu Gly Gly Val
 50 55 60
 Glu Lys Leu Ser Asp Phe Leu Ala Glu Tyr Phe Gln Leu Val Glu Ile
 65 70 75 80
 Gly Ala Gly Ile Arg Ile Tyr Leu Asp Gly Asp Gly Gly Phe Trp Thr
 85 90 95
 Cys Phe Gly His Phe Gln Ala Leu Glu Val Glu Phe Val Gly Cys Gly
 100 105 110
 Glu Arg Leu Asp Glu Arg Arg Gln Asn Phe Ser Gly Trp Lys Ser His
 115 120 125
 Lys Asp Lys Asp Asn Leu Pro Ala Lys Ile Ile Gly Leu Leu His Cys
 130 135 140

Glu Ala Met Arg Arg Arg Ile Pro Ser Val Leu Gly Val Ser Leu Leu
 145 150 155 160
 Ala Ala Phe Leu Val Ala Cys Thr Pro Ser Pro Asn Pro Asn Ala Ala
 165 170 175
 Leu Ala Gln Met Tyr Gln Asp Ala Leu Phe Asp Ser Gln Ala Met Ser
 180 185 190
 Glu Ala Glu Pro Glu Leu Ala Thr Leu Arg Ser Gln His Ala Asp Glu
 195 200 205
 Leu Leu Ala Glu Ile Arg Arg Ile Cys Gly Phe Asp Glu Gly Gln Val
 210 215 220
 Pro Glu Ser Cys Gln Val Thr Val Pro Ala Ile Ala Ile Leu Pro Thr
 225 230 235 240
 Asp Asp Pro Glu Lys Tyr Val Asn Asp Ser Gln Ala Leu Ile Leu Asp
 245 250 255
 Asn Leu Asp Asp Ile Pro Glu Asp Ser Val Ala Leu Val Val Glu Gln
 260 265 270
 Tyr Ile Ala Gln Ala Glu Phe Ala Glu Gly Ser Glu Val Ser Val Pro
 275 280 285
 Val Asp Leu Glu Leu Thr Glu Ala Glu Leu Ala Ala Ala Lys Asp Leu
 290 295 300
 Ala Asp Arg Glu Phe Ser Ala Ala Trp Ser Leu Gly Val Ala Leu Ala
 305 310 315 320
 Gln Leu Pro Glu Thr Asp Arg Glu Glu Val Glu Thr Ala Ile Ser Asn
 325 330 335
 His His Asp Arg Ala Ser Gln Leu Gln Ile Ile Thr Ser Gly Thr Thr
 340 345 350
 Pro Ala Pro Gly Tyr Val Ser Glu Leu Pro Asp Pro Thr Asp Glu Thr
 355 360 365
 Ser Ala Arg Ser Asn Ile Glu Thr Val Glu Asn Asn Val Thr Gln Ala
 370 375 380
 Trp His Ala Ala Ala Ser Ala Ala Thr Thr Asp Ala Trp Arg Val Phe
 385 390 395 400
 Cys Ala His Ile Ala Gly Asp Thr Ala Arg Glu Leu Thr Leu Ile Asp
 405 410 415
 Val Ser

<210> 1925

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXA00763

<400> 1925

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gtttgaatct cttgcaggaa cgtggggtaa agatatagat gtg gaa aaa tcc aga 115
 Val Glu Lys Ser Arg
 1 5

aaa cga ctt gtg acc atc gca gca tcg aca att ggg gcc gtt gcg gtg 163
 Lys Arg Leu Val Thr Ile Ala Ala Ser Thr Ile Gly Ala Val Ala Val
 10 15 20

gct ggc ggc gct ttt tgg atc gtt gat gct tcc atc gct gcg cac gcg 211
 Ala Gly Gly Ala Phe Trp Ile Val Asp Ala Ser Ile Ala Ala His Ala
 25 30 35

gaa cgc aac ttg tct aaa gca gtt gcg gaa tcc gca gat ctt gaa aac 259
 Glu Arg Asn Leu Ser Lys Ala Val Ala Glu Ser Ala Asp Leu Glu Asn
 40 45 50

gac ccg cga gta ttc ctc ggc agc tcc att tac tcc acg gcg ttt ttt 307
 Asp Pro Arg Val Phe Leu Gly Ser Ser Ile Tyr Ser Thr Ala Phe Phe
 55 60 65

acc ggc aaa ctc gac tcc gta agc atc gac atg ctg gac gtg gaa atc 355
 Thr Gly Lys Leu Asp Ser Val Ser Ile Asp Met Leu Asp Val Glu Ile
 70 75 80 85

ccc ggc gtc ggc atg gtg aat gca cgc aca gag gta gaa agc gtg gaa 403
 Pro Gly Val Gly Met Val Asn Ala Arg Thr Glu Val Glu Ser Val Glu
 90 95 100

gtc tca cgg gat caa atc ctc tcc ggt gac ctc gac ggc acc act gcg 451
 Val Ser Arg Asp Gln Ile Leu Ser Gly Asp Leu Asp Gly Thr Thr Ala
 105 110 115

gaa acc ttc acg cgc aca tta cgc atg gac ggc gtc gca atc ggc gcg 499
 Glu Thr Phe Thr Arg Thr Leu Arg Met Asp Gly Val Ala Ile Gly Ala
 120 125 130

cag ctc gga atc acc gac ctc gac atc tcc cac ccc atc gac atc tcc 547
 Gln Leu Gly Ile Thr Asp Leu Asp Ile Ser His Pro Ile Asp Ile Ser
 135 140 145

ccc tcc ggc ggc atc acc tca gaa gcg ctc ctg aca gga acc cca cca 595
 Pro Ser Gly Gly Ile Thr Ser Glu Ala Leu Leu Thr Gly Thr Pro Pro
 150 155 160 165

gac atg gaa gac ccg gtc agt gtg ctg gtc acc ctt cgc cta gtc ggc 643
 Asp Met Glu Asp Pro Val Ser Val Leu Val Thr Leu Arg Leu Val Gly
 170 175 180

tca gaa ttc cag atg ctg ccg tac gag ctt atc gac gca ccc tcc gga 691
 Ser Glu Phe Gln Met Leu Pro Tyr Glu Leu Ile Asp Ala Pro Ser Gly
 185 190 195

ctc acc ctc gac gat gtc gcc ccc gac ttc acg tgg aaa atc gac acc 739

Leu Thr Leu Asp Asp Val Ala Pro Asp Phe Thr Trp Lys Ile Asp Thr
 200 205 210

ctg caa cta ccc ctc gca gat cgg gca atg gcg gtt tac cta tct ggt 787
 Leu Gln Leu Pro Leu Ala Asp Arg Ala Met Ala Val Tyr Leu Ser Gly
 215 220 225

ggc tcc gtc cat ttc caa tct gaa gcc cgc aac gtc cag ctc acc acc 835
 Gly Ser Val His Phe Gln Ser Glu Ala Arg Asn Val Gln Leu Thr Thr
 230 235 240 245

cgc gaa cta tca cca cta gct gca ccg gaa gaa aac tcc gat gaa tcc 883
 Arg Glu Leu Ser Pro Leu Ala Ala Pro Glu Glu Asn Ser Asp Glu Ser
 250 255 260

tagatgccaa acgtgcgcac ccg 906

<210> 1926

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 1926

Val Glu Lys Ser Arg Lys Arg Leu Val Thr Ile Ala Ala Ser Thr Ile
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Gly Ala Val Ala Val Ala Gly Gly Ala Phe Trp Ile Val Asp Ala Ser
 20 25 30

Ile Ala Ala His Ala Glu Arg Asn Leu Ser Lys Ala Val Ala Glu Ser
 35 40 45

Ala Asp Leu Glu Asn Asp Pro Arg Val Phe Leu Gly Ser Ser Ile Tyr
 50 55 60

Ser Thr Ala Phe Phe Thr Gly Lys Leu Asp Ser Val Ser Ile Asp Met
 65 70 75 80

Leu Asp Val Glu Ile Pro Gly Val Gly Met Val Asn Ala Arg Thr Glu
 85 90 95

Val Glu Ser Val Glu Val Ser Arg Asp Gln Ile Leu Ser Gly Asp Leu
 100 105 110

Asp Gly Thr Thr Ala Glu Thr Phe Thr Arg Thr Leu Arg Met Asp Gly
 115 120 125

Val Ala Ile Gly Ala Gln Leu Gly Ile Thr Asp Leu Asp Ile Ser His
 130 135 140

Pro Ile Asp Ile Ser Pro Ser Gly Gly Ile Thr Ser Glu Ala Leu Leu
 145 150 155 160

Thr Gly Thr Pro Pro Asp Met Glu Asp Pro Val Ser Val Leu Val Thr
 165 170 175

Leu Arg Leu Val Gly Ser Glu Phe Gln Met Leu Pro Tyr Glu Leu Ile
 180 185 190

Asp Ala Pro Ser Gly Leu Thr Leu Asp Asp Val Ala Pro Asp Phe Thr

195 200 205

Trp Lys Ile Asp Thr Leu Gln Leu Pro Leu Ala Asp Arg Ala Met Ala
210 215 220

Val Tyr Leu Ser Gly Gly Ser Val His Phe Gln Ser Glu Ala Arg Asn
225 230 235 240

Val Gln Leu Thr Thr Arg Glu Leu Ser Pro Leu Ala Ala Pro Glu Glu
245 250 255

Asn Ser Asp Glu Ser
260

<210> 1927
<211> 810
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(787)
<223> RXA00765

<400> 1927
acggaaaagt ttctgcgtct gcgtggtcga ctcaggattc gcaatcagaa gaacatgcac 60

gttatctaag agtagtgcca aaacgctagt cttgagtgtc atg agc gaa aat tcc 115
Met Ser Glu Asn Ser
1 5

acc cct aat aat cca gtc gtc cca ggt gca ggc gca gac ggc cca tca 163
Thr Pro Asn Asn Pro Val Val Pro Gly Ala Gly Ala Asp Gly Pro Ser
10 15 20

ctg tcc gat tct gca agc atc agc gga tcc gac gca gta aac ctc gct 211
Leu Ser Asp Ser Ala Ser Ile Ser Gly Ser Asp Ala Val Asn Leu Ala
25 30 35

gcc gaa caa tcc aag agc acc gct cac cgc aac atc cca ggc cta ggt 259
Ala Glu Gln Ser Lys Ser Thr Ala His Arg Asn Ile Pro Gly Leu Gly
40 45 50

gac ctt cct atc cct gac gac acc gct aac ctc cgc gaa ggc ccc aac 307
Asp Leu Pro Ile Pro Asp Asp Thr Ala Asn Leu Arg Glu Gly Pro Asn
55 60 65

ctc cac gac gga ctc ctc ggc ctc ctc cct ctc gtc ggc gtc tgg cgc 355
Leu His Asp Gly Leu Leu Ala Leu Leu Pro Leu Val Gly Val Trp Arg
70 75 80 85

ggc gaa ggc caa gcc gac acc gca gaa gac gga caa tac gca ttc ggc 403
Gly Glu Gly Gln Ala Asp Thr Ala Glu Asp Gly Gln Tyr Ala Phe Gly
90 95 100

cag caa atc acc ttc gcc cac gac ggt gaa aac tac ctc tcc ttc gaa 451
Gln Gln Ile Thr Phe Ala His Asp Gly Glu Asn Tyr Leu Ser Phe Glu
105 110 115

tcc cgc atg tgg aaa ctc gac gaa gaa gga aac ccc acc ggc gtc gac 499

Ser Arg Met Trp Lys Leu Asp Glu Glu Gly Asn Pro Thr Gly Val Asp
 120 125 130
 cag cgc gaa tcc ggc ttc tgg cgc atc aat ctc aaa gat gaa atc gaa 547
 Gln Arg Glu Ser Gly Phe Trp Arg Ile Asn Leu Lys Asp Glu Ile Glu
 135 140 145
 ttc gtc tgc acc cac gcc ggc gga gtt gta gaa atc tac tac ggc cag 595
 Phe Val Cys Thr His Ala Gly Gly Val Val Glu Ile Tyr Tyr Gly Gln
 150 155 160 165
 cca ctc aat gag cgc gcc tgg cag ctt gaa tcc gca tct acc atg gtc 643
 Pro Leu Asn Glu Arg Ala Trp Gln Leu Glu Ser Ala Ser Thr Met Val
 170 175 180
 acc gcc acc ggc cca tcc acc ctt gga cca gga aag cgt ctc tac gga 691
 Thr Ala Thr Gly Pro Ser Thr Leu Gly Pro Gly Lys Arg Leu Tyr Gly
 185 190 195
 ctg ctt cca acc aac gaa ctc ggc tgg gtt gat gag cgt ctc gtt ggc 739
 Leu Leu Pro Thr Asn Glu Leu Gly Trp Val Asp Glu Arg Leu Val Gly
 200 205 210
 gac gcc ctc aag cca cgc atg tcc gca cag ctc acc cgc gtg atc ggc 787
 Asp Ala Leu Lys Pro Arg Met Ser Ala Gln Leu Thr Arg Val Ile Gly
 215 220 225
 tagtttttttc tagttcaccg tca 810

 <210> 1928
 <211> 229
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1928
 Met Ser Glu Asn Ser Thr Pro Asn Asn Pro Val Val Pro Gly Ala Gly
 1 5 10 15
 Ala Asp Gly Pro Ser Leu Ser Asp Ser Ala Ser Ile Ser Gly Ser Asp
 20 25 30
 Ala Val Asn Leu Ala Ala Glu Gln Ser Lys Ser Thr Ala His Arg Asn
 35 40 45
 Ile Pro Gly Leu Gly Asp Leu Pro Ile Pro Asp Asp Thr Ala Asn Leu
 50 55 60
 Arg Glu Gly Pro Asn Leu His Asp Gly Leu Leu Ala Leu Leu Pro Leu
 65 70 75 80
 Val Gly Val Trp Arg Gly Glu Gly Gln Ala Asp Thr Ala Glu Asp Gly
 85 90 95
 Gln Tyr Ala Phe Gly Gln Gln Ile Thr Phe Ala His Asp Gly Glu Asn
 100 105 110
 Tyr Leu Ser Phe Glu Ser Arg Met Trp Lys Leu Asp Glu Gly Asn
 115 120 125
 Pro Thr Gly Val Asp Gln Arg Glu Ser Gly Phe Trp Arg Ile Asn Leu

ttc

411

<210> 1930

<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 1930

Met Ser Glu Asn Lys Asn Ile Glu Ile Val His Asn Glu Gly Gln Lys
 1 5 10 15

Arg Phe Val Ile Ser Val Asp Gly Thr Pro Ala Gly Phe Ala Ser Tyr
 20 25 30

Leu Asp Gly Pro Asp Ile Arg Asn Phe Asn His Thr Val Ile Lys Pro
 35 40 45

Glu Phe Arg Gly Gln Gly Leu Ser Ala Pro Leu Ile Lys Phe Ala Leu
 50 55 60

Asp Asp Ala Arg Glu Ser Gly Ile Arg Ile His Asp Ala Cys Ser Ala
 65 70 75 80

Val Ala Gly Phe Ile Gln Lys Asn Pro Glu Tyr Lys Asp Leu Lys Asn
 85 90 95

<210> 1931

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA00788

<400> 1931

cgcacccctc tagttttcca tcacctcaat gaacggcgct aactccggtt cattgcgcaa 60

ttgatccagc actgcttgca gtgaggcctc attagttggc atg gcc tcc tcc atc 115
 Met Ala Ser Ser Ile
 1 5

aac atc gga gtg ttc aac ctt gga aat gct gtt gct gcc tgg ctt gct 163
 Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val Ala Ala Trp Leu Ala
 10 15 20

ggt gca acc atc acc act tcc ctt gga ctc aca tca gcc gga tta gtt 211
 Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr Ser Ala Gly Leu Val
 25 30 35

ggc ggt ttg atg acg tcc ctc gga cta gtg ttg gcc atc gtg gct gtg 259
 Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu Ala Ile Val Ala Val
 40 45 50

gtt ttg cgt cga aaa gcg caa ggc acc caa gcg acc atc agc gtt gtg 307
 Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala Thr Ile Ser Val Val
 55 60 65

gag cac cag ccc gcc caa taaataattt ctctcttcta att
 Glu His Gln Pro Ala Gln
 70 75

348

<210> 1932

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 1932

Met Ala Ser Ser Ile Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val
 1 5 10 15

Ala Ala Trp Leu Ala Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr
 20 25 30

Ser Ala Gly Leu Val Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu
 35 40 45

Ala Ile Val Ala Val Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala
 50 55 60

Thr Ile Ser Val Val Glu His Gln Pro Ala Gln
 65 70 75

<210> 1933

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA00804

<400> 1933

aatctagtagc aagttccagc gaaaaccttc caaaactgac caagtttaag aagattcgct 60

accctatgaa tcagttgtag gagtaagagg ggagtttagag atg aag atc aga agt 115
 Met Lys Ile Arg Ser
 1 5

gca cgt gaa atc gcg gag tgg ttc gtt gcc tgg gga gat gaa ctc gat 163
 Ala Arg Glu Ile Ala Glu Trp Phe Val Ala Trp Gly Asp Glu Leu Asp
 10 15 20

gct gaa gtc tcc cct ttg aaa ttg cag aag ctc ctt tat tac tcc cag 211
 Ala Glu Val Ser Pro Leu Lys Leu Gln Lys Leu Leu Tyr Tyr Ser Gln
 25 30 35

ggt gag cat ata gct gca aca ggg cga aaa ctt ttc tcg gat aag att 259
 Gly Glu His Ile Ala Ala Thr Gly Arg Lys Leu Phe Ser Asp Lys Ile
 40 45 50

ctg gcg tgg cag cac gga cct gtc act ccg ggc gtt tat tca gat aca 307
 Leu Ala Trp Gln His Gly Pro Val Thr Pro Gly Val Tyr Ser Asp Thr
 55 60 65

aaa tca tac ggc cga aac cca att gat cct gat gag ttt gtg tca gat 355
 Lys Ser Tyr Gly Arg Asn Pro Ile Asp Pro Asp Glu Phe Val Ser Asp
 70 75 80 85

gaa ttt aac tgg gat gac tac tca gat gtg tca gat gag ctt gta acc 403
 Glu Phe Asn Trp Asp Asp Tyr Ser Asp Val Ser Asp Glu Leu Val Thr
 90 95 100

gta tgg cga aaa tac ggc atc tat tcg gcg tgg gca ctg agg gaa aaa 451
 Val Trp Arg Lys Tyr Gly Ile Tyr Ser Ala Trp Ala Leu Arg Glu Lys
 105 110 115

act cac agt gaa tcg ccg tgg ctc gat gcc tgg gca caa ggg caa aat 499
 Thr His Ser Glu Ser Pro Trp Leu Asp Ala Trp Ala Gln Gly Gln Asn
 120 125 130

att gaa att aca gat gct gcg ctg aaa gat ttc ttc ttg gtg cat 544
 Ile Glu Ile Thr Asp Ala Ala Leu Lys Asp Phe Phe Leu Val His
 135 140 145

tagaaatttg aaaaagaaac gaa 567

<210> 1934

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 1934

Met Lys Ile Arg Ser Ala Arg Glu Ile Ala Glu Trp Phe Val Ala Trp
 1 5 10 15

Gly Asp Glu Leu Asp Ala Glu Val Ser Pro Leu Lys Leu Gln Lys Leu
 20 25 30

Leu Tyr Tyr Ser Gln Gly Glu His Ile Ala Ala Thr Gly Arg Lys Leu
 35 40 45

Phe Ser Asp Lys Ile Leu Ala Trp Gln His Gly Pro Val Thr Pro Gly
 50 55 60

Val Tyr Ser Asp Thr Lys Ser Tyr Gly Arg Asn Pro Ile Asp Pro Asp
 65 70 75 80

Glu Phe Val Ser Asp Glu Phe Asn Trp Asp Asp Tyr Ser Asp Val Ser
 85 90 95

Asp Glu Leu Val Thr Val Trp Arg Lys Tyr Gly Ile Tyr Ser Ala Trp
 100 105 110

Ala Leu Arg Glu Lys Thr His Ser Glu Ser Pro Trp Leu Asp Ala Trp
 115 120 125

Ala Gln Gly Gln Asn Ile Glu Ile Thr Asp Ala Ala Leu Lys Asp Phe
 130 135 140

Phe Leu Val His
 145

<210> 1935

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA00805

<400> 1935

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tgctccgctg acagtgggtgc gcctgagcag cccaaaagag acaaagcgct ggttgagggc 60
atatgggggaa agcgtgaaac tctgataggg tgccatatcc atg gca gaa agt ttt 115
                                     Met Ala Glu Ser Phe
                                     1 5

ata gag gtc tcg gcg ggg cat gcg gat cgg cgg ata gat aag ttt ttg 163
Ile Glu Val Ser Ala Gly His Ala Asp Arg Arg Ile Asp Lys Phe Leu
          10          15          20

cgg gca cag cta aag ggc gtg ccc gcg tcg ttg att ttc cgt caa atg 211
Arg Ala Gln Leu Lys Gly Val Pro Ala Ser Leu Ile Phe Arg Gln Met
          25          30          35

cgt aaa ggc gac att cgg gtg aat ggt cgt aaa gtg gat ccg aat tac 259
Arg Lys Gly Asp Ile Arg Val Asn Gly Arg Lys Val Asp Pro Asn Tyr
          40          45          50

cgg ttg caa gaa ggc gac cga att cga atg tgg cag atg gat ttg ctg 307
Arg Leu Gln Glu Gly Asp Arg Ile Arg Met Trp Gln Met Asp Leu Leu
          55          60          65

gca gat ttg ccg cca ccg gtc gtc gat aag cat att ttt aag gct gtc 355
Ala Asp Leu Pro Pro Val Val Asp Lys His Ile Phe Lys Ala Val
          70          75          80          85

gca gac agc gtg ctt ttt gag gac gcc gaa tta ctg gtg atc aat aag 403
Ala Asp Ser Val Leu Phe Glu Asp Ala Glu Leu Leu Val Ile Asn Lys
          90          95          100

cca gct gga att cct gtg cac ggt ggc acg ggg cac ggc ggt ggc gtg 451
Pro Ala Gly Ile Pro Val His Gly Gly Thr Gly His Gly Gly Gly Val
          105          110          115

att gag gcg ctg cgg cag aag ttt ccg cag gaa cgc gac ctg gaa ttg 499
Ile Glu Ala Leu Arg Gln Lys Phe Pro Gln Glu Arg Asp Leu Glu Leu
          120          125          130

gtg cat cgt ttg gat cgg gac acc tca ggt ttg ttg ctg gtt tct aaa 547
Val His Arg Leu Asp Arg Asp Thr Ser Gly Leu Leu Leu Val Ser Lys
          135          140          145

acg aca tct gtg ttg cgc gag ttg cag gaa att ttg cga gac cgc gaa 595
Thr Thr Ser Val Leu Arg Glu Leu Gln Glu Ile Leu Arg Asp Arg Glu
          150          155          160          165

gag gag att ttt cgg ggg tat tta ctc aag gtc gag ggg gct tgg cct 643
Glu Glu Ile Phe Arg Gly Tyr Leu Leu Lys Val Glu Gly Ala Trp Pro
          170          175          180

ggc gat ttg cga caa att gat gtg ccg ttg aag cgg acg gag aca act 691

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Gly Asp Leu Arg Gln Ile Asp Val	Pro Leu Lys Arg Thr Glu Thr Thr	
185	190	195
gtt gtg cca cat tcg gat ggt ttg cgg gcg cgg acg tat ttt gag gtt	739	
Val Val Pro His Ser Asp Gly Leu Arg Ala Arg Thr Tyr Phe Glu Val		
200	205	210
gta aag cgt ttg ccg ggt gcg acc ttg gtg aag gcg cag ttg gcg acc	787	
Val Lys Arg Leu Pro Gly Ala Thr Leu Val Lys Ala Gln Leu Ala Thr		
215	220	225
ggg cgg aaa cat cag att cgg gtc cat gcg cag tat gcg ggt cac cct	835	
Gly Arg Lys His Gln Ile Arg Val His Ala Gln Tyr Ala Gly His Pro		
230	235	240
att gtt ggc gat cca cga tac ggg tcg cgt ggg ggc aga gct gcg acg	883	
Ile Val Gly Asp Pro Arg Tyr Gly Ser Arg Gly Gly Arg Ala Ala Thr		
250	255	260
atg cat ttg cat gcg gcg gaa ttg gtg gcg cct cgt ggg gcg ggg aag	931	
Met His Leu His Ala Ala Glu Leu Val Ala Pro Arg Gly Ala Gly Lys		
265	270	275
cgt cag aaa ttc act gca ccg ttg ccg aag gag tgg ggt atg gga cgg	979	
Arg Gln Lys Phe Thr Ala Pro Leu Pro Lys Glu Trp Gly Met Gly Arg		
280	285	290
gtc tgagtcgggc cttcgtggaa tcg	1005	
Val		

<210> 1936

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 1936

Met Ala Glu Ser Phe Ile Glu Val Ser Ala Gly His Ala Asp Arg Arg	
1	15
Ile Asp Lys Phe Leu Arg Ala Gln Leu Lys Gly Val Pro Ala Ser Leu	
20	30
Ile Phe Arg Gln Met Arg Lys Gly Asp Ile Arg Val Asn Gly Arg Lys	
35	45
Val Asp Pro Asn Tyr Arg Leu Gln Glu Gly Asp Arg Ile Arg Met Trp	
50	60
Gln Met Asp Leu Leu Ala Asp Leu Pro Pro Pro Val Val Asp Lys His	
65	80
Ile Phe Lys Ala Val Ala Asp Ser Val Leu Phe Glu Asp Ala Glu Leu	
85	95
Leu Val Ile Asn Lys Pro Ala Gly Ile Pro Val His Gly Gly Thr Gly	
100	110
His Gly Gly Gly Val Ile Glu Ala Leu Arg Gln Lys Phe Pro Gln Glu	
115	125

Arg Asp Leu Glu Leu Val His Arg Leu Asp Arg Asp Thr Ser Gly Leu
 130 135 140
 Leu Leu Val Ser Lys Thr Thr Ser Val Leu Arg Glu Leu Gln Glu Ile
 145 150 155 160
 Leu Arg Asp Arg Glu Glu Glu Ile Phe Arg Gly Tyr Leu Leu Lys Val
 165 170 175
 Glu Gly Ala Trp Pro Gly Asp Leu Arg Gln Ile Asp Val Pro Leu Lys
 180 185 190
 Arg Thr Glu Thr Thr Val Val Pro His Ser Asp Gly Leu Arg Ala Arg
 195 200 205
 Thr Tyr Phe Glu Val Val Lys Arg Leu Pro Gly Ala Thr Leu Val Lys
 210 215 220
 Ala Gln Leu Ala Thr Gly Arg Lys His Gln Ile Arg Val His Ala Gln
 225 230 235 240
 Tyr Ala Gly His Pro Ile Val Gly Asp Pro Arg Tyr Gly Ser Arg Gly
 245 250 255
 Gly Arg Ala Ala Thr Met His Leu His Ala Ala Glu Leu Val Ala Pro
 260 265 270
 Arg Gly Ala Gly Lys Arg Gln Lys Phe Thr Ala Pro Leu Pro Lys Glu
 275 280 285
 Trp Gly Met Gly Arg Val
 290

<210> 1937

<211> 701

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(678)

<223> RXA00808

<400> 1937

gct ggc ttc aat gag atg atg cgt ggc ctg cgt gaa cgt cag cgc gtc 48
 Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val
 1 5 10 15

cgt gac ctt ttc ggt cgc tac gtg ggc gct gaa gtg gcc aag cgt gcg 96
 Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala
 20 25 30

ctg gag gaa cgc ccc act ctg ggt ggc gag gac cgt aag gtt gcc gtg 144
 Leu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val
 35 40 45

ttg ttt gtc gat gtc atc ggc tcc act acc ttt gcc gtc aac cac act 192
 Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr
 50 55 60

cct gaa gag gtt gtg gag gcg ctc aat gag ttc ttc gag cac gtc gtg 240
 Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val
 65 70 75 80

gag gtt gtg cac cgc aac aag ggt gtt atc aac aag ttc cag ggt gac 288
 Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp
 85 90 95

gcg gcg ttg gcg att ttc ggc gct ccc ctg ccc ctg tct gat gcc acc 336
 Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr
 100 105 110

ggt cat gcg ctt gcg gct gcc cgt gag ctc cgc gca gag ctg aaa gat 384
 Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp
 115 120 125

ctc cag ctc aag gcc gga att ggt gtg gct gct ggc cat gtc gtt gct 432
 Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala
 130 135 140

ggt cat atc ggc ggt cac gcg agg ttt gag tac act gtg atc ggc gac 480
 Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp
 145 150 155 160

gcg gtg aac cag gct gcg cgc ctg acg gag atc gcg aaa acg acc cca 528
 Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro
 165 170 175

ggc cgc acc gtc acc aac gct tcc acg ctg cgt gag gcc aac gag gcg 576
 Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala
 180 185 190

gag cag gct cgc tgg acg ctc atg aag tcc gtg gag ctg cgc gga cgt 624
 Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg
 195 200 205

agc cag atg acg cag att gcg cgg cct att cgg ccg acg ttg gcg gat 672
 Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp
 210 215 220

agg tcc taatacgctt ttcgacgcaa aaa 701
 Arg Ser
 225

<210> 1938

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 1938

Ala Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val
 1 5 10 15

Arg Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala
 20 25 30

Leu Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val
 35 40 45

Leu Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr
 50 55 60
 Pro Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val
 65 70 75 80
 Glu Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp
 85 90 95
 Ala Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr
 100 105 110
 Gly His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp
 115 120 125
 Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala
 130 135 140
 Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp
 145 150 155 160
 Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro
 165 170 175
 Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala
 180 185 190
 Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg
 195 200 205
 Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp
 210 215 220
 Arg Ser
 225

<210> 1939
 <211> 1182
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1159)
 <223> RXA00812

<400> 1939
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 gtcgttgaaa gcacgtaagc ctcaggccac agtaggtgcc atg aac acc atc aca 115
 Met Asn Thr Ile Thr
 1 5
 cac caa gca att ctc atc gca gtg gaa gat ccg gtc ctg cac cca gag 163
 His Gln Ala Ile Leu Ile Ala Val Glu Asp Pro Val Leu His Pro Glu
 10 15 20
 gcc atg cac gta gct gca gcc act ggt cgg ccg gtt att gaa aca aca 211
 Ala Met His Val Ala Ala Ala Thr Gly Arg Pro Val Ile Glu Thr Thr
 25 30 35

aat ttg atg gac atc tcc agg cat ttt cac cgc aca tcg gca gtg ctc Asn Leu Met Asp Ile Ser Arg His Phe His Arg Thr Ser Ala Val Leu 40 45 50	259
att gat gcg tcg atg gcc tct caa tta tca cct ggg aaa cgc cgc gac Ile Asp Ala Ser Met Ala Ser Gln Leu Ser Pro Gly Lys Arg Arg Asp 55 60 65	307
agg gtg ttt ctt ctc gat tct gat cca ggg ccc tct gat tgg aaa acg Arg Val Phe Leu Leu Asp Ser Asp Pro Gly Pro Ser Asp Trp Lys Thr 70 75 80 85	355
gcg atg aaa atc cac gct gag caa gcc atg ttg ctt ccc gct cag gca Ala Met Lys Ile His Ala Glu Gln Ala Met Leu Leu Pro Ala Gln Ala 90 95 100	403
ggg gag ttg ctc agc gct tta ggc aga gat gac aaa caa ctg ccg gtg Gly Glu Leu Leu Ser Ala Leu Gly Arg Asp Asp Lys Gln Leu Pro Val 105 110 115	451
gct tcg ggc cat gtc atc ggt gtt gcc ggg gtg gtg gga gga aca ggc Ala Ser Gly His Val Ile Gly Val Ala Gly Val Val Gly Gly Thr Gly 120 125 130	499
gcg agc acg ttt gct gcg gcg ctc gca aag cgg cgt gcg gag tca gtc Ala Ser Thr Phe Ala Ala Leu Ala Lys Arg Arg Ala Glu Ser Val 135 140 145	547
acc act gtg ctt atc gac gcc gac cct tcc tct ggc ggc atc gac ctg Thr Thr Val Leu Ile Asp Ala Asp Pro Ser Ser Gly Gly Ile Asp Leu 150 155 160 165	595
ttg cta gga atc gaa gat gtg ccc ggc gcg cgg tgg cct gat gtg ggg Leu Leu Gly Ile Glu Asp Val Pro Gly Ala Arg Trp Pro Asp Val Gly 170 175 180	643
ttg cgt cgc gga act gtc cag gct gct gat gtg ttg aaa gcg ctg ccg Leu Arg Arg Gly Thr Val Gln Ala Ala Asp Val Leu Lys Ala Leu Pro 185 190 195	691
agc act cct gat gag gtc gtg gtg ttg tct acg gcg cgg tct aat att Ser Thr Pro Asp Glu Val Val Val Leu Ser Thr Ala Arg Ser Asn Ile 200 205 210	739
ctg gat cct ttt gca tta tcc gag tct gat gtt tca gcg gcg att gat Leu Asp Pro Phe Ala Leu Ser Glu Ser Asp Val Ser Ala Ala Ile Asp 215 220 225	787
tgt ttc tta agc gcc gat agg tcg gtg gat gtg gtg gtg gat ctg cct Cys Phe Leu Ser Ala Asp Arg Ser Val Asp Val Val Val Asp Leu Pro 230 235 240 245	835
cat gcg aga gtg cat cca gat att gcg gag cgc tta tcc cac ctg gtg His Ala Arg Val His Pro Asp Ile Ala Glu Arg Leu Ser His Leu Val 250 255 260	883
tta gtc atc cct gca gag gtc cga gcg gtg gct gct gcc agg gct ccg Leu Val Ile Pro Ala Glu Val Arg Ala Val Ala Ala Arg Ala Arg 265 270 275	931

tgt ctg gaa tta caa caa ttg cat gta tcc atc acg tgc gtg ttg agg 979
 Cys Leu Glu Leu Gln Gln Leu His Val Ser Ile Thr Cys Val Leu Arg
 280 285 290

cat cgc ggg tgg tca ggt ttg gat gtt gca gaa gtg gaa gag att tta 1027
 His Arg Gly Trp Ser Gly Leu Asp Val Ala Glu Val Glu Glu Ile Leu
 295 300 305

ggt gcg gat att acc gcg gag gtt ggc tgc atc cag cgg ctg gct aag 1075
 Gly Ala Asp Ile Thr Ala Glu Val Gly Ser Ile Gln Arg Leu Ala Lys
 310 315 320 325

tcc gtg gag atg cat ggg ctg acc ggt tct ttg ccg agg gtt tta agc 1123
 Ser Val Glu Met His Gly Leu Thr Gly Ser Leu Pro Arg Val Leu Ser
 330 335 340

tca gca tgc gac gcg gtc ctc ggg gag gtg gcg gca tgactgacat 1169
 Ser Ala Cys Asp Ala Val Leu Gly Glu Val Ala Ala
 345 350

tgatctggtg gtg 1182

<210> 1940

<211> 353

<212> PRT

<213> Corynebacterium glutamicum

<400> 1940

Met Asn Thr Ile Thr His Gln Ala Ile Leu Ile Ala Val Glu Asp Pro
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Val Leu His Pro Glu Ala Met His Val Ala Ala Ala Thr Gly Arg Pro
 20 25 30

Val Ile Glu Thr Thr Asn Leu Met Asp Ile Ser Arg His Phe His Arg
 35 40 45

Thr Ser Ala Val Leu Ile Asp Ala Ser Met Ala Ser Gln Leu Ser Pro
 50 55 60

Gly Lys Arg Arg Asp Arg Val Phe Leu Leu Asp Ser Asp Pro Gly Pro
 65 70 75 80

Ser Asp Trp Lys Thr Ala Met Lys Ile His Ala Glu Gln Ala Met Leu
 85 90 95

Leu Pro Ala Gln Ala Gly Glu Leu Leu Ser Ala Leu Gly Arg Asp Asp
 100 105 110

Lys Gln Leu Pro Val Ala Ser Gly His Val Ile Gly Val Ala Gly Val
 115 120 125

Val Gly Gly Thr Gly Ala Ser Thr Phe Ala Ala Ala Leu Ala Lys Arg
 130 135 140

Arg Ala Glu Ser Val Thr Thr Val Leu Ile Asp Ala Asp Pro Ser Ser
 145 150 155 160

Gly Gly Ile Asp Leu Leu Leu Gly Ile Glu Asp Val Pro Gly Ala Arg
 165 170 175

Trp Pro Asp Val Gly Leu Arg Arg Gly Thr Val Gln Ala Ala Asp Val
 180 185 190
 Leu Lys Ala Leu Pro Ser Thr Pro Asp Glu Val Val Val Leu Ser Thr
 195 200 205
 Ala Arg Ser Asn Ile Leu Asp Pro Phe Ala Leu Ser Glu Ser Asp Val
 210 215 220
 Ser Ala Ala Ile Asp Cys Phe Leu Ser Ala Asp Arg Ser Val Asp Val
 225 230 235 240
 Val Val Asp Leu Pro His Ala Arg Val His Pro Asp Ile Ala Glu Arg
 245 250 255
 Leu Ser His Leu Val Leu Val Ile Pro Ala Glu Val Arg Ala Val Ala
 260 265 270
 Ala Ala Arg Ala Arg Cys Leu Glu Leu Gln Gln Leu His Val Ser Ile
 275 280 285
 Thr Cys Val Leu Arg His Arg Gly Trp Ser Gly Leu Asp Val Ala Glu
 290 295 300
 Val Glu Glu Ile Leu Gly Ala Asp Ile Thr Ala Glu Val Gly Ser Ile
 305 310 315 320
 Gln Arg Leu Ala Lys Ser Val Glu Met His Gly Leu Thr Gly Ser Leu
 325 330 335
 Pro Arg Val Leu Ser Ser Ala Cys Asp Ala Val Leu Gly Glu Val Ala
 340 345 350

Ala

<210> 1941
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXA00814

<400> 1941
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 gggatttgga ccacggcatg cacgaaggga gcgaagaggc atg gtt tat gcc cta 115
 Met Val Tyr Ala Leu
 1 5
 ggc ctt ctt agc gtg gcg gtg ttg atc tct ggt tca agg ggc ccc ggc 163
 Gly Leu Leu Ser Val Ala Val Leu Ile Ser Gly Ser Arg Gly Pro Gly
 10 15 20
 gcg cgt acc agg cca cca aca cct ggg aat ggc gtc cat cta ttc gcc 211
 Ala Arg Thr Arg Pro Pro Thr Pro Gly Asn Gly Val His Leu Phe Ala

25	30	35	
cta att gca cta ttt tgc ctg gcc aca gtg cta ttt atc gtc gtt gac Leu Ile Ala Leu Phe Cys Leu Ala Thr Val Leu Phe Ile Val Val Asp 40 45 50			259
gcc tac acg atg atc gcc ggc atc atc atc gcc aca act cta ttc tgg Ala Tyr Thr Met Ile Ala Gly Ile Ile Ile Ala Thr Leu Phe Trp 55 60 65			307
tat ctc cgc cag aca cac gcc gca gcc caa cgc acc aaa caa tcc ctc Tyr Leu Arg Gln Thr His Ala Ala Ala Gln Arg Thr Lys Gln Ser Leu 70 75 80 85			355
caa tta gcc agc ttc tta agc ctc tgc gca ggc aat tta cgc gcc ggg Gln Leu Ala Ser Phe Leu Ser Leu Cys Ala Gly Asn Leu Arg Ala Gly 90 95 100			403
gtc acc atg gtc gac gcc atg gac tac gcg ctc gac aac acc acg ccg Val Thr Met Val Asp Ala Met Asp Tyr Ala Leu Asp Asn Thr Thr Pro 105 110 115			451
gac aaa ttc tta agc ccc acg ttg cag acc gca gcc agg cag gcg cgc Asp Lys Phe Leu Ser Pro Thr Leu Gln Thr Ala Ala Arg Gln Ala Arg 120 125 130			499
tcg ggc ggc agc ggg ccg cga gtg ctt atc gac gcc tcc ctc ccc gat Ser Gly Gly Ser Gly Pro Arg Val Leu Ile Asp Ala Ser Leu Pro Asp 135 140 145			547
ctt caa cgc ctc ggc cat ttg tgg gaa aca tca gaa cga cac ggc atc Leu Gln Arg Leu Gly His Leu Trp Glu Thr Ser Glu Arg His Gly Ile 150 155 160 165			595
ccg ctg gtc gcc ctc att gat caa atg agg tcc cgg att tca tcg aag Pro Leu Val Ala Leu Ile Asp Gln Met Arg Ser Arg Ile Ser Ser Lys 170 175 180			643
caa cgc cac ggc gaa tcc acc cga gct gca ctc caa gga ccg caa gca Gln Arg His Gly Glu Ser Thr Arg Ala Ala Leu Gln Gly Pro Gln Ala 185 190 195			691
acc gca gtg atc ctt acc gtg ttg cca cta gca gga atg ctc atg ggc Thr Ala Val Ile Leu Thr Val Leu Pro Leu Ala Gly Met Leu Met Gly 200 205 210			739
aca gcc atg gga gca aac ccc ctt ggg cta ctc acc ggt ggt ggg atc Thr Ala Met Gly Ala Asn Pro Leu Gly Leu Leu Thr Gly Gly Gly Ile 215 220 225			787
ggt ggg ttc ctg ctt gtc atc ggt gtg ggc ctc gat gct gca ggg ttt Gly Gly Phe Leu Leu Val Ile Gly Val Gly Leu Asp Ala Ala Gly Phe 230 235 240 245			835
gtg ctc acc cac aaa att ctc cag agc gcg agc ccc tca tgattacagc Val Leu Thr His Lys Ile Leu Gln Ser Ala Ser Pro Ser 250 255			884
actagttctt gca			897

<210> 1942

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 1942

Met Val Tyr Ala Leu Gly Leu Leu Ser Val Ala Val Leu Ile Ser Gly
1 5 10 15
Ser Arg Gly Pro Gly Ala Arg Thr Arg Pro Pro Thr Pro Gly Asn Gly
20 25 30
Val His Leu Phe Ala Leu Ile Ala Leu Phe Cys Leu Ala Thr Val Leu
35 40 45
Phe Ile Val Val Asp Ala Tyr Thr Met Ile Ala Gly Ile Ile Ile Ala
50 55 60
Thr Thr Leu Phe Trp Tyr Leu Arg Gln Thr His Ala Ala Ala Gln Arg
65 70 75 80
Thr Lys Gln Ser Leu Gln Leu Ala Ser Phe Leu Ser Leu Cys Ala Gly
85 90 95
Asn Leu Arg Ala Gly Val Thr Met Val Asp Ala Met Asp Tyr Ala Leu
100 105 110
Asp Asn Thr Thr Pro Asp Lys Phe Leu Ser Pro Thr Leu Gln Thr Ala
115 120 125
Ala Arg Gln Ala Arg Ser Gly Gly Ser Gly Pro Arg Val Leu Ile Asp
130 135 140
Ala Ser Leu Pro Asp Leu Gln Arg Leu Gly His Leu Trp Glu Thr Ser
145 150 155 160
Glu Arg His Gly Ile Pro Leu Val Ala Leu Ile Asp Gln Met Arg Ser
165 170 175
Arg Ile Ser Ser Lys Gln Arg His Gly Glu Ser Thr Arg Ala Ala Leu
180 185 190
Gln Gly Pro Gln Ala Thr Ala Val Ile Leu Thr Val Leu Pro Leu Ala
195 200 205
Gly Met Leu Met Gly Thr Ala Met Gly Ala Asn Pro Leu Gly Leu Leu
210 215 220
Thr Gly Gly Gly Ile Gly Gly Phe Leu Leu Val Ile Gly Val Gly Leu
225 230 235 240
Asp Ala Ala Gly Phe Val Leu Thr His Lys Ile Leu Gln Ser Ala Ser
245 250 255
Pro Ser

<210> 1943

<211> 696

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA00815

<400> 1943

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ttgtgctcac	ccacaaaatt	ctccagagcg	cgagcccctc	atg	att	aca	gca	cta	115
				Met	Ile	Thr	Ala	Leu	
				1				5	

ggt	ctt	gca	gca	gtg	gcc	atg	ttc	ctc	ggt	tca	ccc	aac	cct	gga	ggt	163
Val	Leu	Ala	Ala	Val	Ala	Met	Phe	Leu	Gly	Ser	Pro	Asn	Pro	Gly	Val	
				10					15					20		

cgc	ggt	gga	ttg	ata	agc	ccc	aaa	tcc	ggt	aaa	agc	ctg	cgt	atc	cga	211
Arg	Gly	Gly	Leu	Ile	Ser	Pro	Lys	Ser	Gly	Lys	Ser	Leu	Arg	Ile	Arg	
			25					30					35			

gct	ggc	cca	aaa	aag	ctg	ggc	aac	gct	gac	cca	gtg	gat	gtc	tct	gca	259
Ala	Gly	Pro	Lys	Lys	Leu	Gly	Asn	Ala	Asp	Pro	Val	Asp	Val	Ser	Ala	
		40					45					50				

gat	atc	gaa	ctg	ttt	tca	gcg	tgt	ttg	gat	gcg	ggt	tta	aac	aca	cgt	307
Asp	Ile	Glu	Leu	Phe	Ser	Ala	Cys	Leu	Asp	Ala	Gly	Leu	Asn	Thr	Arg	
	55					60					65					

gat	gca	gcg	cag	gtg	gtg	gct	cat	ggt	gca	gcc	att	acg	cac	cgc	gaa	355
Asp	Ala	Ala	Gln	Val	Val	Ala	His	Val	Ala	Ala	Ile	Thr	His	Arg	Glu	
	70				75				80						85	

ctg	tgg	aca	cat	gtg	gtg	gca	ttg	cta	tcg	att	gga	gtg	agt	gcc	cct	403
Leu	Trp	Thr	His	Val	Val	Ala	Leu	Leu	Ser	Ile	Gly	Val	Ser	Ala	Pro	
				90					95					100		

caa	gca	ttc	gcc	ctg	atg	gca	gga	ggt	gat	ggg	ctg	gat	gaa	cta	gcc	451
Gln	Ala	Phe	Ala	Leu	Met	Ala	Gly	Val	Asp	Gly	Leu	Asp	Glu	Leu	Ala	
			105					110					115			

aat	tta	gcc	acc	gtg	tcg	cac	agg	tcg	ggc	agt	gca	tta	agt	gat	ggg	499
Asn	Leu	Ala	Thr	Val	Ser	His	Arg	Ser	Gly	Ser	Ala	Leu	Ser	Asp	Gly	
		120					125					130				

tgc	agg	aac	att	tcc	acc	tcg	ttg	ttg	gcc	tct	gct	ggt	gac	aag	cgc	547
Cys	Arg	Asn	Ile	Ser	Thr	Ser	Leu	Leu	Ala	Ser	Ala	Gly	Asp	Lys	Arg	
	135					140					145					

acc	gcc	gca	gca	gaa	cgc	gca	gga	gtg	ttc	atc	gcc	ctg	cca	ctt	gct	595
Thr	Ala	Ala	Ala	Glu	Arg	Ala	Gly	Val	Phe	Ile	Ala	Leu	Pro	Leu	Ala	
	150				155				160					165		

ctg	tgt	ttc	ctc	ccc	gca	ttc	atg	att	gtc	ggg	ctt	gca	cca	gtg	gtg	643
Leu	Cys	Phe	Leu	Pro	Ala	Phe	Met	Ile	Val	Gly	Leu	Ala	Pro	Val	Val	
				170					175					180		

ctc	agc	ttg	ggt	acg	caa	ctt	atc	aat	ttc	tagaaaacac	acacaggaga	693
Leu	Ser	Leu	Gly	Thr	Gln	Leu	Ile	Asn	Phe			
			185					190				

aaa

696

<210> 1944
<211> 191
<212> PRT
<213> Corynebacterium glutamicum

<400> 1944
Met Ile Thr Ala Leu Val Leu Ala Ala Val Ala Met Phe Leu Gly Ser
1 5 10 15
Pro Asn Pro Gly Val Arg Gly Gly Leu Ile Ser Pro Lys Ser Gly Lys
20 25 30
Ser Leu Arg Ile Arg Ala Gly Pro Lys Lys Leu Gly Asn Ala Asp Pro
35 40 45
Val Asp Val Ser Ala Asp Ile Glu Leu Phe Ser Ala Cys Leu Asp Ala
50 55 60
Gly Leu Asn Thr Arg Asp Ala Ala Gln Val Val Ala His Val Ala Ala
65 70 75 80
Ile Thr His Arg Glu Leu Trp Thr His Val Val Ala Leu Leu Ser Ile
85 90 95
Gly Val Ser Ala Pro Gln Ala Phe Ala Leu Met Ala Gly Val Asp Gly
100 105 110
Leu Asp Glu Leu Ala Asn Leu Ala Thr Val Ser His Arg Ser Gly Ser
115 120 125
Ala Leu Ser Asp Gly Cys Arg Asn Ile Ser Thr Ser Leu Leu Ala Ser
130 135 140
Ala Gly Asp Lys Arg Thr Ala Ala Ala Glu Arg Ala Gly Val Phe Ile
145 150 155 160
Ala Leu Pro Leu Ala Leu Cys Phe Leu Pro Ala Phe Met Ile Val Gly
165 170 175
Leu Ala Pro Val Val Leu Ser Leu Gly Thr Gln Leu Ile Asn Phe
180 185 190

<210> 1945
<211> 420
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(397)
<223> RXA00816

<400> 1945
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ttcccggtgg aaaactagct gtgcaaatga cgaaggctac atg acc atc gcc agc 115

Met Thr Ile Ala Ser
1 5

gct ggt gtc gcc tcc atc ctc att agc ctg ctg gtg gtg ctg gcc tgg 163
Ala Gly Val Ala Ser Ile Leu Ile Ser Leu Leu Val Val Leu Ala Trp
10 15 20

cag gcg gga aac ctc gtg gcc agg gaa caa gca cag gta gcg gcc gat 211
Gln Ala Gly Asn Leu Val Ala Arg Glu Gln Ala Gln Val Ala Ala Asp
25 30 35

gtt tca gct gtt gcc gga gcc tac gcc ttt gcc cgc ggg gaa cta ccc 259
Val Ser Ala Val Ala Gly Ala Tyr Ala Phe Ala Arg Gly Glu Leu Pro
40 45 50

gac gct gcc tgc gcc acc gcg aaa cac aca gcc gaa gca aac aac gca 307
Asp Ala Ala Cys Ala Thr Ala Lys His Thr Ala Glu Ala Asn Asn Ala
55 60 65

caa cta gaa aac tgc gca aca gaa ggg gag gat ctc acg ctc acc gtc 355
Gln Leu Glu Asn Cys Ala Thr Glu Gly Glu Asp Leu Thr Leu Thr Val
70 75 80 85

acc gtt cgt gga caa gaa gcc cac gca aaa gca gga cct tta 397
Thr Val Arg Gly Gln Glu Ala His Ala Lys Ala Gly Pro Leu
90 95

tgagggttccc aacaagggtca cca 420

<210> 1946

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 1946

Met Thr Ile Ala Ser Ala Gly Val Ala Ser Ile Leu Ile Ser Leu Leu
1 5 10 15

Val Val Leu Ala Trp Gln Ala Gly Asn Leu Val Ala Arg Glu Gln Ala
20 25 30

Gln Val Ala Ala Asp Val Ser Ala Val Ala Gly Ala Tyr Ala Phe Ala
35 40 45

Arg Gly Glu Leu Pro Asp Ala Ala Cys Ala Thr Ala Lys His Thr Ala
50 55 60

Glu Ala Asn Asn Ala Gln Leu Glu Asn Cys Ala Thr Glu Gly Glu Asp
65 70 75 80

Leu Thr Leu Thr Val Thr Val Arg Gly Gln Glu Ala His Ala Lys Ala
85 90 95

Gly Pro Leu

<210> 1947

<211> 654

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(631)

<223> RXA00826

<400> 1947

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ccgtgtccat tcagactggt ttctttaagt tcttgggcac atg atc aca gtt tta 115
                                         Met Ile Thr Val Leu
                                         1                               5

att gat gga caa tcc ggt gcg ggc aaa acc acc ttg gcg ggt gag tta 163
Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr Leu Ala Gly Glu Leu
                        10                        15                        20

gct gcc cgc acc ggg ttt cag ttg gtt cat ttg gat gac ttt tat cct 211
Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu Asp Asp Phe Tyr Pro
                        25                        30                        35

ggt tgg act ggc ctt gaa gcg gca tcg gag att gtt gca cgc cat gtt 259
Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile Val Ala Arg His Val
                        40                        45                        50

ttg gac gcg gac aac ccc ggt ttc ttc acg tgg gat tgg cac aac aat 307
Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn
                        55                        60                        65

tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc 355
Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly Arg Ser Leu Ile Ile
                        70                        75                        80                        85

gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tcg ctg 403
Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu
                        90                        95                        100

ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga 451
Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg
                        105                        110                        115

aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa 499
Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys
                        120                        125                        130

gtg tgg gcg cag cag gag caa cgc cat ttc tct tta ggc gtt gag gtg 547
Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val
                        135                        140                        145

gat cat gag att gtg cta ggt tct gat gag gct tcg gga cga ccc gaa 595
Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu
                        150                        155                        160                        165

gaa atc tat gac agc ctg gga acg gcc cag agt tct taagaaagtt 641
Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser Ser
                        170                        175

tgactagaga aca 654

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<210> 1948
 <211> 177
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1948
 Met Ile Thr Val Leu Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr
 1 5 10 15
 Leu Ala Gly Glu Leu Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu
 20 25 30
 Asp Asp Phe Tyr Pro Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile
 35 40 45
 Val Ala Arg His Val Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp
 50 55 60
 Asp Trp His Asn Asn Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly
 65 70 75 80
 Arg Ser Leu Ile Ile Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys
 85 90 95
 Arg Lys Ala Ser Leu Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly
 100 105 110
 Pro Glu Ala Leu Arg Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr
 115 120 125
 Ala Pro Phe Trp Lys Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser
 130 135 140
 Leu Gly Val Glu Val Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala
 145 150 155 160
 Ser Gly Arg Pro Glu Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser
 165 170 175
 Ser

<210> 1949
 <211> 846
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(823)
 <223> RXA00830

<400> 1949
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 aacaggacgc caccttaaag cttatgtaga ttagtttctt atg gaa aac cct ggt 115
 Met Glu Asn Pro Gly
 1 5
 gat ctc ggc gct atg cca cag tac ggt ttt gag cat att tcg atg ctc 163

Asp	Leu	Gly	Ala	Met	Pro	Gln	Tyr	Gly	Phe	Glu	His	Ile	Ser	Met	Leu	
				10					15					20		
atc	acc	gct	gtg	gtt	tta	gcg	att	ctt	gtc	gtc	ccc	att	gct	cgt	cga	211
Ile	Thr	Ala	Val	Val	Leu	Ala	Ile	Leu	Val	Val	Pro	Ile	Ala	Arg	Arg	
				25					30					35		
ttc	aac	ttc	gca	ccg	gca	ttt	ggc	tgg	gtg	cta	ctc	atc	gca	aca	ctt	259
Phe	Asn	Phe	Ala	Pro	Ala	Phe	Gly	Trp	Val	Leu	Leu	Ile	Ala	Thr	Leu	
				40					45					50		
ctg	tcg	aac	ctg	tgg	aat	ttt	atg	ccc	ggc	tat	tac	acg	ctg	gac	caa	307
Leu	Ser	Asn	Leu	Trp	Asn	Phe	Met	Pro	Gly	Tyr	Tyr	Thr	Leu	Asp	Gln	
				55					60					65		
tct	tgg	cca	ttc	cac	ttc	tca	gat	gca	ttg	cgc	att	att	gct	gcc	atc	355
Ser	Trp	Pro	Phe	His	Phe	Ser	Asp	Ala	Leu	Arg	Ile	Ile	Ala	Ala	Ile	
				70					75					80		
gca	ttg	att	aat	cgc	gcg	cgg	tgg	gca	gtt	tca	gtg	act	att	ttg	tgg	403
Ala	Leu	Ile	Asn	Arg	Ala	Arg	Trp	Ala	Val	Ser	Val	Thr	Ile	Leu	Trp	
				90					95					100		
ggc	acc	acg	atc	aac	ctg	atg	tca	ctg	ctc	act	cca	gat	gtt	cag	tat	451
Gly	Thr	Thr	Ile	Asn	Leu	Met	Ser	Leu	Leu	Thr	Pro	Asp	Val	Gln	Tyr	
				105					110					115		
tta	cag	gtt	ccc	tgg	ctg	gag	ttt	tta	atg	tac	tgg	ttt	atg	cac	att	499
Leu	Gln	Val	Pro	Trp	Leu	Glu	Phe	Leu	Met	Tyr	Trp	Phe	Met	His	Ile	
				120					125					130		
tct	gtg	ttc	cta	gca	gct	ata	att	ctc	att	ttc	gct	ttt	gga	gaa	aag	547
Ser	Val	Phe	Leu	Ala	Ala	Ile	Ile	Leu	Ile	Phe	Ala	Phe	Gly	Glu	Lys	
				135					140					145		
cca	ggg	ctg	tcc	gga	gtg	gtt	atg	tcc	gtt	gca	gtg	gcg	att	agc	tgg	595
Pro	Gly	Leu	Ser	Gly	Val	Val	Met	Ser	Val	Ala	Val	Ala	Ile	Ser	Trp	
				150					155					160		
ggc	atc	atg	tgc	ctc	atg	gtc	aac	gca	ttt	ttg	gga	acc	aac	tac	ggg	643
Gly	Ile	Met	Cys	Leu	Met	Val	Asn	Ala	Phe	Leu	Gly	Thr	Asn	Tyr	Gly	
				170					175					180		
tac	ctc	tcc	aca	gaa	cca	gaa	tca	gcg	tca	att	ctg	gat	ttg	ttg	gga	691
Tyr	Leu	Ser	Thr	Glu	Pro	Glu	Ser	Ala	Ser	Ile	Leu	Asp	Leu	Leu	Gly	
				185					190					195		
gga	tgg	ccg	ttc	tac	atc	gtc	gcg	gaa	gta	tta	ctc	ctg	tgt	gca	gtg	739
Gly	Trp	Pro	Phe	Tyr	Ile	Val	Ala	Glu	Val	Leu	Leu	Leu	Cys	Ala	Val	
				200					205					210		
tgg	gct	ttg	tgg	tct	tat	ctg	att	gat	aag	ctg	cct	atc	acg	tat	cgc	787
Trp	Ala	Leu	Trp	Ser	Tyr	Leu	Ile	Asp	Lys	Leu	Pro	Ile	Thr	Tyr	Arg	
				215					220					225		
cct	gct	tac	cgt	ccg	aaa	act	cgg	aag	gcc	gct	gcg	taaccgcct				833

<210> 1950

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 1950

Met Glu Asn Pro Gly Asp Leu Gly Ala Met Pro Gln Tyr Gly Phe Glu
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His Ile Ser Met Leu Ile Thr Ala Val Val Leu Ala Ile Leu Val Val
20 25 30

Pro Ile Ala Arg Arg Phe Asn Phe Ala Pro Ala Phe Gly Trp Val Leu
35 40 45

Leu Ile Ala Thr Leu Leu Ser Asn Leu Trp Asn Phe Met Pro Gly Tyr
50 55 60

Tyr Thr Leu Asp Gln Ser Trp Pro Phe His Phe Ser Asp Ala Leu Arg
65 70 75 80

Ile Ile Ala Ala Ile Ala Leu Ile Asn Arg Ala Arg Trp Ala Val Ser
85 90 95

Val Thr Ile Leu Trp Gly Thr Thr Ile Asn Leu Met Ser Leu Leu Thr
100 105 110

Pro Asp Val Gln Tyr Leu Gln Val Pro Trp Leu Glu Phe Leu Met Tyr
115 120 125

Trp Phe Met His Ile Ser Val Phe Leu Ala Ala Ile Ile Leu Ile Phe
130 135 140

Ala Phe Gly Glu Lys Pro Gly Leu Ser Gly Val Val Met Ser Val Ala
145 150 155 160

Val Ala Ile Ser Trp Gly Ile Met Cys Leu Met Val Asn Ala Phe Leu
165 170 175

Gly Thr Asn Tyr Gly Tyr Leu Ser Thr Glu Pro Glu Ser Ala Ser Ile
180 185 190

Leu Asp Leu Leu Gly Gly Trp Pro Phe Tyr Ile Val Ala Glu Val Leu
195 200 205

Leu Leu Cys Ala Val Trp Ala Leu Trp Ser Tyr Leu Ile Asp Lys Leu
210 215 220

Pro Ile Thr Tyr Arg Pro Ala Tyr Arg Pro Lys Thr Arg Lys Ala Ala
225 230 235 240

Ala

<210> 1951

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> RXA00853

<400> 1951

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agcttgcttg ttgaacactg ttcaggtgta tgattttttc atg cct aca tcc tct 115
 Met Pro Thr Ser Ser
 1 5

tct cct gca act gtg act ccg cta aag aag cag tct tca cgt aaa cag 163
 Ser Pro Ala Thr Val Thr Pro Leu Lys Lys Gln Ser Ser Arg Lys Gln
 10 15 20

ctc caa gac atc gcg ctt att gca gtt ttt gca gca ctg atc att gtg 211
 Leu Gln Asp Ile Ala Leu Ile Ala Val Phe Ala Ala Leu Ile Ile Val
 25 30 35

ctt gct ttt gtt tcc atc cca gtt ggc aca gcg gga gtg cct att gtt 259
 Leu Ala Phe Val Ser Ile Pro Val Gly Thr Ala Gly Val Pro Ile Val
 40 45 50

ttg cag aat gcc tcc atc gtt ttg gct ggc ctg att ctt ggt ggt cga 307
 Leu Gln Asn Ala Ser Ile Val Leu Ala Gly Leu Ile Leu Gly Gly Arg
 55 60 65

cgt ggt ttt ctc act gct ttg ctg ttc ctg gca ctc ggc ctg att ggc 355
 Arg Gly Phe Leu Thr Ala Leu Leu Phe Leu Ala Leu Gly Leu Ile Gly
 70 75 80 85

ctg cct gtc ctt gca ggt ggt cgt acc act ttg gcc gca ctt gct ggc 403
 Leu Pro Val Leu Ala Gly Gly Arg Thr Thr Leu Ala Ala Leu Ala Gly
 90 95 100

cca aca gct ggc tac atc gtg ggt tac ctc att tcc cca ctt gtt gca 451
 Pro Thr Ala Gly Tyr Ile Val Gly Tyr Leu Ile Ser Pro Leu Val Ala
 105 110 115

ggc atc atc gct tac ctc gca cct aaa aag cgt ggc gct gga atg ttc 499
 Gly Ile Ile Ala Tyr Leu Ala Pro Lys Lys Arg Gly Ala Gly Met Phe
 120 125 130

atc gtt tta ggc ctg gcg ggt ctc gcg ggt ctg atc acc caa tac gct 547
 Ile Val Leu Gly Leu Ala Gly Leu Ala Gly Leu Ile Thr Gln Tyr Ala
 135 140 145

tgc ggc atc gtg ggt ctc gtc ctt cgt gcg ggt cta agc ttg agt gaa 595
 Cys Gly Ile Val Gly Leu Val Leu Arg Ala Gly Leu Ser Leu Ser Glu
 150 155 160 165

gca aca att gct caa ggt gcc ttt gtg ctg cca gat ttg gcc aag atc 643
 Ala Thr Ile Ala Gln Gly Ala Phe Val Leu Pro Asp Leu Ala Lys Ile
 170 175 180

acc gtc atg gtc ata atc gcc gct gga gtt cat gca gca ttc cct gac 691
 Thr Val Met Val Ile Ile Ala Ala Gly Val His Ala Ala Phe Pro Asp
 185 190 195

atc cgt aag aaa tagttccaac ccacttttcc tca 726

Ile Arg Lys Lys
200

<210> 1952

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1952

Met Pro Thr Ser Ser Ser Pro Ala Thr Val Thr Pro Leu Lys Lys Gln
1 5 10 15

Ser Ser Arg Lys Gln Leu Gln Asp Ile Ala Leu Ile Ala Val Phe Ala
20 25 30

Ala Leu Ile Ile Val Leu Ala Phe Val Ser Ile Pro Val Gly Thr Ala
35 40 45

Gly Val Pro Ile Val Leu Gln Asn Ala Ser Ile Val Leu Ala Gly Leu
50 55 60

Ile Leu Gly Gly Arg Arg Gly Phe Leu Thr Ala Leu Leu Phe Leu Ala
65 70 75 80

Leu Gly Leu Ile Gly Leu Pro Val Leu Ala Gly Gly Arg Thr Thr Leu
85 90 95

Ala Ala Leu Ala Gly Pro Thr Ala Gly Tyr Ile Val Gly Tyr Leu Ile
100 105 110

Ser Pro Leu Val Ala Gly Ile Ile Ala Tyr Leu Ala Pro Lys Lys Arg
115 120 125

Gly Ala Gly Met Phe Ile Val Leu Gly Leu Ala Gly Leu Ala Gly Leu
130 135 140

Ile Thr Gln Tyr Ala Cys Gly Ile Val Gly Leu Val Leu Arg Ala Gly
145 150 155 160

Leu Ser Leu Ser Glu Ala Thr Ile Ala Gln Gly Ala Phe Val Leu Pro
165 170 175

Asp Leu Ala Lys Ile Thr Val Met Val Ile Ile Ala Ala Gly Val His
180 185 190

Ala Ala Phe Pro Asp Ile Arg Lys Lys
195 200

<210> 1953

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(426)

<223> RXA00861

<400> 1953

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 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15
 cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc 96
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30
 act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45
 ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60
 ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc 240
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80
 cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95
 aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac 336
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110
 aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125
 gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca 426
 Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 1954

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 1954

Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
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 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 1955

<211> 680

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXA00862

<400> 1955

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cggtcacaacg cctacaacct ctgctagtcc tgctccagtt gtg aca gaa act gaa 115
 Val Thr Glu Thr Glu
 1 5

acc gct aac ccg gtc acc aca act cgc acg cct tca gat gct gcc ccg 163
 Thr Ala Asn Pro Val Thr Thr Thr Arg Thr Pro Ser Asp Ala Ala Pro
 10 15 20

tcg cct acc act tca gag ccc act ggt tca gag tcc acc aac tcc cct 211
 Ser Pro Thr Thr Ser Glu Pro Thr Gly Ser Glu Ser Thr Asn Ser Pro
 25 30 35

tcc ccc act gct ttg ccg ccg ttg ggt tcc ccg tcg atg gat cag aag 259
 Ser Pro Thr Ala Leu Pro Pro Leu Gly Ser Pro Ser Met Asp Gln Lys
 40 45 50

cag cag gct caa gtt ggt gac tcc gat atg tcg atc gct ggc atc cgc 307
 Gln Gln Ala Gln Val Gly Asp Ser Asp Met Ser Ile Ala Gly Ile Arg
 55 60 65

gtt gcc gag cac gaa acg ttc aca cga gtt gtt ttt gat atc gcc ggt 355
 Val Ala Glu His Glu Thr Phe Thr Arg Val Val Phe Asp Ile Ala Gly
 70 75 80 85

aat ggc caa cct ggt tgg tgg gtc gat tgg gcc act gat cca att cag 403
 Asn Gly Gln Pro Gly Trp Trp Val Asp Trp Ala Thr Asp Pro Ile Gln
 90 95 100

cag gcg tca ggt ctt cca gtt gag atg gct ggt gat tcc ttc ctc aac 451
 Gln Ala Ser Gly Leu Pro Val Glu Met Ala Gly Asp Ser Phe Leu Asn
 105 110 115

gtc aat att caa ggc act gga tat cct gat cag gtt gtc gtt cca ggt 499
 Val Asn Ile Gln Gly Thr Gly Tyr Pro Asp Gln Val Val Val Pro Gly
 120 125 130

atc gat acc gga tca tat cct ggt gca ggc att gtt gaa gac atc aac 547
 Ile Asp Thr Gly Ser Tyr Pro Gly Ala Gly Ile Val Glu Asp Ile Asn

135	140	145	
ttc acc agt att ttt gaa gcc cgt tcc caa gtt ctc att ggt gta tct			595
Phe Thr Ser Ile Phe Glu Ala Arg Ser Gln Val Leu Ile Gly Val Ser			
150	155	160	165
ggt caa ccc cga aat tac tcg gtc tca ttg ctg cag gaa cca acc agg			643
Gly Gln Pro Arg Asn Tyr Ser Val Ser Leu Leu Gln Glu Pro Thr Arg			
	170	175	180
ctt gtg gtg gac atc gtt cac tagcgctgga acgccg			680
Leu Val Val Asp Ile Val His			
	185		

<210> 1956

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 1956

Val Thr Glu Thr Glu Thr Ala Asn Pro Val Thr Thr Thr Arg Thr Pro
1 5 10 15

Ser Asp Ala Ala Pro Ser Pro Thr Thr Ser Glu Pro Thr Gly Ser Glu
20 25 30

Ser Thr Asn Ser Pro Ser Pro Thr Ala Leu Pro Pro Leu Gly Ser Pro
35 40 45

Ser Met Asp Gln Lys Gln Gln Ala Gln Val Gly Asp Ser Asp Met Ser
50 55 60

Ile Ala Gly Ile Arg Val Ala Glu His Glu Thr Phe Thr Arg Val Val
65 70 75 80

Phe Asp Ile Ala Gly Asn Gly Gln Pro Gly Trp Trp Val Asp Trp Ala
85 90 95

Thr Asp Pro Ile Gln Gln Ala Ser Gly Leu Pro Val Glu Met Ala Gly
100 105 110

Asp Ser Phe Leu Asn Val Asn Ile Gln Gly Thr Gly Tyr Pro Asp Gln
115 120 125

Val Val Val Pro Gly Ile Asp Thr Gly Ser Tyr Pro Gly Ala Gly Ile
130 135 140

Val Glu Asp Ile Asn Phe Thr Ser Ile Phe Glu Ala Arg Ser Gln Val
145 150 155 160

Leu Ile Gly Val Ser Gly Gln Pro Arg Asn Tyr Ser Val Ser Leu Leu
165 170 175

Gln Glu Pro Thr Arg Leu Val Val Asp Ile Val His
180 185

<210> 1957

<211> 1212

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (1189)

<223> RXA00874

<400> 1957

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tctggtttga tctcaccgcc gatgaaaagg acgatatgga atg agc att ggc caa															115
Met Ser Ile Gly Gln															5
cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac															163
His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp															20
aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct															211
Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala															35
gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat															259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp															50
ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc															307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe															65
gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca															355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro															85
ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa															403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys															100
gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat															451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp															115
gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc															499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile															130
ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc															547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val															145
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg															595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu															165
act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa															643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu															180
gcc acc cgc aat gtt cac act gct ctt gca tcg gcc ttc cct act cgg															691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg															195

gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat 739
 Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn
 200 205 210

gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc 787
 Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala
 215 220 225

atc gac ctc tac caa tcg ttg gaa ggc gaa gcc cac atc caa cgc atc 835
 Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile
 230 235 240 245

cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac 883
 His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr
 250 255 260

atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga 931
 Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg
 265 270 275

cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc 979
 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser
 280 285 290

atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac 1027
 Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn
 295 300 305

gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa 1075
 Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln
 310 315 320 325

gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc 1123
 Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala
 330 335 340

tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg 1171
 Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala
 345 350 355

gtc gaa agg ctt cta gac tagttagtta ctctgcgtca aac 1212
 Val Glu Arg Leu Leu Asp
 360

<210> 1958

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 1958

Met Ser Ile Gly Gln His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys
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 20 25 30

Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
 35 40 45

Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
50 55 60

Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
65 70 75 80

Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
85 90 95

Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
100 105 110

Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala
130 135 140

Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
145 150 155 160

Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
165 170 175

Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
180 185 190

Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
195 200 205

Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
210 215 220

Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
225 230 235 240

His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
245 250 255

Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
260 265 270

Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
275 280 285

Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His
290 295 300

Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly
305 310 315 320

Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala
325 330 335

Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys
340 345 350

Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp
355 360

<210> 1959
 <211> 1878
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1855)
 <223> RXA00876

<400> 1959

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                                         Met Thr Leu Lys Ile
                                         1 5

gat ccc tcg tcc atc agt agt gct gtg tct cgc ttg aat gag ctt cag 163
Asp Pro Ser Ser Ile Ser Ser Ala Val Ser Arg Leu Asn Glu Leu Gln
                        10 15 20

cat caa gct att act gca tct caa gtg gga atg aaa tca aca att cta 211
His Gln Ala Ile Thr Ala Ser Gln Val Gly Met Lys Ser Thr Ile Leu
                        25 30 35

tcc gcg ttt tcg ccc gtc tct gga ctc gat caa ttg ggt tcc ggt cac 259
Ser Ala Phe Ser Pro Val Ser Gly Leu Asp Gln Leu Gly Ser Gly His
                        40 45 50

ggg aat gtg att aat ggt ggg gca ggc gca gca aac tct gtg ctg aat 307
Gly Asn Val Ile Asn Gly Gly Ala Gly Ala Ala Asn Ser Val Leu Asn
                        55 60 65

tcc tat gcc gaa caa atc gag tgg ttg tct gcg gct ttg cag gct tct 355
Ser Tyr Ala Glu Gln Ile Glu Trp Leu Ser Ala Ala Leu Gln Ala Ser
                        70 75 80 85

ggt gcg gct ttg act ggc cag gat gaa tta ttc gct agg ggt atg gat 403
Gly Ala Ala Leu Thr Gly Gln Asp Glu Leu Phe Ala Arg Gly Met Asp
                        90 95 100

gta gcg gat acc ggt ggc agg gtt gta gaa gag tca gta atg ttc ccg 451
Val Ala Asp Thr Gly Gly Arg Val Val Glu Glu Ser Val Met Phe Pro
                        105 110 115

gcg cgg ccg gca cct cgg ttt gag tct ttc gtt ttt aat cca cca gct 499
Ala Arg Pro Ala Pro Arg Phe Glu Ser Phe Val Phe Asn Pro Pro Ala
                        120 125 130

gtt agt cct tcg ttg tcg ttg gat gcg ttg tgt agt cag ttt tcc gga 547
Val Ser Pro Ser Leu Ser Leu Asp Ala Leu Cys Ser Gln Phe Ser Gly
                        135 140 145

acc aac tcg ggg gcg gtt ttg gag gcg cag ggg tct tgg ggc tct atg 595
Thr Asn Ser Gly Ala Val Leu Glu Ala Gln Gly Ser Trp Gly Ser Met
                        150 155 160 165

gcg tcg gct att agc aat gtg tcg gct tcg ttg tcg tcg att gct ggt 643
Ala Ser Ala Ile Ser Asn Val Ser Ala Ser Leu Ser Ser Ile Ala Gly
                        170 175 180

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gag att ttg gcg gag aac tca ggc gaa acg ttt gag cag gct gct gct	691
Glu Ile Leu Ala Glu Asn Ser Gly Glu Thr Phe Glu Gln Ala Ala Ala	
185 190 195	
cgg att aat gag gtg gcg gct gcg ggg gcg acg ttt gct gcg aat gcg	739
Arg Ile Asn Glu Val Ala Ala Ala Gly Ala Thr Phe Ala Ala Asn Ala	
200 205 210	
aaa atg atg ggg gcg tcg gtg ggg acg ctg aat cgg att tat atg ggg	787
Lys Met Met Gly Ala Ser Val Gly Thr Leu Asn Arg Ile Tyr Met Gly	
215 220 225	
cat cgc atg cag gtg ttt atg gct gcg acg tcg att aag gcg att ttg	835
His Arg Met Gln Val Phe Met Ala Ala Thr Ser Ile Lys Ala Ile Leu	
230 235 240 245	
gat ccg gtg cag agg ctt gct gcg gag agg gcg ttt ttg gcg tcg ttt	883
Asp Pro Val Gln Arg Leu Ala Ala Glu Arg Ala Phe Leu Ala Ser Phe	
250 255 260	
cag gct act ttt cag gcg gat gtg ttg acg ggt atg cct cct gtg agc	931
Gln Ala Thr Phe Gln Ala Asp Val Leu Thr Gly Met Pro Pro Val Ser	
265 270 275	
aat ttg atg cag atg aag ggg gcg aat ggt tct gcg ggg gaa att gct	979
Asn Leu Met Gln Met Lys Gly Ala Asn Gly Ser Ala Gly Glu Ile Ala	
280 285 290	
ctg ggg atg gat gag att gct ggc agt ggg cag gca tgg tct gcg gcg	1027
Leu Gly Met Asp Glu Ile Ala Gly Ser Gly Gln Ala Trp Ser Ala Ala	
295 300 305	
ggg ttg act ccg tcg ggg gct gcg cag ggt ggt gtc gcc aat gcg ggc	1075
Gly Leu Thr Pro Ser Gly Ala Ala Gln Gly Gly Val Ala Asn Ala Gly	
310 315 320 325	
agt atc gcg ccg gat gca gcg gtt caa ggt gct gcg ggg cag agt ggg	1123
Ser Ile Ala Pro Asp Ala Ala Val Gln Gly Ala Ala Gly Gln Ser Gly	
330 335 340	
gtt gga agt ttt ggc act gtc act gat cag ttg gat ggc atc aat att	1171
Val Gly Ser Phe Gly Thr Val Thr Asp Gln Leu Asp Gly Ile Asn Ile	
345 350 355	
ggg gat atg ttg acc tct gct gcc tca gct ggg cag agc ctt gcg aat	1219
Gly Asp Met Leu Thr Ser Ala Ala Ser Ala Gly Gln Ser Leu Ala Asn	
360 365 370	
ggt ttg gcg atg cct act tct acg cct aat tcg gcg tcc ggt gcg att	1267
Gly Leu Ala Met Pro Thr Ser Thr Pro Asn Ser Ala Ser Gly Ala Ile	
375 380 385	
cct tcc tcg atg tct gcg gca tcg ccg ctt ggt gcg ttt ggc agc ggt	1315
Pro Ser Ser Met Ser Ala Ala Ser Pro Leu Gly Ala Phe Gly Ser Gly	
390 395 400 405	
gca ggg ttg ggc gca cag ggt ggc tcg att gga tct tcg gca cct gga	1363
Ala Gly Leu Gly Ala Gln Gly Gly Ser Ile Gly Ser Ser Ala Pro Gly	
410 415 420	
gcg atc agt agt cga gcg gcc gga tcc gca ggt ggt tcg gta ccg gga	1411

Ala Ile Ser Ser Arg Ala Ala Gly Ser Ala Gly Gly Ser Val Pro Gly
425 430 435

atg act ggt ggt cct ggc gcg ccg ggg att acc tcg gat tcg ttg atg 1459
Met Thr Gly Gly Pro Gly Ala Pro Gly Ile Thr Ser Asp Ser Leu Met
440 445 450

gga gct cga act cat ggt gct tct tcc gcg gga gct gtc gct ccg atg 1507
Gly Ala Arg Thr His Gly Ala Ser Ser Ala Gly Ala Val Ala Pro Met
455 460 465

atg ggt ggt gct ggc gga atg tct ggt ggc gtc gtt ggt gca ggt ggt 1555
Met Gly Gly Ala Gly Gly Met Ser Gly Gly Val Val Gly Ala Gly Gly
470 475 480 485

act ggt tct cag agc aag tat gcg cgc cag act gga tcg tcg gtt gga 1603
Thr Gly Ser Gln Ser Lys Tyr Ala Arg Gln Thr Gly Ser Ser Val Gly
490 495 500

tct agt tcg cag tcg ggt tct ggc ctg ggg atg gtg gga tca ggg agt 1651
Ser Ser Ser Gln Ser Gly Ser Gly Leu Gly Met Val Gly Ser Gly Ser
505 510 515

ggg aag ccg tcg ata agc aat ttt ggg cgc ggc atg atg ccg atg atg 1699
Gly Lys Pro Ser Ile Ser Asn Phe Gly Arg Gly Met Met Pro Met Met
520 525 530

ccc atg atg ccc atg gga ggc gcc ggc ggt ggg cag aag aat acc ggc 1747
Pro Met Met Pro Met Gly Gly Ala Gly Gly Gly Gln Lys Asn Thr Gly
535 540 545

aag gtg aaa acg gtg acg tct gcg gtg gag gaa gac cgc aat ttg gcg 1795
Lys Val Lys Thr Val Thr Ser Ala Val Glu Glu Asp Arg Asn Leu Ala
550 555 560 565

gcg ctg ctg ggt gat cgg ggg ccg gtt gtt ccg ggt gtg att ggt gac 1843
Ala Leu Leu Gly Asp Arg Gly Pro Val Val Pro Gly Val Ile Gly Asp
570 575 580

tgg gtg agg ggc taacgcaaca atgtgtctaa gct 1878
Trp Val Arg Gly
585

<210> 1960

<211> 585

<212> PRT

<213> Corynebacterium glutamicum

<400> 1960

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20 25 30

Lys Ser Thr Ile Leu Ser Ala Phe Ser Pro Val Ser Gly Leu Asp Gln
35 40 45

Leu Gly Ser Gly His Gly Asn Val Ile Asn Gly Gly Ala Gly Ala Ala
50 55 60

Asn Ser Val Leu Asn Ser Tyr Ala Glu Gln Ile Glu Trp Leu Ser Ala
65 70 75 80

Ala Leu Gln Ala Ser Gly Ala Ala Leu Thr Gly Gln Asp Glu Leu Phe
85 90 95

Ala Arg Gly Met Asp Val Ala Asp Thr Gly Gly Arg Val Val Glu Glu
100 105 110

Ser Val Met Phe Pro Ala Arg Pro Ala Pro Arg Phe Glu Ser Phe Val
115 120 125

Phe Asn Pro Pro Ala Val Ser Pro Ser Leu Ser Leu Asp Ala Leu Cys
130 135 140

Ser Gln Phe Ser Gly Thr Asn Ser Gly Ala Val Leu Glu Ala Gln Gly
145 150 155 160

Ser Trp Gly Ser Met Ala Ser Ala Ile Ser Asn Val Ser Ala Ser Leu
165 170 175

Ser Ser Ile Ala Gly Glu Ile Leu Ala Glu Asn Ser Gly Glu Thr Phe
180 185 190

Glu Gln Ala Ala Ala Arg Ile Asn Glu Val Ala Ala Ala Gly Ala Thr
195 200 205

Phe Ala Ala Asn Ala Lys Met Met Gly Ala Ser Val Gly Thr Leu Asn
210 215 220

Arg Ile Tyr Met Gly His Arg Met Gln Val Phe Met Ala Ala Thr Ser
225 230 235 240

Ile Lys Ala Ile Leu Asp Pro Val Gln Arg Leu Ala Ala Glu Arg Ala
245 250 255

Phe Leu Ala Ser Phe Gln Ala Thr Phe Gln Ala Asp Val Leu Thr Gly
260 265 270

Met Pro Pro Val Ser Asn Leu Met Gln Met Lys Gly Ala Asn Gly Ser
275 280 285

Ala Gly Glu Ile Ala Leu Gly Met Asp Glu Ile Ala Gly Ser Gly Gln
290 295 300

Ala Trp Ser Ala Ala Gly Leu Thr Pro Ser Gly Ala Ala Gln Gly Gly
305 310 315 320

Val Ala Asn Ala Gly Ser Ile Ala Pro Asp Ala Ala Val Gln Gly Ala
325 330 335

Ala Gly Gln Ser Gly Val Gly Ser Phe Gly Thr Val Thr Asp Gln Leu
340 345 350

Asp Gly Ile Asn Ile Gly Asp Met Leu Thr Ser Ala Ala Ser Ala Gly
355 360 365

Gln Ser Leu Ala Asn Gly Leu Ala Met Pro Thr Ser Thr Pro Asn Ser
370 375 380

Ala Ser Gly Ala Ile Pro Ser Ser Met Ser Ala Ala Ser Pro Leu Gly
 385 390 395 400

Ala Phe Gly Ser Gly Ala Gly Leu Gly Ala Gln Gly Gly Ser Ile Gly
 405 410 415

Ser Ser Ala Pro Gly Ala Ile Ser Ser Arg Ala Ala Gly Ser Ala Gly
 420 425 430

Gly Ser Val Pro Gly Met Thr Gly Gly Pro Gly Ala Pro Gly Ile Thr
 435 440 445

Ser Asp Ser Leu Met Gly Ala Arg Thr His Gly Ala Ser Ser Ala Gly
 450 455 460

Ala Val Ala Pro Met Met Gly Gly Ala Gly Gly Met Ser Gly Gly Val
 465 470 475 480

Val Gly Ala Gly Gly Thr Gly Ser Gln Ser Lys Tyr Ala Arg Gln Thr
 485 490 495

Gly Ser Ser Val Gly Ser Ser Ser Gln Ser Gly Ser Gly Leu Gly Met
 500 505 510

Val Gly Ser Gly Ser Gly Lys Pro Ser Ile Ser Asn Phe Gly Arg Gly
 515 520 525

Met Met Pro Met Met Pro Met Met Pro Met Gly Gly Ala Gly Gly Gly
 530 535 540

Gln Lys Asn Thr Gly Lys Val Lys Thr Val Thr Ser Ala Val Glu Glu
 545 550 555 560

Asp Arg Asn Leu Ala Ala Leu Leu Gly Asp Arg Gly Pro Val Val Pro
 565 570 575

Gly Val Ile Gly Asp Trp Val Arg Gly
 580 585

<210> 1961

<211> 501

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXA00881

<400> 1961

acctgaccga ggaagccgac gagctgaccc caacgctgaa ggtcaagcgc aacgttggtg 60

ttcgccgtta cgcagacgcc atcgaccaca tctacaaccg atg agt aac aca gag 115
 Met Ser Asn Thr Glu
 1 5

acc caa ttt gat tgg gat gga tcg aca tgg acc cgc acc gaa gtc ggc 163
 Thr Gln Phe Asp Trp Asp Gly Ser Thr Trp Thr Arg Thr Glu Val Gly
 10 15 20

gaa gca cca aca cgc ttc gct gtg ggc gtg atg gag gat ttc gcc tac 211
 Glu Ala Pro Thr Arg Phe Ala Val Gly Val Met Glu Asp Phe Ala Tyr
 25 30 35

att gca gcc act ggc acg gac ggg gat gaa gag ttc ttt act ttg ggc 259
 Ile Ala Ala Thr Gly Thr Asp Gly Asp Glu Glu Phe Phe Thr Leu Gly
 40 45 50

tca aat ccg ggt ctg acg ttt ggt gat ccc gag tgg ctt ttc gct cag 307
 Ser Asn Pro Gly Leu Thr Phe Gly Asp Pro Glu Trp Leu Phe Ala Gln
 55 60 65

gat aat ccg cag tat gtg gtg gag tgc att ggc cag cag gga acc gag 355
 Asp Asn Pro Gln Tyr Val Val Glu Cys Ile Gly Gln Gln Gly Thr Glu
 70 75 80 85

ccg gca gcc ctg aag gtt gta gat aaa tat ttg tcg cga cta tct gat 403
 Pro Ala Ala Leu Lys Val Val Asp Lys Tyr Leu Ser Arg Leu Ser Asp
 90 95 100

gag gag tca cgt ggc gaa ccc acg cgg att ctc aat gaa ttg gtc tcg 451
 Glu Glu Ser Arg Gly Glu Pro Thr Arg Ile Leu Asn Glu Leu Val Ser
 105 110 115

gcg atg gag ttg ccg gca ttg ccg tgg tgatttttct cgggcttttag 498
 Ala Met Glu Leu Pro Ala Leu Pro Trp
 120 125

tga 501

<210> 1962

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 1962

Met Ser Asn Thr Glu Thr Gln Phe Asp Trp Asp Gly Ser Thr Trp Thr
 1 5 10 15

Arg Thr Glu Val Gly Glu Ala Pro Thr Arg Phe Ala Val Gly Val Met
 20 25 30

Glu Asp Phe Ala Tyr Ile Ala Ala Thr Gly Thr Asp Gly Asp Glu Glu
 35 40 45

Phe Phe Thr Leu Gly Ser Asn Pro Gly Leu Thr Phe Gly Asp Pro Glu
 50 55 60

Trp Leu Phe Ala Gln Asp Asn Pro Gln Tyr Val Val Glu Cys Ile Gly
 65 70 75 80

Gln Gln Gly Thr Glu Pro Ala Ala Leu Lys Val Val Asp Lys Tyr Leu
 85 90 95

Ser Arg Leu Ser Asp Glu Glu Ser Arg Gly Glu Pro Thr Arg Ile Leu
 100 105 110

Asn Glu Leu Val Ser Ala Met Glu Leu Pro Ala Leu Pro Trp
 115 120 125

ggc acc gcc aat ccg gcg tat gtg cgc acc atg cga ggc agc aac ccg 691
 Gly Thr Ala Asn Pro Ala Tyr Val Arg Thr Met Arg Gly Ser Asn Pro
 185 190 195

cca cgt ttc ctg ctt gag cgt gcg cgt atc gac gct gtc gtg gcc cgg 739
 Pro Arg Phe Leu Leu Glu Arg Ala Arg Ile Asp Ala Val Val Ala Arg
 200 205 210

gtt gca gac aag ctt gcg caa aag cgc aac gct gtt tcc tagaaatctc 788
 Val Ala Asp Lys Leu Ala Gln Lys Arg Asn Ala Val Ser
 215 220 225

ggtgcagcaa aaa 801

<210> 1964

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 1964

Met Ser Ser Thr Thr Ala Gln Leu Arg His Arg Glu Leu Thr Gln Glu
 1 5 10 15

Ile Tyr Asn Ile Gly Asp Glu Val Ala Glu Tyr Ile Glu His Ile Met
 20 25 30

Glu Ala Val Ser Asp Trp Asp Leu Glu Leu Val Glu Asp Cys Leu Ala
 35 40 45

Glu Phe Asp Glu Ile Ile Thr Glu Ala Arg Asp Asp Ser Arg Thr Val
 50 55 60

Val Ala Glu Leu Ser Gly Leu Arg His Ala Leu Thr Thr Gly Ile Arg
 65 70 75 80

Gln Gly Thr Val Ser Ala Arg Ala Thr Val Glu Val Asp Val Asp Lys
 85 90 95

Pro Glu Arg Leu Thr Ala Ser Glu Leu Glu Arg Asp Phe Asp Ile Asp
 100 105 110

Ala Gly Leu Val Asp Val Arg Asp Leu Ser Thr Ala Leu Asn Ala Arg
 115 120 125

Thr Asp Ala Val Val Lys Arg Leu Glu Ala Thr Val Glu Trp Val Leu
 130 135 140

Ala Glu Thr Asp Lys Val Ala Asn Asp Leu Asp Ser Leu Ser Leu Pro
 145 150 155 160

Leu Leu Tyr Gly Arg Val Ala Ala Val Ile Glu Ser Ala Thr Ser Ala
 165 170 175

Trp Ile Asn Ala Val Gly Thr Ala Asn Pro Ala Tyr Val Arg Thr Met
 180 185 190

Arg Gly Ser Asn Pro Pro Arg Phe Leu Leu Glu Arg Ala Arg Ile Asp
 195 200 205

Ala Val Val Ala Arg Val Ala Asp Lys Leu Ala Gln Lys Arg Asn Ala
 210 215 220

Val Ser
 225

<210> 1965
 <211> 642
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(619)
 <223> RXA00883

<400> 1965

aatatacaca ccaaaaactg acatgccccca agcctagtgc ctgcccccta tacatgatta 60

attgatgtta aacatagcga attcctaaga acagggtaga gtg cag ggt atg aaa 115
 Val Gln Gly Met Lys
 1 5

cgg aag atg gtc gca gcg gcg ctg gca aca gcg ctt ctt ttt ggg gct 163
 Arg Lys Met Val Ala Ala Ala Leu Ala Thr Ala Leu Leu Phe Gly Ala
 10 15 20

gca cct gcg cac gct tcc gaa ttg gta gag ccc acc aca gtt gca gag 211
 Ala Pro Ala His Ala Ser Glu Leu Val Glu Pro Thr Thr Val Ala Glu
 25 30 35

tca gtg gca ctc gat ccc aac aaa gca atc aat att ctc acc cca gat 259
 Ser Val Ala Leu Asp Pro Asn Lys Ala Ile Asn Ile Leu Thr Pro Asp
 40 45 50

ctc tgg gaa gac att gag gca aaa cca ggc gat atc gtc cac atc ccc 307
 Leu Trp Glu Asp Ile Glu Ala Lys Pro Gly Asp Ile Val His Ile Pro
 55 60 65

tac cag ggc acc cga aac tac gag gac ctc acc gta gaa gtc gcg aaa 355
 Tyr Gln Gly Thr Arg Asn Tyr Glu Asp Leu Thr Val Glu Val Ala Lys
 70 75 80 85

cct ttc gaa gat ttc caa atc ctc gtc gga ctc gac aac agc atc gtc 403
 Pro Phe Glu Asp Phe Gln Ile Leu Val Gly Leu Asp Asn Ser Ile Val
 90 95 100

atc gca gtg cca aag aac tta agt ggc gca gca tca gtc gcc cca gtt 451
 Ile Ala Val Pro Lys Asn Leu Ser Gly Ala Ala Ser Val Ala Pro Val
 105 110 115

ttc act gtc tct gac aaa aac ggt gag atc gac tct ttc acc atc aaa 499
 Phe Thr Val Ser Asp Lys Asn Gly Glu Ile Asp Ser Phe Thr Ile Lys
 120 125 130

gta agc gtc gag cca cgc cgc caa agc gac gaa gaa aag cgc tcc gca 547
 Val Ser Val Glu Pro Arg Arg Gln Ser Asp Glu Glu Lys Arg Ser Ala
 135 140 145

cta ttt gat gtc atc tct gag ctt gcc tac cgc atg cct cat ctg cca 595

Leu Phe Asp Val Ile Ser Glu Leu Ala Tyr Arg Met Pro His Leu Pro
150 155 160 165

ttc gtg tca gag ttg ctg aag tac tagaacagta acgagaaaac ccc 642
Phe Val Ser Glu Leu Leu Lys Tyr
170

<210> 1966

<211> 173

<212> PRT

<213> Corynebacterium glutamicum

<400> 1966

Val Gln Gly Met Lys Arg Lys Met Val Ala Ala Ala Leu Ala Thr Ala
1 5 10 15

Leu Leu Phe Gly Ala Ala Pro Ala His Ala Ser Glu Leu Val Glu Pro
20 25 30

Thr Thr Val Ala Glu Ser Val Ala Leu Asp Pro Asn Lys Ala Ile Asn
35 40 45

Ile Leu Thr Pro Asp Leu Trp Glu Asp Ile Glu Ala Lys Pro Gly Asp
50 55 60

Ile Val His Ile Pro Tyr Gln Gly Thr Arg Asn Tyr Glu Asp Leu Thr
65 70 75 80

Val Glu Val Ala Lys Pro Phe Glu Asp Phe Gln Ile Leu Val Gly Leu
85 90 95

Asp Asn Ser Ile Val Ile Ala Val Pro Lys Asn Leu Ser Gly Ala Ala
100 105 110

Ser Val Ala Pro Val Phe Thr Val Ser Asp Lys Asn Gly Glu Ile Asp
115 120 125

Ser Phe Thr Ile Lys Val Ser Val Glu Pro Arg Arg Gln Ser Asp Glu
130 135 140

Glu Lys Arg Ser Ala Leu Phe Asp Val Ile Ser Glu Leu Ala Tyr Arg
145 150 155 160

Met Pro His Leu Pro Phe Val Ser Glu Leu Leu Lys Tyr
165 170

<210> 1967

<211> 846

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(823)

<223> RXA00887

<400> 1967

aagaaatccg caaccatcgc agcgacaacg cttccgtgca tcgcgaaggc ggagaagaat 60

Ala Leu Ala Ala Ile Gly Val Leu Ser Asp Arg Trp
230 235 240

ctgacataac ctt

846

<210> 1968

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 1968

Met Ser Leu Pro Val Phe Ile Ser Asp Ser Ala Ala Gly Pro Gly Glu
1 5 10 15

Thr Ile Glu Leu Ala Gly Pro Glu Gly Arg His Ala Val Thr Val Lys
20 25 30

Arg Ile Gln Val Gly Glu Lys Ile Ser Leu Ile Asp Gly Arg Gly Thr
35 40 45

Ala Arg Thr Cys Thr Val Thr Ala Leu Gln Gly Lys Asp Arg Leu Asn
50 55 60

Ala Val Val Asp Leu Val Glu Glu Ile Pro Ala Pro Asn Pro Gln Val
65 70 75 80

Thr Ile Val Gln Ala Ile Pro Lys Ser Glu Arg Ser Glu Leu Thr Ile
85 90 95

Asp Leu Leu Thr Gln Ala Gly Ala Asp Arg Ile Val Ala Trp Gln Ala
100 105 110

Ser Arg Cys Val Ala Lys Trp Gly Gly Lys Glu Ala Lys Ser Leu Ala
115 120 125

Lys Trp Gln Val Ala Ala Glu Ala Ala Ala Lys Gln Ser Arg Arg Ala
130 135 140

Thr Ile Pro Glu Ile Leu Gly Val Val Gly Glu Glu Gly Val Glu Lys
145 150 155 160

Leu Ile Asp Glu Ser Asp Leu Ala Ile Ile Leu His Glu Glu Ala Thr
165 170 175

Ala Ala Ile Arg Glu Leu Glu Phe Ser Gly Asn Val Val Val Ile Ile
180 185 190

Gly Pro Glu Gly Gly Val Ala Pro Ser Glu Ile Ser Arg Phe Val Asp
195 200 205

Ala Gly Ala His Thr Val Lys Leu Gly Pro Glu Val Leu Arg Thr Ala
210 215 220

Ser Ala Gly Met Val Ala Leu Ala Ala Ile Gly Val Leu Ser Asp Arg
225 230 235 240

Trp

<210> 1969
 <211> 711
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(688)
 <223> RXA00889

<400> 1969

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tgggtccgccca ccaactgggtt ggacacattg tggatgcata cgaagactat gaagaacgcg 60
aggccccgcga attgaaacgc aaacgccagg agacacggcc atg agc att gag gta 115
                                         Met Ser Ile Glu Val
                                         1 5

ttc aac gaa tca gga tac gac ggc gtc aat gaa gaa atg ctc att gat 163
Phe Asn Glu Ser Gly Tyr Asp Gly Val Asn Glu Glu Met Leu Ile Asp
      10 15 20

gtc ctc tcc ttc gca ctc ggg gaa atg gac atc cac ccc gac gcc gaa 211
Val Leu Ser Phe Ala Leu Gly Glu Met Asp Ile His Pro Asp Ala Glu
      25 30 35

gca tcc atc cac atc gtc gac gtc gac acc atc gcc gat ctc cac gtg 259
Ala Ser Ile His Ile Val Asp Val Asp Thr Ile Ala Asp Leu His Val
      40 45 50

aaa tgg ctt gat ctt gaa ggc cca acc gac gtg atg agc ttc ccg atg 307
Lys Trp Leu Asp Leu Glu Gly Pro Thr Asp Val Met Ser Phe Pro Met
      55 60 65

gat gag ctc acc ccc ggc tac tcc cgc ccc gac ggc gcc acc ccc ggc 355
Asp Glu Leu Thr Pro Gly Tyr Ser Arg Pro Asp Gly Ala Thr Pro Gly
      70 75 80 85

ccc gcc atg ctg ggc gac att gtg ctg tgc cca gag ttc gcg gca aag 403
Pro Ala Met Leu Gly Asp Ile Val Leu Cys Pro Glu Phe Ala Ala Lys
      90 95 100

caa gcg acc aaa gca ggc cac gac tta gcc cac gag cta gct ttg ctg 451
Gln Ala Thr Lys Ala Gly His Asp Leu Ala His Glu Leu Ala Leu Leu
      105 110 115

acc gtg cac ggc agc ctg cac ctg ctt ggc tac gac cac gtc gat cca 499
Thr Val His Gly Ser Leu His Leu Leu Gly Tyr Asp His Val Asp Pro
      120 125 130

gcc gaa gag cgt gaa atg ttc gcc ctt caa aac gag ctg ctt gcc gat 547
Ala Glu Glu Arg Glu Met Phe Ala Leu Gln Asn Glu Leu Leu Ala Asp
      135 140 145

tgg tac gac aac gtc gaa gcc cgt ggc gtc acc tac cag cca aaa cca 595
Trp Tyr Asp Asn Val Glu Ala Arg Gly Val Thr Tyr Gln Pro Lys Pro
      150 155 160 165

tcc ggc gcc ggt gca ttc ccc acc gct gct gat cgt ctg gaa ttg gac 643
Ser Gly Ala Gly Ala Phe Pro Thr Ala Ala Asp Arg Leu Glu Leu Asp
      170 175 180

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gaa aag atg gaa gcg gat gac tct ggc ttt gga ggc gtt gag tcc 688
 Glu Lys Met Glu Ala Asp Asp Ser Gly Phe Gly Gly Val Glu Ser
 185 190 195

taggtggaat cctcagttat atg 711

<210> 1970

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 1970

Met Ser Ile Glu Val Phe Asn Glu Ser Gly Tyr Asp Gly Val Asn Glu
 1 5 10 15

Glu Met Leu Ile Asp Val Leu Ser Phe Ala Leu Gly Glu Met Asp Ile
 20 25 30

His Pro Asp Ala Glu Ala Ser Ile His Ile Val Asp Val Asp Thr Ile
 35 40 45

Ala Asp Leu His Val Lys Trp Leu Asp Leu Glu Gly Pro Thr Asp Val
 50 55 60

Met Ser Phe Pro Met Asp Glu Leu Thr Pro Gly Tyr Ser Arg Pro Asp
 65 70 75 80

Gly Ala Thr Pro Gly Pro Ala Met Leu Gly Asp Ile Val Leu Cys Pro
 85 90 95

Glu Phe Ala Ala Lys Gln Ala Thr Lys Ala Gly His Asp Leu Ala His
 100 105 110

Glu Leu Ala Leu Leu Thr Val His Gly Ser Leu His Leu Leu Gly Tyr
 115 120 125

Asp His Val Asp Pro Ala Glu Glu Arg Glu Met Phe Ala Leu Gln Asn
 130 135 140

Glu Leu Leu Ala Asp Trp Tyr Asp Asn Val Glu Ala Arg Gly Val Thr
 145 150 155 160

Tyr Gln Pro Lys Pro Ser Gly Ala Gly Ala Phe Pro Thr Ala Ala Asp
 165 170 175

Arg Leu Glu Leu Asp Glu Lys Met Glu Ala Asp Asp Ser Gly Phe Gly
 180 185 190

Gly Val Glu Ser
 195

<210> 1971

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(697)

<223> RXA00893

<400> 1971

acgccaacgc agagtgttta aagaaactgg cagttggaaa gctgcagttg atttagcctg 60

cgacgaactc aacgacctca aagcactgga ctaaataagct atg gtg gaa tcc caa 115
Met Val Glu Ser Gln
1 5

cac atc att ttc atc ccg gaa tcc caa caa aca ccc gac gag ttt acc 163
His Ile Ile Phe Ile Pro Glu Ser Gln Gln Thr Pro Asp Glu Phe Thr
10 15 20

gag gta gtc aac gag att ccc gcc gga atc aaa cca cgg atc gta ccg 211
Glu Val Val Asn Glu Ile Pro Ala Gly Ile Lys Pro Arg Ile Val Pro
25 30 35

tgg agc ggt agt gtt tcc gca ggt gtg cag gct gtg gaa tcc atc ctc 259
Trp Ser Gly Ser Val Ser Ala Gly Val Gln Ala Val Glu Ser Ile Leu
40 45 50

gac cgt gaa gaa atc ccg cgc gtc atc ctg gtc ggc gct gga acc gga 307
Asp Arg Glu Glu Ile Arg Arg Val Ile Leu Val Gly Ala Gly Thr Gly
55 60 65

gct gga gtg gcg ttg gaa att gcc aag aac caa ccc cgc cgc gtg gaa 355
Ala Gly Val Ala Leu Glu Ile Ala Lys Asn Gln Pro Arg Arg Val Glu
70 75 80 85

cgc ctc gtg ctg gat tca ccg ttg gtg acc ttt gat gag aaa caa ctc 403
Arg Leu Val Leu Asp Ser Pro Leu Val Thr Phe Asp Glu Lys Gln Leu
90 95 100

aaa ggc atg agc acc gca ctg aaa atg atg cca gga ttc ttc ttc cga 451
Lys Gly Met Ser Thr Ala Leu Lys Met Met Pro Gly Phe Phe Phe Arg
105 110 115

aag aag aac aag aaa gac ctc ctg cag cag gta gaa gaa gcc cgt act 499
Lys Lys Asn Lys Lys Asp Leu Leu Gln Gln Val Glu Glu Ala Arg Thr
120 125 130

gca gtt ccg atg gga ttt tcc gag att acc atg ccg acg tta atc atc 547
Ala Val Pro Met Gly Phe Ser Glu Ile Thr Met Pro Thr Leu Ile Ile
135 140 145

cga ggc tcc gct gcg aag gct gga att gat tct gac ttg gaa aaa caa 595
Arg Gly Ser Ala Ala Lys Ala Gly Ile Asp Ser Asp Leu Glu Lys Gln
150 155 160 165

atc ccg agc gct cgg gct acc acc att att ggt gcc aat tgg ctg act 643
Ile Pro Ser Ala Arg Ala Thr Thr Ile Ile Gly Ala Asn Trp Leu Thr
170 175 180

tac aca acg cat gga cgc caa act ggt gct gcg att gcg gaa ttc ctc 691
Tyr Thr Thr His Gly Arg Gln Thr Gly Ala Ala Ile Ala Glu Phe Leu
185 190 195

gcc caa tagaagggca cgcctaaacg cca 720
Ala Gln

<210> 1972

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 1972

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Met Val Glu Ser Gln His Ile Ile Phe Ile Pro Glu Ser Gln Gln Thr
  1             5             10             15

Pro Asp Glu Phe Thr Glu Val Val Asn Glu Ile Pro Ala Gly Ile Lys
      20             25             30

Pro Arg Ile Val Pro Trp Ser Gly Ser Val Ser Ala Gly Val Gln Ala
      35             40             45

Val Glu Ser Ile Leu Asp Arg Glu Glu Ile Arg Arg Val Ile Leu Val
      50             55             60

Gly Ala Gly Thr Gly Ala Gly Val Ala Leu Glu Ile Ala Lys Asn Gln
      65             70             75             80

Pro Arg Arg Val Glu Arg Leu Val Leu Asp Ser Pro Leu Val Thr Phe
      85             90             95

Asp Glu Lys Gln Leu Lys Gly Met Ser Thr Ala Leu Lys Met Met Pro
      100            105            110

Gly Phe Phe Phe Arg Lys Lys Asn Lys Lys Asp Leu Leu Gln Gln Val
      115            120            125

Glu Glu Ala Arg Thr Ala Val Pro Met Gly Phe Ser Glu Ile Thr Met
      130            135            140

Pro Thr Leu Ile Ile Arg Gly Ser Ala Ala Lys Ala Gly Ile Asp Ser
      145            150            155            160

Asp Leu Glu Lys Gln Ile Pro Ser Ala Arg Ala Thr Thr Ile Ile Gly
      165            170            175

Ala Asn Trp Leu Thr Tyr Thr Thr His Gly Arg Gln Thr Gly Ala Ala
      180            185            190

Ile Ala Glu Phe Leu Ala Gln
      195

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<210> 1973

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXA00895

<400> 1973

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gtcgcgcgcgg aaagatagac taagccacat gacttcggac atgcagaatt ctccacagca 60
ctcggccacg ccttcagaag aaaaacaagg cggactgccc atg cgc ggt ttg gcc 115

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	Met	Arg	Gly	Leu	Ala	
	1				5	
atg att ttg atc gcc gtg gcc gta ttg ctc gca gcg tgg gca ctg tgg						163
Met Ile Leu Ile Ala Val Ala Val Leu Leu Ala Ala Trp Ala Leu Trp						
			10		15	20
tca atg cag ggc aaa gac gac acc tcc acc acc agc gcc gga caa acc						211
Ser Met Gln Gly Lys Asp Asp Thr Ser Thr Thr Ser Ala Gly Gln Thr						
			25		30	35
cag tcc acg gaa acc aac gcg gga act att gct gaa tct tct ggc tct						259
Gln Ser Thr Glu Thr Asn Ala Gly Thr Ile Ala Glu Ser Ser Gly Ser						
			40		45	50
tcg gat tcc gag cag gca tca gca gaa cct gga acc tcc gaa gaa acc						307
Ser Asp Ser Ser Glu Gln Ala Ser Ala Glu Pro Gly Thr Ser Glu Glu Thr						
			55		60	65
tct gct gag cag cca gct gca gat ggc gaa gcc gct aat gct gct ggg						355
Ser Ala Glu Gln Pro Ala Ala Asp Gly Glu Ala Ala Asn Ala Ala Gly						
			70		75	80
gcc gct gct gct ggt ggc gct agt tcg gct aac ggc aac tcc acc cca						403
Ala Ala Ala Ala Gly Gly Ala Ser Ser Ala Asn Gly Asn Ser Thr Pro						
			90		95	100
gtg aac act ctg tac gtg ctc aac aac tcc acc gtc cca caa ctt gca						451
Val Asn Thr Leu Tyr Val Leu Asn Asn Ser Thr Val Pro Gln Leu Ala						
			105		110	115
gca cga gtg gca gac agc cta agc ggt gac tac caa aag gta gag tcc						499
Ala Arg Val Ala Asp Ser Leu Ser Gly Asp Tyr Gln Lys Val Glu Ser						
			120		125	130
gga aac ctt cca gac acc atc att ccg cag aac act gtg tac ttc acc						547
Gly Asn Leu Pro Asp Thr Ile Ile Pro Gln Asn Thr Val Tyr Phe Thr						
			135		140	145
gct gga aac acc gaa gct gaa aag gct gca cgt gaa ctc gct gac cgc						595
Ala Gly Asn Thr Glu Ala Glu Lys Ala Ala Arg Glu Leu Ala Asp Arg						
			150		155	160
gtc agt ggc gta gca atg gaa cgc agc gat gca ctg cca acc gaa aca						643
Val Ser Gly Val Ala Met Glu Arg Ser Asp Ala Leu Pro Thr Glu Thr						
			170		175	180
gaa ggc aaa gat gcc ctc gtt ttg gtg ctg gtc caa gac gta gcg ctg						691
Glu Gly Lys Asp Ala Leu Val Leu Val Leu Val Gln Asp Val Ala Leu						
			185		190	195
tagttttctc ggatttggtg gaa						714

<210> 1974

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 1974

Met Arg Gly Leu Ala Met Ile Leu Ile Ala Val Ala Val Leu Leu Ala

1 5 10 15
 Ala Trp Ala Leu Trp Ser Met Gln Gly Lys Asp Asp Thr Ser Thr Thr
 20 25 30
 Ser Ala Gly Gln Thr Gln Ser Thr Glu Thr Asn Ala Gly Thr Ile Ala
 35 40 45
 Glu Ser Ser Gly Ser Ser Asp Ser Glu Gln Ala Ser Ala Glu Pro Gly
 50 55 60
 Thr Ser Glu Glu Thr Ser Ala Glu Gln Pro Ala Ala Asp Gly Glu Ala
 65 70 75 80
 Ala Asn Ala Ala Gly Ala Ala Ala Ala Gly Gly Ala Ser Ser Ala Asn
 85 90 95
 Gly Asn Ser Thr Pro Val Asn Thr Leu Tyr Val Leu Asn Asn Ser Thr
 100 105 110
 Val Pro Gln Leu Ala Ala Arg Val Ala Asp Ser Leu Ser Gly Asp Tyr
 115 120 125
 Gln Lys Val Glu Ser Gly Asn Leu Pro Asp Thr Ile Ile Pro Gln Asn
 130 135 140
 Thr Val Tyr Phe Thr Ala Gly Asn Thr Glu Ala Glu Lys Ala Ala Arg
 145 150 155 160
 Glu Leu Ala Asp Arg Val Ser Gly Val Ala Met Glu Arg Ser Asp Ala
 165 170 175
 Leu Pro Thr Glu Thr Glu Gly Lys Asp Ala Leu Val Leu Val Leu Val
 180 185 190
 Gln Asp Val Ala Leu
 195

<210> 1975

<211> 815

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (37)..(792)

<223> RXA00904

<400> 1975

aagcagtgcg gtaccaggct ggaagtgtgg acaaca atg att aat acc atc cgc 54
 Met Ile Asn Thr Ile Arg
 1 5

tcc gaa tgg acc aaa ctt gtc acc acc aaa tcc ttc tgg tgg aca acc 102
 Ser Glu Trp Thr Lys Leu Val Thr Thr Lys Ser Phe Trp Trp Thr Thr
 10 15 20

gca cta att ctg gtc ttc agc ctg gga tac gca gcg ctc acc gga tca 150
 Ala Leu Ile Leu Val Phe Ser Leu Gly Tyr Ala Ala Leu Thr Gly Ser
 25 30 35

ctc gcc acc ggc gaa agc ttt gca tca ctg ttc ctt ctc gca ggc agc 198
 Leu Ala Thr Gly Glu Ser Phe Ala Ser Leu Phe Leu Leu Ala Gly Ser
 40 45 50

aca gtc acc ggc ctt tac ctc ctt ggc ttc gtg gtg atc atg atc caa 246
 Thr Val Thr Gly Leu Tyr Leu Leu Gly Phe Val Val Ile Met Ile Gln
 55 60 65 70

tcc atc atg atg ttc acc acc gaa ttt cga ttc ggc tac caa acc caa 294
 Ser Ile Met Met Phe Thr Thr Glu Phe Arg Phe Gly Tyr Gln Thr Gln
 75 80 85

acc ttc ctc gcc aca cca aaa cgc tgg gtt gtc gcc gtt tcc aaa tgg 342
 Thr Phe Leu Ala Thr Pro Lys Arg Trp Val Val Ala Val Ser Lys Trp
 90 95 100

ttg ctg tac ctc gtg ttc gcc gta gtg ttg acc ttc atc acc gtg att 390
 Leu Leu Tyr Leu Val Phe Ala Val Val Leu Thr Phe Ile Thr Val Ile
 105 110 115

ctg tgc ttc tat cta gcc aaa gcc ctg gca tca gac act gca agc tcc 438
 Leu Cys Phe Tyr Leu Ala Lys Ala Leu Ala Ser Asp Thr Ala Ser Ser
 120 125 130

acc ctg gtg gtg tgg gaa gat acg caa gca cga cga atc atg tgg caa 486
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<210> 1976

<211> 252

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<213> Corynebacterium glutamicum

<400> 1976

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Phe Cys Ser Gly Ile Ala Leu Leu Leu Arg Gln Thr Ala Gly Ala Val
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Ala Leu Val Leu Met Trp His Phe Ala Ile Glu Asn Leu Leu Ser Phe
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<210> 1977

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Gln Thr Arg Asn His Thr Met Glu Pro Ile Gln Ser Glu Pro Arg Ile
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<210> 1978

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

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<211> 1197

<212> PRT

<213> Corynebacterium glutamicum

<400> 1980

Met	Lys	Lys	Val	Leu	Val	Val	Gly	Cys	Gly	Gly	Ser	Gly	Ala	Lys	Thr
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Leu Ala Tyr Met Met Asp Gln Leu Lys Thr Thr Leu Ala Asp Ser Leu
20 25 30

Pro Glu Arg Tyr Pro Asn Pro Lys Glu Ala Lys Leu Pro Gly Ala Trp
35 40 45

Gln Phe Val Ser Val Asp Val Pro Thr Ser Pro Glu Ser Pro Gly Pro
50 55 60

Asn Leu Pro Asn Val Pro Glu Ala Gly Gly Arg Tyr Ile Ser Cys Gly
65 70 75 80

Ser Ser Asp Arg Tyr Ala Thr Val Asp Thr Ala Val Ser Asn Gln Leu
85 90 95

Ser Ser Arg Gly Ala Leu Gly Gly Val Ser Ser Trp Ala Leu Arg Asn
100 105 110

Pro Asp Ser Glu Thr Thr Pro Ile Ser Lys Gly Ala Gly Gln Tyr Arg
115 120 125

Ser Ile Gly Arg Met Leu Ile Leu Ser Arg Leu Gln Glu Ile Gln Ala
130 135 140

Glu Leu Arg Lys Ser Trp Asp Val Leu Phe Ser Gly Glu Thr Glu Arg
145 150 155 160

Glu Leu Ala Asp Leu Arg Ser Ala Leu Tyr Gly Thr Ser Val Ser Ser
165 170 175

Gly Glu Thr Ser Lys Glu Gln Pro Ile Ile Phe Gly Val Ser Ser Met
180 185 190

Ala Gly Gly Ala Gly Ala Ser Met Ala Leu Asp Ile Cys Arg Leu Leu
195 200 205

Thr Gly Leu Glu Gly Asn Ala Val Gly Leu Ser Ser Leu Phe Met Val
210 215 220

Thr Pro Asp Ile Phe Ser Gln Leu Ser Pro Asp Gln Val Ala Gly Thr
225 230 235 240

Asn Pro Asn Ala Leu Ala Met Phe Ala Glu Leu Ala Ala Ala Gln Met
245 250 255

Gly Ala Ala Ser Glu Glu Asp Ala Arg Leu Phe Asn Ala Leu Gly Val
260 265 270

Ser Val Gly Asp Asp Ser Ile Pro Val Gly Arg Ile Phe Pro Val Gly
275 280 285

Ile Arg Ser Gly Glu Asn Gly Ala Leu Leu Gly Asp Gly Lys Pro Asp
290 295 300

Thr Val Tyr Arg Ala Leu Gly Arg Gly Leu Ala Ala Leu Met Ala Asp
305 310 315 320

Glu Val Ser Met Asp Asn Phe Glu Gln Phe Thr Leu Gly Asn Arg Gly
325 330 335

Gly Gly Ser Ala Asp Gln Ser Lys Tyr Ala Trp Gly Ala Gln Glu Ala

340	345	350
Lys Asn Ile Pro Trp Gly Ser Tyr Gly Tyr Ser Gln Leu Ser Met Gly 355 360 365		
Arg Asp Arg Tyr Ala Glu Tyr Ala Ala Gln Arg Leu Ala Arg Ser Ala 370 375 380		
Val Asp Arg Leu Leu Lys Gly His Phe Asp Pro Ser Asn Asp Ala Ala 385 390 395 400		
Ser Asp Gln Gln Leu Gln Lys Arg Leu Glu Asn Asn Arg Pro Ser Leu 405 410 415		
Met Gly Asn Leu Ser Asp Val Leu Pro Val Asn Ala Pro Ala Gly Asp 420 425 430		
Trp Ile Phe His Ser Phe Asn Gln Met Ile Glu Asn Trp Thr Gln Arg 435 440 445		
Met Lys Ala Ile Ile Lys Ser Gln Ile Pro Ala Ala Asn Gly Gln Arg 450 455 460		
Gly Ser Glu Trp Leu Gly Asp Val Gln Arg Ala Phe Gln Ser Ser Ser 465 470 475 480		
Gln Met Ile Asp Asn Asp Ser Arg His Glu Leu Tyr Met Gly Val Ala 485 490 495		
Asp Trp Ala Ser Ala Asp Val Leu Gln Arg Arg Val Val Glu Leu Leu 500 505 510		
Arg Asp Glu Ile Ala Lys Leu Gly Val Pro Tyr Gly Val Ser Val Ile 515 520 525		
Glu Ser Leu Ser Ala Thr Ile Gln Asn Gln Leu Ile Gly Gln Leu Ser 530 535 540		
Asp Leu Ala Asn Asn Arg Ala Pro Glu Ala Val Gln Leu Asp Asp Val 545 550 555 560		
Ser Arg Ser Glu Leu Asp Asn Ser Lys Gly Arg Ile Asp Asp Ser Asp 565 570 575		
Ser Tyr Ile Gln Glu Ile Val Ser Arg Ser Thr Gly Gln Leu His Thr 580 585 590		
Arg Ala Val Gln Tyr Ile Ala Asp His Met Ala Ser Val Leu Asp Asp 595 600 605		
Phe Leu Lys Asn Phe Ile Tyr Pro Leu Gln Arg Thr Ile Gln Arg Glu 610 615 620		
His His Ser Leu Glu Lys Asp Tyr Gln Leu Thr Asn Asp Val Asn Leu 625 630 635 640		
Gly Ile Ser Gln Leu Lys Thr Asn Val Pro Ala Leu Trp Pro Asp Glu 645 650 655		
Ser Gln Thr Thr Val Pro Ser Arg Phe Ser Gln Ala Ala Asn Glu Val 660 665 670		

Phe Leu Thr Asp Val Ala Ser Phe Pro Glu Gln Phe Gln Ala His Val
 675 680 685
 Arg Ser Ser Thr Asp Asp Ile Asn Glu Gln Asn Asp Tyr Ser Ser Ala
 690 695 700
 Leu Gln Glu Ala Ser Thr Arg Val Val Ser Gly Val Trp Glu Ser Lys
 705 710 715 720
 Ser Gly Ser Glu Lys Ala Pro Arg Asp Leu Ile Arg Leu Ile Asp Val
 725 730 735
 Trp Val Ala Arg Asp Leu Thr Arg Asp Pro Ser Gly Ser Gly Ser Leu
 740 745 750
 Arg Asp Pro Lys Gln Ala Arg Phe Glu Leu Lys Ile Asp Thr Gly Glu
 755 760 765
 Val Leu Glu Arg Ser Arg Gln Tyr Ile Arg Arg Pro Gly Phe Ser Phe
 770 775 780
 Gln Gln Phe Ile Ala Ser Ser Leu Arg Glu Phe Ile Thr Ala Pro Gly
 785 790 795 800
 Leu Ala Asp His Glu Arg Arg Ala Arg Arg Gln Gln Val Leu Ser Lys
 805 810 815
 Phe Ser Glu Ala Met Thr Tyr Ala Leu Pro Leu Ala Gln Ile Asn Pro
 820 825 830
 Gln Leu Val Arg Ala Leu Tyr Gly Asp Glu Val Arg Tyr Asn Phe Asn
 835 840 845
 Phe Ser Arg Ile Pro Phe Ala Gly Asp Glu Leu Gly Ser Ser Leu Glu
 850 855 860
 Gln Ala Val Arg Asp Tyr Pro Asn His Arg Pro Ala Asp Ile Ser Lys
 865 870 875 880
 Pro Leu Gly Lys Ala Leu Val Ser Gln Gly Glu Glu Arg Ser Ile Asp
 885 890 895
 Ile Phe Gly Ser Tyr Pro Asn Tyr Ala Pro Ile Val Phe Asp Ser Leu
 900 905 910
 Leu Pro Pro Ile Glu Lys Gln Trp Arg Gln Ile Thr Gly Asp Arg Thr
 915 920 925
 Glu Phe Trp His Gly Arg Arg Thr Arg Pro Leu Thr Ala Ala Leu Pro
 930 935 940
 Met Thr Asp Leu Glu Arg Asn Ala Met Val Lys Gly Trp Tyr Ile Gly
 945 950 955 960
 Arg Leu Val Gly Arg Val Phe Phe Pro Ala Thr Leu Asp Thr Ala Asp
 965 970 975
 Thr Thr Pro Val Gln Ile Tyr Asp Glu Lys Ser Asp Ser Trp Ile Asn
 980 985 990

Phe Ser Thr Pro Met Leu Thr Pro Val Ser Arg Phe Arg Gly Ser Leu
 995 1000 1005
 Asp Trp Leu Pro Asn Leu Leu Glu Ser Ala Ser Leu Ala Trp Ala Arg
 1010 1015 1020
 Ala Gly Glu Arg Pro Val Phe Glu Ser Val Glu Pro Tyr Ile Gln Leu
 1025 1030 1035 1040
 Arg Gln Leu Trp Asp Asp Ala Ala Ser Pro Ser Leu Pro Gly Arg Thr
 1045 1050 1055
 Thr Arg Gly Glu Lys Leu Leu His Asp Trp Leu Phe Asp Gly Asn Arg
 1060 1065 1070
 Met Ala Gly Asn Val Leu Gln Ile Pro Gly Thr Glu Ala Gly Val Thr
 1075 1080 1085
 Pro Ala Ala Arg Phe Glu Ala Ala Lys Asn Phe Leu Gln Arg Gln Asn
 1090 1095 1100
 Glu Ile Ser Gln Asn Tyr Val Pro Ser Asp Lys Leu Arg Gln Gly Arg
 1105 1110 1115 1120
 Leu Phe Thr Thr Ala Asp Arg Pro Phe Gly Asp Val Lys Asp Arg Glu
 1125 1130 1135
 Leu Ala Ala Gln Ile Pro Val Phe Ala Asp Leu Ala Ala Asp Val Phe
 1140 1145 1150
 Asp Gly Thr Gln Glu Ile Ile Asp Ile Leu Glu Lys Cys Leu Ala Ala
 1155 1160 1165
 Gly Pro Pro Ser Ala Gln Val Phe Asp Met Asn Val Ala Arg Arg Asp
 1170 1175 1180
 Val Ser Ser Gly Pro Ser Leu Pro Gly Glu Gly Glu Phe
 1185 1190 1195

 <210> 1981
 <211> 486
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(463)
 <223> RXA00926

 <400> 1981
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 Met Asp Ile Val Phe
 1 5

 ctc ata att ctt cta gcc att ttt atc gtt ccc act ttc ctc atg agc 163
 Leu Ile Ile Leu Leu Ala Ile Phe Ile Val Pro Thr Phe Leu Met Ser
 10 15 20

cgc cgc cag cgc gca cgg atg act gaa atc caa aag ctg cag gac tct 211
 Arg Arg Gln Arg Ala Arg Met Thr Glu Ile Gln Lys Leu Gln Asp Ser
 25 30 35

 gtc gtc cca ggc gac cgc atc gtc acc acc gcc gga cag cac gca acg 259
 Val Val Pro Gly Asp Arg Ile Val Thr Thr Ala Gly Gln His Ala Thr
 40 45 50

 gtc att tcc acc act gca gaa acc gtt gat cta gag atc gcc ccg ggt 307
 Val Ile Ser Thr Thr Ala Glu Thr Val Asp Leu Glu Ile Ala Pro Gly
 55 60 65

 atg atc agc act ttt gaa aag ctt gct atc gtg cgt gtg ctg tcc aag 355
 Met Ile Ser Thr Phe Glu Lys Leu Ala Ile Val Arg Val Leu Ser Lys
 70 75 80 85

 gcc aat gaa cct cag atg ttg gat gag ccg acg ctg ttt gat cag cca 403
 Ala Asn Glu Pro Gln Met Leu Asp Glu Pro Thr Leu Phe Asp Gln Pro
 90 95 100

 gaa gac gat cag ccg aac gat ggt ttc gat gga cgc act gac gga cat 451
 Glu Asp Asp Gln Pro Asn Asp Gly Phe Asp Gly Arg Thr Asp Gly His
 105 110 115

 cct gag aat cgt tagaaattaa taataattca gca 486
 Pro Glu Asn Arg
 120

<210> 1982

<211> 121

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1982

Met Asp Ile Val Phe Leu Ile Ile Leu Leu Ala Ile Phe Ile Val Pro
 1 5 10 15

 Thr Phe Leu Met Ser Arg Arg Gln Arg Ala Arg Met Thr Glu Ile Gln
 20 25 30

 Lys Leu Gln Asp Ser Val Val Pro Gly Asp Arg Ile Val Thr Thr Ala
 35 40 45

 Gly Gln His Ala Thr Val Ile Ser Thr Thr Ala Glu Thr Val Asp Leu
 50 55 60

 Glu Ile Ala Pro Gly Met Ile Ser Thr Phe Glu Lys Leu Ala Ile Val
 65 70 75 80

 Arg Val Leu Ser Lys Ala Asn Glu Pro Gln Met Leu Asp Glu Pro Thr
 85 90 95

 Leu Phe Asp Gln Pro Glu Asp Asp Gln Pro Asn Asp Gly Phe Asp Gly
 100 105 110

 Arg Thr Asp Gly His Pro Glu Asn Arg
 115 120

<210> 1983

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXA00930

<400> 1983

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acggcgccacc acacatttgg tggtgtattg agctatctct gggctgctg agaaaccatt 60
ttccggtgga tgatggaagc tagacgacga aaggggagcat atg tct ggc cac tca 115
                                         Met Ser Gly His Ser
                                         1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163
Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
                        10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211
Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg
                        25 30 35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259
Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile
                        40 45 50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307
Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala
                        55 60 65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355
Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn
                        70 75 80 85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403
Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu
                        90 95 100

tgt ctg acc gac aac cgt aac ccg gca gct acc gaa gtt cgc acc gca 451
Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala
                        105 110 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499
Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr
                        120 125 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547
Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser
                        135 140 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595
Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val
                        150 155 160 165

aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643
Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile
                        170 175 180

cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691

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Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp
 185 190 195

tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp
 200 205 210

ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp
 215 220 225

gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu
 230 235 240 245

aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876
 Thr Glu Leu Glu Asn Asp
 250

<210> 1984

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 1984

Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
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Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
 20 25 30

Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
 35 40 45

Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
 50 55 60

Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
 65 70 75 80

Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
 85 90 95

Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
 100 105 110

Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
 115 120 125

Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
 145 150 155 160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
 165 170 175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
 180 185 190

Ile Glu Val Glu Asp Ser. Glu Ser Asp Phe Arg Ala Ser Val Gln Val
 195 200 205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
 210 215 220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
 225 230 235 240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
 245 250

<210> 1985

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXA00932

<400> 1985

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aataaggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa 115
 Met Thr Pro Gln Lys
 1 5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg 163
 Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
 10 15 20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc 211
 Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
 25 30 35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc 259
 Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
 40 45 50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt 307
 Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
 55 60 65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt 355
 Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
 70 75 80 85

gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt 403
 Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
 90 95 100

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct 451
 Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala
 105 110 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att 499
 Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile

120 125 130
 atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547
 Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
 135 140 145

 cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac 594
 Pro Asp Ala Ile Ala Asn Thr Val Asp
 150 155

 atg 597

 <210> 1986
 <211> 158
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1986
 Met Thr Pro Gln Lys Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly
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 20 25 30
 Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
 35 40 45
 Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
 50 55 60
 Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65 70 75 80
 Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
 85 90 95
 Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
 100 105 110
 Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
 115 120 125
 Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
 130 135 140
 Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
 145 150 155

<210> 1987
 <211> 585
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(562)
 <223> RXA00933

<400> 1987

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cagtctatga aaccattgcg atcgacaaag tgaggcttgg atg acc ctt gtt tac 115
                                         Met Thr Leu Val Tyr
                                         1           5

ctc ctc atc gct gtc gtt gtc acc gca act gtt ctg tgg gcg tat ttc 163
Leu Leu Ile Ala Val Val Val Thr Ala Thr Val Leu Trp Ala Tyr Phe
                        10                15                20

aca gca caa cgc ctc aac cgg ctc cac atc cgc acc gac tca gca aga 211
Thr Ala Gln Arg Leu Asn Arg Leu His Ile Arg Thr Asp Ser Ala Arg
                        25                30                35

caa gcc ctg caa gca gca ctg gat cgc cga gca gca cta gta ggt gcg 259
Gln Ala Leu Gln Ala Ala Leu Asp Arg Arg Ala Ala Leu Val Gly Ala
                        40                45                50

ttg ttg ccc gat gca gca gaa gcc tca aaa cgc gct gag gca att ccc 307
Leu Leu Pro Asp Ala Ala Glu Ala Ser Lys Arg Ala Glu Ala Ile Pro
                        55                60                65

ctg gaa tac tcc cgc ttc tcc caa cgc gcc cgc gcc gaa cga gaa atc 355
Leu Glu Tyr Ser Arg Phe Ser Gln Arg Ala Arg Ala Glu Arg Glu Ile
                        70                75                80                85

tct gaa ctc atc ttg aaa cag ggg aag acc ctt cca gat tcc atc gtg 403
Ser Glu Leu Ile Leu Lys Gln Gly Lys Thr Leu Pro Asp Ser Ile Val
                        90                95                100

gac gct gcc acc cgc gtg gaa tta gcc cac cgc ttc tac aac gaa gcc 451
Asp Ala Ala Thr Arg Val Glu Leu Ala His Arg Phe Tyr Asn Glu Ala
                        105                110                115

gtc agt gac acc cgc gat ctt cga acc cga ttg atg gtc aga tcc ttc 499
Val Ser Asp Thr Arg Asp Leu Arg Thr Arg Leu Met Val Arg Ser Phe
                        120                125                130

cga ctc ggc ggc acc gca ccc ttg ccg gag tac ttc gaa cta ctc gat 547
Arg Leu Gly Gly Thr Ala Pro Leu Pro Glu Tyr Phe Glu Leu Leu Asp
                        135                140                145

aca gat ctg ctg act taaatgtaaa aaagcctcct tca 585
Thr Asp Leu Leu Thr
150

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<210> 1988

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 1988

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Met Thr Leu Val Tyr Leu Leu Ile Ala Val Val Val Thr Ala Thr Val
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Leu Trp Ala Tyr Phe Thr Ala Gln Arg Leu Asn Arg Leu His Ile Arg
  20           25           30

Thr Asp Ser Ala Arg Gln Ala Leu Gln Ala Ala Leu Asp Arg Arg Ala
  35           40           45

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Ala Leu Val Gly Ala Leu Leu Pro Asp Ala Ala Glu Ala Ser Lys Arg
 50 55 60

Ala Glu Ala Ile Pro Leu Glu Tyr Ser Arg Phe Ser Gln Arg Ala Arg
 65 70 75 80

Ala Glu Arg Glu Ile Ser Glu Leu Ile Leu Lys Gln Gly Lys Thr Leu
 85 90 95

Pro Asp Ser Ile Val Asp Ala Ala Thr Arg Val Glu Leu Ala His Arg
 100 105 110

Phe Tyr Asn Glu Ala Val Ser Asp Thr Arg Asp Leu Arg Thr Arg Leu
 115 120 125

Met Val Arg Ser Phe Arg Leu Gly Gly Thr Ala Pro Leu Pro Glu Tyr
 130 135 140

Phe Glu Leu Leu Asp Thr Asp Leu Leu Thr
 145 150

<210> 1989

<211> 519

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(496)

<223> RXA00940

<400> 1989

tgctcaacgg cacgctgaag ggcacggaca tggacatcat cacggcaggc gacccggacg 60

tggtcgcggt ggacgtgctg gcagaggcga tctgcgcaat gtg att ttg gtg ctg 115
 Val Ile Leu Val Leu 5

ctg gaa gct gag tca atg cgc ggc tac cag atc atc acc acc atc agt 163
 Leu Glu Ala Glu Ser Met Arg Gly Tyr Gln Ile Ile Thr Thr Ile Ser 10 15 20

gag caa aca gaa ggt aac tgg act cca agc cca gga acc atc tat cca 211
 Glu Gln Thr Glu Gly Asn Trp Thr Pro Ser Pro Gly Thr Ile Tyr Pro 25 30 35

acc ttg tcc atg ctt gaa gat gaa ggc ctg att tcc atc tcc cat gaa 259
 Thr Leu Ser Met Leu Glu Asp Glu Gly Leu Ile Ser Ile Ser His Glu 40 45 50

atg ggc aga aaa atg gcg cgc ctt aca gaa gaa ggc gcg cag gaa gtg 307
 Met Gly Arg Lys Met Ala Arg Leu Thr Glu Glu Gly Ala Gln Glu Val 55 60 65

gca aag aac aag gat gcg tgg gga tca att ctg gag gct tat cgc aat 355
 Ala Lys Asn Lys Asp Ala Trp Gly Ser Ile Leu Glu Ala Tyr Arg Asn 70 75 80 85

cca gaa tcc cga gag gtg cgg gtg ttt aac att cgc tct gag ttt cac 403

Pro Glu Ser Arg Glu Val Arg Val Phe Asn Ile Arg Ser Glu Phe His
90 95 100
aag gtc agg gaa gca gcg aaa gct gct ccc gac gat aaa gca gag caa 451
Lys Val Arg Glu Ala Ala Lys Ala Ala Pro Asp Asp Lys Ala Glu Gln
105 110 115
ata atc gag att tta agg aga gca gca gat gac atc aag aga cta 496
Ile Ile Glu Ile Leu Arg Arg Ala Ala Asp Asp Ile Lys Arg Leu
120 125 130
taacccccagt accatgcagc tgc 519

<210> 1990

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 1990

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20 25 30
Gly Thr Ile Tyr Pro Thr Leu Ser Met Leu Glu Asp Glu Gly Leu Ile
35 40 45
Ser Ile Ser His Glu Met Gly Arg Lys Met Ala Arg Leu Thr Glu Glu
50 55 60
Gly Ala Gln Glu Val Ala Lys Asn Lys Asp Ala Trp Gly Ser Ile Leu
65 70 75 80
Glu Ala Tyr Arg Asn Pro Glu Ser Arg Glu Val Arg Val Phe Asn Ile
85 90 95
Arg Ser Glu Phe His Lys Val Arg Glu Ala Ala Lys Ala Ala Pro Asp
100 105 110
Asp Lys Ala Glu Gln Ile Ile Glu Ile Leu Arg Arg Ala Ala Asp Asp
115 120 125
Ile Lys Arg Leu
130

<210> 1991

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(748)

<223> RXA00949

<400> 1991

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Met Lys Val Phe Ile	
1 5	
atc ggc gct gcg ggt ggc atc ggc aat cga ctt tcc agc ctg ctt cac	163
Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu Ser Ser Leu Leu His	
10 15 20	
gcc agg gga gat gca gtt agc ggc atg cac cgc aat ctt gag cag gcc	211
Ala Arg Gly Asp Ala Val Ser Gly Met His Arg Asn Leu Glu Gln Ala	
25 30 35	
tca aaa atc aca gac act ggg gca act gcc gta ctc ggg gat ctc atc	259
Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val Leu Gly Asp Leu Ile	
40 45 50	
cac aac agc acg gag gag ctt gcg gag ctt ttc cgc ggt cac gat gcc	307
His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe Arg Gly His Asp Ala	
55 60 65	
atc gta ttt tct gca ggc gcc cac gga aca ggg caa gaa aat acc acg	355
Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly Gln Glu Asn Thr Thr	
70 75 80 85	
ctt atc gac ggc gcc ggc ctc cgt aaa gcc gcc gac gct gcc agc gcg	403
Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala Asp Ala Ala Ser Ala	
90 95 100	
gcc aac gtt tca cgc ttc atc ttg gtc tct gcg ttt ccg gaa tcc tcc	451
Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala Phe Pro Glu Ser Ser	
105 110 115	
cgc ggg gag aac acc acc gag aac ttt gag cac tat atg aag gtg aag	499
Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His Tyr Met Lys Val Lys	
120 125 130	
aag tcc gcc gat gtc tac ctc agt cac act gac cta gac tgg gtt att	547
Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp Leu Asp Trp Val Ile	
135 140 145	
gtc cga cca ggc gtg ctt caa gat gag gca ggg gat ggt tta gtc act	595
Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly Asp Gly Leu Val Thr	
150 155 160 165	
gct ggc tta gcg att aat tac ggc aat gtt gct cgc gat aat gtc gca	643
Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala Arg Asp Asn Val Ala	
170 175 180	
gcg ttc att gat gaa gct ctg cat caa ccg cag ttg tca aag atc att	691
Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln Leu Ser Lys Ile Ile	
185 190 195	
gtt gaa ctc acc gac ggt tca act ccg gtg gcg gaa gcc gta gaa cgc	739
Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala Glu Ala Val Glu Arg	
200 205 210	
ctc atc aag taaagacgaa aagaggggaga atg	771
Leu Ile Lys	
215	

<210> 1992

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 1992

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Met Lys Val Phe Ile Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu
  1             5             10             15

Ser Ser Leu Leu His Ala Arg Gly Asp Ala Val Ser Gly Met His Arg
          20             25             30

Asn Leu Glu Gln Ala Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val
          35             40             45

Leu Gly Asp Leu Ile His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe
  50             55             60

Arg Gly His Asp Ala Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly
  65             70             75             80

Gln Glu Asn Thr Thr Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala
          85             90             95

Asp Ala Ala Ser Ala Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala
          100            105            110

Phe Pro Glu Ser Ser Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His
          115            120            125

Tyr Met Lys Val Lys Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp
          130            135            140

Leu Asp Trp Val Ile Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly
          145            150            155            160

Asp Gly Leu Val Thr Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala
          165            170            175

Arg Asp Asn Val Ala Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln
          180            185            190

Leu Ser Lys Ile Ile Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala
          195            200            205

Glu Ala Val Glu Arg Leu Ile Lys
          210            215

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<210> 1993

<211> 170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(147)

<223> RXA00969

<400> 1993

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atc cga cag gaa gag cgc gat gat gat gca cgt ctg atc gtg gtc acc 48

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Ile Arg Gln Glu Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr
 1 5 10 15
 cac tct gcg ctg gaa tct gat ctt tcc cgc acc gtt gaa ctg ctg aag 96
 His Ser Ala Leu Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys
 20 25 30
 gct aag cct gtt gtt aag gca atc aac agt gtg atc cgc ctc gaa agg 144
 Ala Lys Pro Val Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg
 35 40 45
 gac taattttact gacatggcaa ttg 170
 Asp

<210> 1994
 <211> 49
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1994
 Ile Arg Gln Glu Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr
 1 5 10 15
 His Ser Ala Leu Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys
 20 25 30
 Ala Lys Pro Val Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg
 35 40 45
 Asp

<210> 1995
 <211> 726
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(703)
 <223> RXA00973

<400> 1995
 ttgttggtgc aggcottaca gccattgcac tgagttccat gctgtcgcag ccagtacagg 60
 ccttcacat gaccattgag atggtgagtg tatttttcac atg aac cac tct gac 115
 Met Asn His Ser Asp
 1 5
 gac gat cgc atg caa aag tgg ttc cag atc cgc cgc gaa ctg ggc aaa 163
 Asp Asp Arg Met Gln Lys Trp Phe Gln Ile Arg Arg Glu Leu Gly Lys
 10 15 20
 gaa att gtg aaa cag ctt caa aag gat ctg ccc gca gtc gcc tct gac 211
 Glu Ile Val Lys Gln Leu Gln Lys Asp Leu Pro Ala Val Ala Ser Asp
 25 30 35
 atc ggc tcc atg gtg tat tcc tct gat caa gtt ccc ctc gga aac gcc 259

Ile Gly Ser Met Val Tyr Ser Ser Asp Gln Val Pro Leu Gly Asn Ala
 40 45 50
 acg ctc act gca tac gga gac atc ggc aac cga gtc gct tcc gct gca 307
 Thr Leu Thr Ala Tyr Gly Asp Ile Gly Asn Arg Val Ala Ser Ala Ala
 55 60 65
 aca agt gcg aga tac aac gta gag gaa ctc ctg gac gca atc gaa aac 355
 Thr Ser Ala Arg Tyr Asn Val Glu Glu Leu Leu Asp Ala Ile Glu Asn
 70 75 80 85
 gca cga ttt gcc atc tgg gtt cca aat tac gac aac tcc tac tac ctc 403
 Ala Arg Phe Ala Ile Trp Val Pro Asn Tyr Asp Asn Ser Tyr Tyr Leu
 90 95 100
 tcc ggc gag gaa ggt gcc gac gaa ttc caa aca tac ctc atc aaa gat 451
 Ser Gly Glu Glu Gly Ala Asp Glu Phe Gln Thr Tyr Leu Ile Lys Asp
 105 110 115
 gcg tca aga ttt ctt gaa tcc tcc ggg aat act cca ccc gag aac ccg 499
 Ala Ser Arg Phe Leu Glu Ser Ser Gly Asn Thr Pro Pro Glu Asn Pro
 120 125 130
 cag tac agc gac tcc aaa tta acc ttt gct agc gaa cta ctc ccc ttc 547
 Gln Tyr Ser Asp Ser Lys Leu Thr Phe Ala Ser Glu Leu Leu Pro Phe
 135 140 145
 tac acc gca ttt aac aac tcg acc tac cca cta ctt cat gct tgt gtg 595
 Tyr Thr Ala Phe Asn Asn Ser Thr Tyr Pro Leu Leu His Ala Cys Val
 150 155 160 165
 caa ggt gaa cca act gaa gta gac ctc tac ttc tac gag ctc gag cag 643
 Gln Gly Glu Pro Thr Glu Val Asp Leu Tyr Phe Tyr Glu Leu Glu Gln
 170 175 180
 gca gaa ttg aag gaa aaa gag act gca cag ctc tcg agt gga tca agt 691
 Ala Glu Leu Lys Glu Lys Glu Thr Ala Gln Leu Ser Ser Gly Ser Ser
 185 190 195
 ttt ggc tcc agt tagtcagaat tctcctaaag ggc 726
 Phe Gly Ser Ser
 200

<210> 1996

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1996

Met Asn His Ser Asp Asp Asp Arg Met Gln Lys Trp Phe Gln Ile Arg
 1 5 10 15

Arg Glu Leu Gly Lys Glu Ile Val Lys Gln Leu Gln Lys Asp Leu Pro
 20 25 30

Ala Val Ala Ser Asp Ile Gly Ser Met Val Tyr Ser Ser Asp Gln Val
 35 40 45

Pro Leu Gly Asn Ala Thr Leu Thr Ala Tyr Gly Asp Ile Gly Asn Arg
 50 55 60

Val Ala Ser Ala Ala Thr Ser Ala Arg Tyr Asn Val Glu Glu Leu Leu
 65 70 75 80
 Asp Ala Ile Glu Asn Ala Arg Phe Ala Ile Trp Val Pro Asn Tyr Asp
 85 90 95
 Asn Ser Tyr Tyr Leu Ser Gly Glu Glu Gly Ala Asp Glu Phe Gln Thr
 100 105 110
 Tyr Leu Ile Lys Asp Ala Ser Arg Phe Leu Glu Ser Ser Gly Asn Thr
 115 120 125
 Pro Pro Glu Asn Pro Gln Tyr Ser Asp Ser Lys Leu Thr Phe Ala Ser
 130 135 140
 Glu Leu Leu Pro Phe Tyr Thr Ala Phe Asn Asn Ser Thr Tyr Pro Leu
 145 150 155 160
 Leu His Ala Cys Val Gln Gly Glu Pro Thr Glu Val Asp Leu Tyr Phe
 165 170 175
 Tyr Glu Leu Glu Gln Ala Glu Leu Lys Glu Lys Glu Thr Ala Gln Leu
 180 185 190
 Ser Ser Gly Ser Ser Phe Gly Ser Ser
 195 200

<210> 1997

<211> 738

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(715)

<223> RXA00978

<400> 1997

tcctgggtag catgggctta tgagcactga tagccaaaac cctgtaagaa aatcctgcgc 60
 acagccacat tcttggtccc aagaggtgcg attgaaagcg atg tcc agg tca ccg 115
 Met Ser Arg Ser Pro
 1 5
 ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca 163
 Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser
 10 15 20
 cta act gcg tgg tcg tgg gca gaa gat gat cct ttg tac ctc gca ggt 211
 Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly
 25 30 35
 gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc 259
 Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val
 40 45 50
 tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg 307
 Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr
 55 60 65

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ccc ggc gat gtt att ggt gcg ata gat aca gaa cct cag ccg gca gta 355
Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu Pro Gln Pro Ala Val
 70          75          80          85

gat tcc gct tgg gca ata gaa acc acc tgt gcg ctg ttt ctt cca gca 403
Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala Leu Phe Leu Pro Ala
          90          95          100

acc gcg ttg gca act gtg att gaa cag cat cca agt ttt gct ttg gcg 451
Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro Ser Phe Ala Leu Ala
          105          110          115

atg att cgg atg cag cag caa cgt ttg gct aca gcc aga gat cat gaa 499
Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr Ala Arg Asp His Glu
          120          125          130

att aac ctg act acg acc aca gtt gag caa cga gta gct att gca gtg 547
Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg Val Ala Ile Ala Val
          135          140          145

aga act ctg gga cga aaa atc ggg caa cga cga ccc gat gga atc ttg 595
Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg Pro Asp Gly Ile Leu
          150          155          160          165

ctc att caa gtt cga atc cgg cgg gaa gat gtt gcg ggt tta gca ggc 643
Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val Ala Gly Leu Ala Gly
          170          175          180

acc acc gtg gaa tct act tct aga gtt ttg gcg cga tta cgt aaa gaa 691
Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala Arg Leu Arg Lys Glu
          185          190          195

ggg gtc att gat agc ggt agg gaa tgattgccgt ggatcgatgaa cgg 738
Gly Val Ile Asp Ser Gly Arg Glu
          200          205

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<210> 1998

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 1998

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Met Ser Arg Ser Pro Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu
 1          5          10          15

Glu Leu Asp Lys Ser Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro
          20          25          30

Leu Tyr Leu Ala Gly Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala
          35          40          45

Gly Arg Val Arg Val Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr
          50          55          60

Val Asp Ile Ala Thr Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu
          65          70          75          80

Pro Gln Pro Ala Val Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala
          85          90          95

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Leu Phe Leu Pro Ala Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro
 100 105 110
 Ser Phe Ala Leu Ala Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr
 115 120 125
 Ala Arg Asp His Glu Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg
 130 135 140
 Val Ala Ile Ala Val Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg
 145 150 155 160
 Pro Asp Gly Ile Leu Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val
 165 170 175
 Ala Gly Leu Ala Gly Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala
 180 185 190
 Arg Leu Arg Lys Glu Gly Val Ile Asp Ser Gly Arg Glu
 195 200 205

<210> 1999

<211> 424

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (60)..(401)

<223> RXA00986

<400> 1999

ctactttgat aacaccgcca cccaagccaa gccggagtga tctccgtatc ctttaaggc atg 62
 Met
 1
 act tta aaa gat aag tac gac act gaa gta gct gtt tct aat aat cag 110
 Thr Leu Lys Asp Lys Tyr Asp Thr Glu Val Ala Val Ser Asn Asn Gln
 5 10 15
 gac aag cac caa ttt gag gtc agt tac cct gaa gat gcc gtg act gct 158
 Asp Lys His Gln Phe Glu Val Ser Tyr Pro Glu Asp Ala Val Thr Ala
 20 25 30
 ggc ttt gct gca tac ctt gat aaa ggt gat tcg cgg atc ttc tat cac 206
 Gly Phe Ala Ala Tyr Leu Asp Lys Gly Asp Ser Arg Ile Phe Tyr His
 35 40 45
 acc gtt gtt ggc gat gaa ttc ggt ggc aag gga ctt gcg tca att ctt 254
 Thr Val Val Gly Asp Glu Phe Gly Gly Lys Gly Leu Ala Ser Ile Leu
 50 55 60 65
 gtt tca gag gcg tta aaa gcc aca aaa gaa gct ggt ctt acc gtg gtt 302
 Val Ser Glu Ala Leu Lys Ala Thr Lys Glu Ala Gly Leu Thr Val Val
 70 75 80
 ccg gta tgt ccc ttt gtt aaa gga ttc gtg gaa aag aac gca ttc gag 350
 Pro Val Cys Pro Phe Val Lys Gly Phe Val Glu Lys Asn Ala Phe Glu
 85 90 95

gca cta gtt tct gac atc act cga act gga gaa tgg tcg ccc gtg tgt 211
 Ala Leu Val Ser Asp Ile Thr Arg Thr Gly Glu Trp Ser Pro Val Cys
 25 30 35

gag aaa tgc tgg tgg gat gaa gac gaa ggc ccc gtc gtg ggt gcg cac 259
 Glu Lys Cys Trp Trp Asp Glu Asp Glu Gly Pro Val Val Gly Ala His
 40 45 50

ttt act ggc cga aac gtc aca cct gag cgc acc tgg gag aca cgg agc 307
 Phe Thr Gly Arg Asn Val Thr Pro Glu Arg Thr Trp Glu Thr Arg Ser
 55 60 65

gag gtt atc gtc gca gag cca aat cgt tgc ttt ggt tgg agc gtg act 355
 Glu Val Ile Val Ala Glu Pro Asn Arg Cys Phe Gly Trp Ser Val Thr
 70 75 80 85

gat gga aac gtc aag tgg att tat tcc atg gaa ccg tta gaa gaa ggc 403
 Asp Gly Asn Val Lys Trp Ile Tyr Ser Met Glu Pro Leu Glu Glu Gly
 90 95 100

aca gta ttg act gaa tca tgg gaa ttt acc ccc aaa ggt caa cga ttc 451
 Thr Val Leu Thr Glu Ser Trp Glu Phe Thr Pro Lys Gly Gln Arg Phe
 105 110 115

ttc cac gac aaa ttc ggc gac aaa tca att gaa gaa att gaa aag cga 499
 Phe His Asp Lys Phe Gly Asp Lys Ser Ile Glu Glu Ile Glu Lys Arg
 120 125 130

cgc ttg gca gct ata acc gga att cca gaa aca ctg gtt gcc att cag 547
 Arg Leu Ala Ala Ile Thr Gly Ile Pro Glu Thr Leu Val Ala Ile Gln
 135 140 145

cgc att ctg gaa gtt gag tagtttctac atctggctct tca 588
 Arg Ile Leu Glu Val Glu
 150 155

<210> 2002
 <211> 155
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2002
 Met Pro Lys Ser Leu Thr Phe Glu Asp Ser Ile Asn Ile Ala Ala Pro
 1 5 10 15

Ile Asn Gln Val Tyr Ala Leu Val Ser Asp Ile Thr Arg Thr Gly Glu
 20 25 30

Trp Ser Pro Val Cys Glu Lys Cys Trp Trp Asp Glu Asp Glu Gly Pro
 35 40 45

Val Val Gly Ala His Phe Thr Gly Arg Asn Val Thr Pro Glu Arg Thr
 50 55 60

Trp Glu Thr Arg Ser Glu Val Ile Val Ala Glu Pro Asn Arg Cys Phe
 65 70 75 80

Gly Trp Ser Val Thr Asp Gly Asn Val Lys Trp Ile Tyr Ser Met Glu
 85 90 95

Pro Leu Glu Glu Gly Thr Val Leu Thr Glu Ser Trp Glu Phe Thr Pro
 100 105 110

Lys Gly Gln Arg Phe Phe His Asp Lys Phe Gly Asp Lys Ser Ile Glu
 115 120 125

Glu Ile Glu Lys Arg Arg Leu Ala Ala Ile Thr Gly Ile Pro Glu Thr
 130 135 140

Leu Val Ala Ile Gln Arg Ile Leu Glu Val Glu
 145 150 155

<210> 2003
 <211> 546
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(523)
 <223> RXA00988

<400> 2003

tagcagaaga caccgatgta cagtccggat caggtgttgt gatcaccggt tcaatcgtga 60

ccgccggcga tgcgcgcacg ctgtttggaa aggaacctgc atg agc aag cgt gaa 115
 Met Ser Lys Arg Glu
 1 5

gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag 163
 Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
 10 15 20

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg 211
 Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
 25 30 35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac 259
 Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
 40 45 50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc 307
 Asp Gly Ile Tyr Trp Thr Phe Asn Trp Val Tyr Val Ser Ala Val
 55 60 65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc 355
 Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
 70 75 80 85

atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt 403
 Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
 90 95 100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg 451
 Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
 105 110 115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc 499
 Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg

120

125

130

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc 546
 Gly Leu Leu Thr Thr Gln His Ser
 135 140

<210> 2004

<211> 141

<212> PRT

<213> Corynebacterium glutamicum

<400> 2004

Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
 1 5 10 15

His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
 20 25 30

Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
 35 40 45

Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
 50 55 60

Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65 70 75 80

Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
 85 90 95

Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
 100 105 110

Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
 115 120 125

Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
 130 135 140

<210> 2005

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXA01005

<400> 2005

tgggcaccgt caacgattgg actcacgaaa gctccgacga ctagaaatag taactgtgtt 60

ggacactttt cacctccgcg tattgagcga ggatgagtgg atg gaa cta gcc cgc 115
 Met Glu Leu Ala Arg
 1 5

gcc cac cac gcg cgg gct gat tca ttc acc aaa gac cac ttg aag cgt 163
 Ala His His Ala Arg Ala Asp Ser Phe Thr Lys Asp His Leu Lys Arg
 10 15 20

cga caa gcg cat atc aag cac ccc gtc ttc gac ttc ctc ttc gag tac	211
Arg Gln Ala His Ile Lys His Pro Val Phe Asp Phe Leu Phe Glu Tyr	
25 30 35	
tac ccc gtg cgc gtc gcg cac cta aaa acc tgg cac ccc ggc atc ggc	259
Tyr Pro Val Arg Val Ala His Leu Lys Thr Trp His Pro Gly Ile Gly	
40 45 50	
gtg ttt cta gaa ggc aca ccg ccg cat gcc acc atg cgc gat ttt ttg	307
Val Phe Leu Glu Gly Thr Pro Pro His Ala Thr Met Arg Asp Phe Leu	
55 60 65	
ctt gtc gac gcc tcc ctc cat cac gca gcc ggc gtc cag ctt gac ctg	355
Leu Val Asp Ala Ser Leu His His Ala Ala Gly Val Gln Leu Asp Leu	
70 75 80 85	
gcc tcc tat atg caa cgc cgt ggg tcc tct gtg cgc tac atc cac gaa	403
Ala Ser Tyr Met Gln Arg Arg Gly Ser Ser Val Arg Tyr Ile His Glu	
90 95 100	
ctg ttg tcc gcc acc cgc gac aac cac gcc caa ttt gat tgt ttt ggt	451
Leu Leu Ser Ala Thr Arg Asp Asn His Ala Gln Phe Asp Cys Phe Gly	
105 110 115	
ctg cac gaa tgg gca atg gtg tac aaa tca aac gat ctc cgc cat gac	499
Leu His Glu Trp Ala Met Val Tyr Lys Ser Asn Asp Leu Arg His Asp	
120 125 130	
ctt ccc ctg cgc ctt acc cca tcg gaa acc gac cgt gtg gtg gaa agc	547
Leu Pro Leu Arg Leu Thr Pro Ser Glu Thr Asp Arg Val Val Glu Ser	
135 140 145	
cac aac atc aaa tgc acc cac ttt gat gcc tac cga ttc ttc acc aca	595
His Asn Ile Lys Cys Thr His Phe Asp Ala Tyr Arg Phe Phe Thr Thr	
150 155 160 165	
cca gcc atc ccg ttg aac ctc acg gtg tta acc cgc gaa gat cag cca	643
Pro Ala Ile Pro Leu Asn Leu Thr Val Leu Thr Arg Glu Asp Gln Pro	
170 175 180	
cgc aac gat caa tgt ggt tgt ctg cat gcc acg atg gat cta tac aaa	691
Arg Asn Asp Gln Cys Gly Cys Leu His Ala Thr Met Asp Leu Tyr Lys	
185 190 195	
tgg tcc gca aag ctt ggc cct ctt gtg cca ggt gat ctt ttc ttg gac	739
Trp Ser Ala Lys Leu Gly Pro Leu Val Pro Gly Asp Leu Phe Leu Asp	
200 205 210	
gcg ttt gaa cta gcc cgc gac acc cgc atc ttg gac atg gag gct tcg	787
Ala Phe Glu Leu Ala Arg Asp Thr Arg Ile Leu Asp Met Glu Ala Ser	
215 220 225	
cct tac gac gtc cgc gga tac ggc ttt ggc tac gtc ccc att gag acc	835
Pro Tyr Asp Val Arg Gly Tyr Gly Phe Gly Tyr Val Pro Ile Glu Thr	
230 235 240 245	
gcc gag ggc aaa gcc gaa tat gtc agt aga caa cgc gag ctg tct gaa	883
Ala Glu Gly Lys Ala Glu Tyr Val Ser Arg Gln Arg Glu Leu Ser Glu	
250 255 260	

cga gca aaa ccc atc cgt gac cgg ctt gtc tcc att act aaa caa gct 931
 Arg Ala Lys Pro Ile Arg Asp Arg Leu Val Ser Ile Thr Lys Gln Ala
 265 270 275

cta cag gct agt att tagaaaaatta gacttgtcaa tgt 969
 Leu Gln Ala Ser Ile
 280

<210> 2006

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 2006

Met Glu Leu Ala Arg Ala His His Ala Arg Ala Asp Ser Phe Thr Lys
 1 5 10 15

Asp His Leu Lys Arg Arg Gln Ala His Ile Lys His Pro Val Phe Asp
 20 25 30

Phe Leu Phe Glu Tyr Tyr Pro Val Arg Val Ala His Leu Lys Thr Trp
 35 40 45

His Pro Gly Ile Gly Val Phe Leu Glu Gly Thr Pro Pro His Ala Thr
 50 55 60

Met Arg Asp Phe Leu Leu Val Asp Ala Ser Leu His His Ala Ala Gly
 65 70 75 80

Val Gln Leu Asp Leu Ala Ser Tyr Met Gln Arg Arg Gly Ser Ser Val
 85 90 95

Arg Tyr Ile His Glu Leu Leu Ser Ala Thr Arg Asp Asn His Ala Gln
 100 105 110

Phe Asp Cys Phe Gly Leu His Glu Trp Ala Met Val Tyr Lys Ser Asn
 115 120 125

Asp Leu Arg His Asp Leu Pro Leu Arg Leu Thr Pro Ser Glu Thr Asp
 130 135 140

Arg Val Val Glu Ser His Asn Ile Lys Cys Thr His Phe Asp Ala Tyr
 145 150 155 160

Arg Phe Phe Thr Thr Pro Ala Ile Pro Leu Asn Leu Thr Val Leu Thr
 165 170 175

Arg Glu Asp Gln Pro Arg Asn Asp Gln Cys Gly Cys Leu His Ala Thr
 180 185 190

Met Asp Leu Tyr Lys Trp Ser Ala Lys Leu Gly Pro Leu Val Pro Gly
 195 200 205

Asp Leu Phe Leu Asp Ala Phe Glu Leu Ala Arg Asp Thr Arg Ile Leu
 210 215 220

Asp Met Glu Ala Ser Pro Tyr Asp Val Arg Gly Tyr Gly Phe Gly Tyr
 225 230 235 240

Val Pro Ile Glu Thr Ala Glu Gly Lys Ala Glu Tyr Val Ser Arg Gln

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                245                250                255
Arg Glu Leu Ser Glu Arg Ala Lys Pro Ile Arg Asp Arg Leu Val Ser
                260                265                270

Ile Thr Lys Gln Ala Leu Gln Ala Ser Ile
                275                280

<210> 2007
<211> 1830
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1807)
<223> RXA01007

<400> 2007
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                               Val Phe Lys Lys His
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aga cac ggt ctc ggc tcc ccc gaa acc aaa cca cgc tca ata acc cgc 163
Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro Arg Ser Ile Thr Arg
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cgg ttt ttc acc gcg gcc gcc gct acg ctg gca gga ttg gca gtc ctg 211
Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala Gly Leu Ala Val Leu
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tcc ggc tgc aca gca caa ccc tca caa gca gaa gac aac acg ctc act 259
Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu Asp Asn Thr Leu Thr
                40                45                50

tac tta gag cca cag ttc ttc cgc acc ctg tac cca cca tca gcg ggc 307
Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr Pro Pro Ser Ala Gly
                55                60                65

ttt tac ccc aac ggc agt gtg gtg aac aac att gca gac cgc ttg ctc 355
Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile Ala Asp Arg Leu Leu
                70                75                80                85

tac cag gat cct gaa acc ttg gaa ctc aag ccg tgg atc gcc acc gaa 403
Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro Trp Ile Ala Thr Glu
                90                95                100

ctc cca gaa gta aac gaa gac gcc acg gaa ttt acc ttc aac atc cgc 451
Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe Thr Phe Asn Ile Arg
                105                110                115

acc gat gtc acc tac tcc gat ggc acc ccg ctg acg gct gaa aac gtg 499
Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu Thr Ala Glu Asn Val
                120                125                130

gtg aaa aac ttc gat ctc tat ggc ctc ggc gat caa gat cga cgc ctc 547
Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp Gln Asp Arg Arg Leu
                135                140                145

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gag gac acc gtc cga ttc cac ttc tct gag cct gca cct ggt ttt gct Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro Ala Pro Gly Phe Ala 170 175 180	643
cag gcc acc agc tcc ttc aac gct ggc ctt tat gcc gat tcc acc ttg Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr Ala Asp Ser Thr Leu 185 190 195	691
gag ttc gcc aat gag gat ttc gcg cca ggc aac gcc caa aac gtc atc Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn Ala Gln Asn Val Ile 200 205 210	739
ggc tcc ggt cct ttc gtg atc acc gat gaa acc cta ggc acc aac ctc Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr Leu Gly Thr Asn Leu 215 220 225	787
acc ttg act gcg cgt gag gat tac gat tgg gca cca cca tca cgc gaa Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala Pro Pro Ser Arg Glu 230 235 240 245	835
cat caa ggt cgc gcg aag ctt gac gcc gtc aat tat gtc ctc gcg ggt His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn Tyr Val Leu Ala Gly 250 255 260	883
gaa gaa tcc gtc cgc atc gga gcc atc gtt gct ggc caa ggt gat atc Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala Gly Gln Gly Asp Ile 265 270 275	931
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ttc cgc ttc aaa aac gag ctg ctc tca gac atc cgt gtt cgc caa gct Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile Arg Val Arg Gln Ala 310 315 320 325	1075
ctg atc cac gcg atc gac cgc gaa aag atc atg cgt gtg ctg ttt agt Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met Arg Val Leu Phe Ser 330 335 340	1123
gat tcc tat ccg ctg gca act tct gtg ctt gcg caa aat gca ctg ggc Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala Gln Asn Ala Leu Gly 345 350 355	1171
tac aaa gaa caa gta gat gcc tat gtc tac gac cta gac aaa gca aca Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp Leu Asp Lys Ala Thr 360 365 370	1219
gct ctg ctt gac gaa gcc ggc tgg acc ctt gat agc gac ggc atg cgt Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp Ser Asp Gly Met Arg 375 380 385	1267

cgc aag gac ggt gaa ctt cta gag ctc acc ttc aac gaa gcc ctc cca 1315
 Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe Asn Glu Ala Leu Pro
 390 395 400 405

cag cct cgt tca cgc gaa gtt gtc acc atg gtc caa gaa cag ctc ggt 1363
 Gln Pro Arg Ser Arg Glu Val Val Thr Met Val Gln Glu Gln Leu Gly
 410 415 420

gat ctg ggc atc aag gtc aac ctc aac cca ggt gac caa gca gcc cag 1411
 Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly Asp Gln Ala Ala Gln
 425 430 435

gac gct gac tcc aag gat ctc aac aag atc cag gtt cgc cac acc atg 1459
 Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln Val Arg His Thr Met
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 Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser Gln Leu Tyr Ser Thr
 455 460 465

aac cgc aac gag ctg ttg aac atg acc gtg gaa ggg gag acc gcc gat 1555
 Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu Gly Glu Thr Ala Asp
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att ggc gat cct cat ttg gag gaa ctc ctc atg gct att gca tcc agc 1603
 Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met Ala Ile Ala Ser Ser
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cca cgc gaa gag gac cgt gca gca gca tct gcc gca gca cag gat tac 1651
 Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala Ala Ala Gln Asp Tyr
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atc acc gag cag gca tat gtt ctt cca ctg ttt gaa gag cca gtt gtc 1699
 Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe Glu Glu Pro Val Val
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tac ggc gtg cag cct tac gtg aag ggc ttt agc ccc gaa gtg atc ggc 1747
 Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser Pro Glu Val Ile Gly
 535 540 545

cgc ccc agc ttc tat gag acc tac att gac cat tcc agc gac cat tcc 1795
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<210> 2008

<211> 569

<212> PRT

<213> Corynebacterium glutamicum

<400> 2008

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 35 40 45
 Asp Asn Thr Leu Thr Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr
 50 55 60
 Pro Pro Ser Ala Gly Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile
 65 70 75 80
 Ala Asp Arg Leu Leu Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro
 85 90 95
 Trp Ile Ala Thr Glu Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe
 100 105 110
 Thr Phe Asn Ile Arg Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu
 115 120 125
 Thr Ala Glu Asn Val Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp
 130 135 140
 Gln Asp Arg Arg Leu Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His
 145 150 155 160
 Gly Glu Val Val Asp Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro
 165 170 175
 Ala Pro Gly Phe Ala Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr
 180 185 190
 Ala Asp Ser Thr Leu Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn
 195 200 205
 Ala Gln Asn Val Ile Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr
 210 215 220
 Leu Gly Thr Asn Leu Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala
 225 230 235 240
 Pro Pro Ser Arg Glu His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn
 245 250 255
 Tyr Val Leu Ala Gly Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala
 260 265 270
 Gly Gln Gly Asp Ile Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His
 275 280 285
 Leu Lys Asp Ala Gly Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val
 290 295 300
 Asn Asn Ser Phe Asn Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile
 305 310 315 320
 Arg Val Arg Gln Ala Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met
 325 330 335
 Arg Val Leu Phe Ser Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala
 340 345 350
 Gln Asn Ala Leu Gly Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp

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Leu	Asp	Lys	Ala	Thr	Ala	Leu	Leu	Asp	Glu	Ala	Gly	Trp	Thr	Leu	Asp
370					375					380					
Ser	Asp	Gly	Met	Arg	Arg	Lys	Asp	Gly	Glu	Leu	Leu	Glu	Leu	Thr	Phe
385					390					395					400
Asn	Glu	Ala	Leu	Pro	Gln	Pro	Arg	Ser	Arg	Glu	Val	Val	Thr	Met	Val
405					410					415					
Gln	Glu	Gln	Leu	Gly	Asp	Leu	Gly	Ile	Lys	Val	Asn	Leu	Asn	Pro	Gly
420					425					430					
Asp	Gln	Ala	Ala	Gln	Asp	Ala	Asp	Ser	Lys	Asp	Leu	Asn	Lys	Ile	Gln
435					440					445					
Val	Arg	His	Thr	Met	Val	Gly	Arg	Ala	Asp	Tyr	Asp	Val	Leu	Lys	Ser
450					455					460					
Gln	Leu	Tyr	Ser	Thr	Asn	Arg	Asn	Glu	Leu	Leu	Asn	Met	Thr	Val	Glu
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Gly	Glu	Thr	Ala	Asp	Ile	Gly	Asp	Pro	His	Leu	Glu	Glu	Leu	Leu	Met
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Ala	Ile	Ala	Ser	Ser	Pro	Arg	Glu	Glu	Asp	Arg	Ala	Ala	Ala	Ser	Ala
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Ala	Ala	Gln	Asp	Tyr	Ile	Thr	Glu	Gln	Ala	Tyr	Val	Leu	Pro	Leu	Phe
515					520					525					
Glu	Glu	Pro	Val	Val	Tyr	Gly	Val	Gln	Pro	Tyr	Val	Lys	Gly	Phe	Ser
530					535					540					
Pro	Glu	Val	Ile	Gly	Arg	Pro	Ser	Phe	Tyr	Glu	Thr	Tyr	Ile	Asp	His
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Ser	Ser	Asp	His	Ser	Ser	Glu	Glu	Asp							
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<211> 2064
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<223> RXA01008
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Val Ser Thr Thr Asp
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aag cag gta gcc atc gtt gga gtt ggc ccc aga ggt att tcc ata ctc 163
Lys Gln Val Ala Ile Val Gly Val Gly Pro Arg Gly Ile Ser Ile Leu

10										15					20					
gaa agg atc gca gca gct ctc aac aca gtt tcc cgc ccc aaa caa ggc	211																			
Glu Arg Ile Ala Ala Leu Asn Thr Val Ser Arg Pro Lys Gln Gly																				
25 30 35																				
ttg acc atc cac ctg att gag gat gcc cag atg ggt gca ggc aac gtg	259																			
Leu Thr Ile His Leu Ile Glu Asp Ala Gln Met Gly Ala Gly Asn Val																				
40 45 50																				
tgg cgc act gat caa acc cgc acg ctg tgc atg aat act ctg gcc ggt	307																			
Trp Arg Thr Asp Gln Thr Arg Thr Leu Cys Met Asn Thr Leu Ala Gly																				
55 60 65																				
gcg gtg aca tta ttc aca gag cca ggc tct acg gtg agc gct cca gtg	355																			
Ala Val Thr Leu Phe Thr Glu Pro Gly Ser Thr Val Ser Ala Pro Val																				
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90 95 100																				
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Glu Asp Leu Ser Gly Ile Pro Thr Lys Ala Ile Glu Leu Phe Arg Thr																				
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Tyr Pro Pro Ala Ala Ser Val Ala Glu Asp Phe Lys Glu Glu Leu Ala																				
120 125 130																				
gcc act gtt atc cag tcc aat cct tcc cgt gct ctt tat ggc gca tat	547																			
Ala Thr Val Ile Gln Ser Asn Pro Ser Arg Ala Leu Tyr Gly Ala Tyr																				
135 140 145																				
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150 155 160 165																				
aag gtc gag cag cac cat gcg cgc gcg att ggc atc cgc gaa gat ggt	643																			
Lys Val Glu Gln His His Ala Arg Ala Ile Gly Ile Arg Glu Asp Gly																				
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Asp Arg Asp Val Ile Thr Leu Asp Asn Ser Glu Met Ile Ser Ala Asp																				
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Ser Thr Val Leu Ala Val Gly Trp Gln Thr Pro Ala Pro Asn Ala Glu																				
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Glu Leu Ser Ile Ala Ala Ala Leu Glu Glu Asn Pro Asp Leu Val Trp																				
215 220 225																				
gtc aag ccc ggc aac cct gtc gag cag gat gcc agc ctc att ccc gct	835																			
Val Lys Pro Gly Asn Pro Val Glu Gln Asp Ala Ser Leu Ile Pro Ala																				
230 235 240 245																				
ggc gaa cag gtg ctt gtc cgc ggg ctg ggc atg gga ttt ttc gat atc	883																			
Gly Glu Gln Val Leu Val Arg Gly Leu Gly Met Gly Phe Phe Asp Ile																				
250 255 260																				

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Met Ala Leu Thr Thr Ile Asp Arg Gly Gly Ile Phe His Glu Asp Pro	
265 270 275	
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Ser Thr Arg Ser Gly Leu Arg Tyr Glu Ala Ser Gly Glu Glu Pro His	
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Phe Val Ile Ser Ser Gly Arg Gly Tyr Pro Tyr Leu Pro Lys Ser Asp	
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Tyr Lys Ser Leu Pro Pro Gly Ala Lys Leu Ala Arg Leu Lys Ala Val	
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Ile Ala Ala Ile Asn Ala Gln Asn Arg Gly Val Ala Ser Ile Asn Tyr	
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Asp Ala Glu Val Trp Pro Ala Val Ala Arg Asp Ala Tyr Glu Ala Tyr	
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Tyr Glu Thr Leu Asp Arg Val Ser Pro Glu Ser Ile Arg Thr Gly Leu	
360 365 370	
gat aaa att gtg gaa att att gat gag gtg gac gtc gat aag ctt cct	1267
Asp Lys Ile Val Glu Ile Ile Asp Glu Val Asp Val Asp Lys Leu Pro	
375 380 385	
aaa gca ctc gcc gcg cac acc gat gac gtc ttt gac ctg cat gct tgg	1315
Lys Ala Leu Ala Ala His Thr Asp Asp Val Phe Asp Leu His Ala Trp	
390 395 400 405	
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Glu Phe Pro Leu Ala Gly Ile Asn Glu Ser Val Glu Ala Leu Thr Ala	
410 415 420	
cgc atc gcg gac ggc atg gcc cgc gat att cgc cat gca gta acg gcc	1411
Arg Ile Ala Asp Gly Met Ala Arg Asp Ile Arg His Ala Val Thr Ala	
425 430 435	
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Ser Gly Pro Pro Leu Phe Arg Thr Arg Glu Leu Leu Ala Leu Val Asp	
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 Ala Gly Leu Ala His Phe Ala Gly Ala Arg Pro Arg Leu Ser Val Ser
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 Asp Gly Gln Trp Gln Ile Ser Ser Pro Thr Thr Gly Asp Thr Pro Leu
 520 525 530
 aga tcg aaa gtg ctt gtc gac gcg tgg atg cac aac cca gat gtg cgt 1747
 Arg Ser Lys Val Leu Val Asp Ala Trp Met His Asn Pro Asp Val Arg
 535 540 545
 cgc aac gcc gac ccg cta gca ctg tct ttg gaa gat gcc gac cgg gta 1795
 Arg Asn Ala Asp Pro Leu Ala Leu Ser Leu Glu Asp Ala Asp Arg Val
 550 555 560 565
 cgc ccc ttc aac gac tat tcc gtc gac gga acc gct gcc ccc aca ggc 1843
 Arg Pro Phe Asn Asp Tyr Ser Val Asp Gly Thr Ala Ala Pro Thr Gly
 570 575 580
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 Ser Pro Glu Val Asp Pro Ala Thr Arg Leu Leu Val His Pro Asn Gly
 585 590 595
 aac ctc gat ccg cgc gtg cac ctg att ggc atc cca acc tat ggg cag 1939
 Asn Leu Asp Pro Arg Val His Leu Ile Gly Ile Pro Thr Tyr Gly Gln
 600 605 610
 ctg gcc gac acc acc atc tcg ccg atg cct gga acc aac ccg ctc atg 1987
 Leu Ala Asp Thr Thr Ile Ser Pro Met Pro Gly Thr Asn Pro Leu Met
 615 620 625
 ctg caa gaa acc gac aaa aca gcc gtt cac gtg cta aag cag ctc ggc 2035
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 Leu Ile

<210> 2010

<211> 647

<212> PRT

<213> Corynebacterium glutamicum

<400> 2010

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 20 25 30

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 35 40 45

Gly Ala Gly Asn Val Trp Arg Thr Asp Gln Thr Arg Thr Leu Cys Met
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Asn Thr Leu Ala Gly Ala Val Thr Leu Phe Thr Glu Pro Gly Ser Thr
 65 70 75 80

Val Ser Ala Pro Val Val Glu Gly Pro Leu Gln Phe Asp Trp Ile Arg
 85 90 95
 Leu Leu Arg Gly Asp Glu Asp Leu Ser Gly Ile Pro Thr Lys Ala Ile
 100 105 110
 Glu Leu Phe Arg Thr Tyr Pro Pro Ala Ala Ser Val Ala Glu Asp Phe
 115 120 125
 Lys Glu Glu Leu Ala Ala Thr Val Ile Gln Ser Asn Pro Ser Arg Ala
 130 135 140
 Leu Tyr Gly Ala Tyr Leu Arg Trp Ala Phe Asp Val Ala Leu Gln Leu
 145 150 155 160
 Leu Pro Gln Trp Val Lys Val Glu Gln His His Ala Arg Ala Ile Gly
 165 170 175
 Ile Arg Glu Asp Gly Asp Arg Asp Val Ile Thr Leu Asp Asn Ser Glu
 180 185 190
 Met Ile Ser Ala Asp Ser Thr Val Leu Ala Val Gly Trp Gln Thr Pro
 195 200 205
 Ala Pro Asn Ala Glu Glu Leu Ser Ile Ala Ala Ala Leu Glu Glu Asn
 210 215 220
 Pro Asp Leu Val Trp Val Lys Pro Gly Asn Pro Val Glu Gln Asp Ala
 225 230 235 240
 Ser Leu Ile Pro Ala Gly Glu Gln Val Leu Val Arg Gly Leu Gly Met
 245 250 255
 Gly Phe Phe Asp Ile Met Ala Leu Thr Thr Ile Asp Arg Gly Gly Ile
 260 265 270
 Phe His Glu Asp Pro Ser Thr Arg Ser Gly Leu Arg Tyr Glu Ala Ser
 275 280 285
 Gly Glu Glu Pro His Phe Val Ile Ser Ser Gly Arg Gly Tyr Pro Tyr
 290 295 300
 Leu Pro Lys Ser Asp Tyr Lys Ser Leu Pro Pro Gly Ala Lys Leu Ala
 305 310 315 320
 Arg Leu Lys Ala Val Ile Ala Ala Ile Asn Ala Gln Asn Arg Gly Val
 325 330 335
 Ala Ser Ile Asn Tyr Asp Ala Glu Val Trp Pro Ala Val Ala Arg Asp
 340 345 350
 Ala Tyr Glu Ala Tyr Tyr Glu Thr Leu Asp Arg Val Ser Pro Glu Ser
 355 360 365
 Ile Arg Thr Gly Leu Asp Lys Ile Val Glu Ile Ile Asp Glu Val Asp
 370 375 380
 Val Asp Lys Leu Pro Lys Ala Leu Ala Ala His Thr Asp Asp Val Phe
 385 390 395 400

Asp Leu His Ala Trp Glu Phe Pro Leu Ala Gly Ile Asn Glu Ser Val
405 410 415

Glu Ala Leu Thr Ala Arg Ile Ala Asp Gly Met Ala Arg Asp Ile Arg
420 425 430

His Ala Val Thr Ala Trp Asp Ser Pro Leu Lys Ser Ala Leu Trp Ser
435 440 445

Ile Ser Ala Ala Arg Lys Pro Ser Ser Ile Leu Gly Ala Glu Gly Arg
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Leu Thr Phe Glu Ser Arg Arg Asn Arg Phe Ala Ala Val Met Ala Ile
465 470 475 480

Gly Gln Met Val Gly Ser Gly Pro Pro Leu Phe Arg Thr Arg Glu Leu
485 490 495

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500 505 510

Arg Leu Ser Val Ser Asp Gly Gln Trp Gln Ile Ser Ser Pro Thr Thr
515 520 525

Gly Asp Thr Pro Leu Arg Ser Lys Val Leu Val Asp Ala Trp Met His
530 535 540

Asn Pro Asp Val Arg Arg Asn Ala Asp Pro Leu Ala Leu Ser Leu Glu
545 550 555 560

Asp Ala Asp Arg Val Arg Pro Phe Asn Asp Tyr Ser Val Asp Gly Thr
565 570 575

Ala Ala Pro Thr Gly Ser Pro Glu Val Asp Pro Ala Thr Arg Leu Leu
580 585 590

Val His Pro Asn Gly Asn Leu Asp Pro Arg Val His Leu Ile Gly Ile
595 600 605

Pro Thr Tyr Gly Gln Leu Ala Asp Thr Thr Ile Ser Pro Met Pro Gly
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<210> 2011

<211> 1356

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1333)

<223> RXA01011

<400> 2011

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	1 5	
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Gln Ala Arg Asp Asn Ala Gln Lys Ser Phe Glu Ala Leu Leu Glu Pro		
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Val Asn Pro Gly Thr Phe Ser Phe Gly Glu Arg Tyr Ala Val Ala Thr		
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Tyr Val Ala Gly Leu His Gln Phe Ala Pro Ala Val Asp Leu Tyr Gln		
	55 60 65	
gat ttg ctt ctc gac gac gcc cca acc acc ctg gca aac gcc gtc tcc	355	
Asp Leu Leu Leu Asp Asp Ala Pro Thr Thr Leu Ala Asn Ala Val Ser		
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gat gcc atc gac gag ggc cta tcc gca ggc cca tac ggc acc tac cgt	403	
Asp Ala Ile Asp Glu Gly Leu Ser Ala Gly Pro Tyr Gly Thr Tyr Arg		
	90 95 100	
gaa cct gga ctt gag tcc gaa tca gag cca ggc gga tct gtg cgc aac	451	
Glu Pro Gly Leu Glu Ser Glu Ser Glu Pro Gly Gly Ser Val Arg Asn		
	105 110 115	
gat gcc gcc aag ctt ggc gag cga ctt gca gca gca ttt gat tac gca	499	
Asp Ala Ala Lys Leu Gly Glu Arg Leu Ala Ala Ala Phe Asp Tyr Ala		
	120 125 130	
cac cta cta gtt ttc cac ccc cgt gat tcc cgc ccc gag gtc ctt ggt	547	
His Leu Leu Val Phe His Pro Arg Asp Ser Arg Pro Glu Val Leu Gly		
	135 140 145	
cga ctc tcc ggc gct ggc tgg agc gcg gat gac acc gtg aca ttg gct	595	
Arg Leu Ser Gly Ala Gly Trp Ser Ala Asp Asp Thr Val Thr Leu Ala		
	150 155 160 165	
cag ctg gtg tcg ttc ctg gca ttc cag ctg cgt gtt gcc tac ggc ctg	643	
Gln Leu Val Ser Phe Leu Ala Phe Gln Leu Arg Val Ala Tyr Gly Leu		
	170 175 180	
cgc acc ctc aaa ggt gaa gac att cag gtg aaa gct cct cgc ctg agt	691	
Arg Thr Leu Lys Gly Glu Asp Ile Gln Val Lys Ala Pro Arg Leu Ser		
	185 190 195	
att cct gaa gcg aag tgg gaa ctg tcc aac aac ggc ttt gag atc tcc	739	
Ile Pro Glu Ala Lys Trp Glu Leu Ser Asn Asn Gly Phe Glu Ile Ser		
	200 205 210	
acc tat gaa gaa ctc aac cgc cct gaa gcg ttt gtg aac cac tct ttg	787	
Thr Tyr Glu Glu Leu Asn Arg Pro Glu Ala Phe Val Asn His Ser Leu		
	215 220 225	

ggc tgg aag cca tgg gta cca cca gta gca aag gca gat ctc acc gaa 835
 Gly Trp Lys Pro Trp Val Pro Pro Val Ala Lys Ala Asp Leu Thr Glu
 230 235 240 245
 gaa cag ctg gat tct ttg atc cag cct gag cgc gct gat atg cca tac 883
 Glu Gln Leu Asp Ser Leu Ile Gln Pro Glu Arg Ala Asp Met Pro Tyr
 250 255 260
 ttc cgt ctc ttg gca cgc gat cct gca gca ttg aag gcg cgt acc ctg 931
 Phe Arg Leu Leu Ala Arg Asp Pro Ala Ala Leu Lys Ala Arg Thr Leu
 265 270 275
 acc gat ctg gat atc ttc ttc aac act gac ggc gaa ggc cta gga cgt 979
 Thr Asp Leu Asp Ile Phe Phe Asn Thr Asp Gly Glu Gly Leu Gly Arg
 280 285 290
 gca gag cgt gaa ctc ggc gcc acc gtt act tcc cgc tac aac ggc tgc 1027
 Ala Glu Arg Glu Leu Gly Ala Thr Val Thr Ser Arg Tyr Asn Gly Cys
 295 300 305
 gtg tac tgc gca tcc gtg cac gca gga cgt gct cag gaa gaa tcc ggt 1075
 Val Tyr Cys Ala Ser Val His Ala Gly Arg Ala Gln Glu Glu Ser Gly
 310 315 320 325
 cga gct gat gat gtc aac gca ctg ttg gca agc atc gac tcc gat ctg 1123
 Arg Ala Asp Asp Val Asn Ala Leu Leu Ala Ser Ile Asp Ser Asp Leu
 330 335 340
 ggt tct gac cag tgg aat gtc atc cgt gac gct gct cgc gca ctg agc 1171
 Gly Ser Asp Gln Trp Asn Val Ile Arg Asp Ala Ala Arg Ala Leu Ser
 345 350 355
 tcc acc cct gct gct ttc aac cag gga tgc atc acc aag ctg cgt ggc 1219
 Ser Thr Pro Ala Ala Phe Asn Gln Gly Cys Ile Thr Lys Leu Arg Gly
 360 365 370
 gtt gga ttc agc gac ctg cag atc gtg gac ttg atc aac tct gtg gcg 1267
 Val Gly Phe Ser Asp Leu Gln Ile Val Asp Leu Ile Asn Ser Val Ala
 375 380 385
 ttc ttc aac tgg gcg aac cgc ctg atg ttg tca ctg ggt gaa ccc gaa 1315
 Phe Phe Asn Trp Ala Asn Arg Leu Met Leu Ser Leu Gly Glu Pro Glu
 390 395 400 405
 gtg cca aag cgt ttc ctg taaaacgcat aaccccgaaat acc 1356
 Val Pro Lys Arg Phe Leu
 410

<210> 2012

<211> 411

<212> PRT

<213> Corynebacterium glutamicum

<400> 2012

Met Ser Asp Leu Ile Asp Met Leu Val Gly Glu Asp Leu Pro Gln Leu
 1 5 10 15

Arg Asp Asn Arg Pro Gln Ala Arg Asp Asn Ala Gln Lys Ser Phe Glu
 20 25 30

Ala Leu Leu Glu Pro Val Asn Pro Gly Thr Phe Ser Phe Gly Glu Arg
35 40 45

Tyr Ala Val Ala Thr Tyr Val Ala Gly Leu His Gln Phe Ala Pro Ala
50 55 60

Val Asp Leu Tyr Gln Asp Leu Leu Leu Asp Asp Ala Pro Thr Thr Leu
65 70 75 80

Ala Asn Ala Val Ser Asp Ala Ile Asp Glu Gly Leu Ser Ala Gly Pro
85 90 95

Tyr Gly Thr Tyr Arg Glu Pro Gly Leu Glu Ser Glu Ser Glu Pro Gly
100 105 110

Gly Ser Val Arg Asn Asp Ala Ala Lys Leu Gly Glu Arg Leu Ala Ala
115 120 125

Ala Phe Asp Tyr Ala His Leu Leu Val Phe His Pro Arg Asp Ser Arg
130 135 140

Pro Glu Val Leu Gly Arg Leu Ser Gly Ala Gly Trp Ser Ala Asp Asp
145 150 155 160

Thr Val Thr Leu Ala Gln Leu Val Ser Phe Leu Ala Phe Gln Leu Arg
165 170 175

Val Ala Tyr Gly Leu Arg Thr Leu Lys Gly Glu Asp Ile Gln Val Lys
180 185 190

Ala Pro Arg Leu Ser Ile Pro Glu Ala Lys Trp Glu Leu Ser Asn Asn
195 200 205

Gly Phe Glu Ile Ser Thr Tyr Glu Glu Leu Asn Arg Pro Glu Ala Phe
210 215 220

Val Asn His Ser Leu Gly Trp Lys Pro Trp Val Pro Pro Val Ala Lys
225 230 235 240

Ala Asp Leu Thr Glu Glu Gln Leu Asp Ser Leu Ile Gln Pro Glu Arg
245 250 255

Ala Asp Met Pro Tyr Phe Arg Leu Leu Ala Arg Asp Pro Ala Ala Leu
260 265 270

Lys Ala Arg Thr Leu Thr Asp Leu Asp Ile Phe Phe Asn Thr Asp Gly
275 280 285

Glu Gly Leu Gly Arg Ala Glu Arg Glu Leu Gly Ala Thr Val Thr Ser
290 295 300

Arg Tyr Asn Gly Cys Val Tyr Cys Ala Ser Val His Ala Gly Arg Ala
305 310 315 320

Gln Glu Glu Ser Gly Arg Ala Asp Asp Val Asn Ala Leu Leu Ala Ser
325 330 335

Ile Asp Ser Asp Leu Gly Ser Asp Gln Trp Asn Val Ile Arg Asp Ala
340 345 350

Ala Arg Ala Leu Ser Ser Thr Pro Ala Ala Phe Asn Gln Gly Cys Ile

355	360	365
Thr Lys Leu Arg Gly Val Gly Phe Ser Asp Leu Gln Ile Val Asp Leu		
370	375	380
Ile Asn Ser Val Ala Phe Phe Asn Trp Ala Asn Arg Leu Met Leu Ser		
385	390	395
		400
Leu Gly Glu Pro Glu Val Pro Lys Arg Phe Leu		
	405	410

<210> 2013

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXA01017

<400> 2013

gaaatttgag ggggcgctac ccttagaagg tgcgcaatga caccacgata gttcgcgcct 60

agtgtggatt gctagaaaac tttaagaaag aggaaataat	atg gct caa aaa gta	115
	Met Ala Gln Lys Val	
	1 5	

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc	163
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg	
10 15 20	

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt	211
Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val	
25 30 35	

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat	259
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp	
40 45 50	

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca	307
Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala	
55 60 65	

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca	355
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala	
70 75 80 85	

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc	403
Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser	
90 95 100	

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct	451
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala	
105 110 115	

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc	499
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg	
120 125 130	

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547
 Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
 135 140 145
 cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595
 Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
 150 155 160 165
 cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643
 Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
 170 175 180
 aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691
 Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
 185 190 195
 gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732
 Glu Asn Pro Gln Phe Asp
 200

<210> 2014

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 2014

Met Ala Gln Lys Val Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys
 1 5 10 15
 Trp Val Thr Ser Arg Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile
 20 25 30
 Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg
 35 40 45
 Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro
 50 55 60
 Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly
 65 70 75 80
 Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly
 85 90 95
 Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu
 100 105 110
 Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp
 115 120 125
 Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly
 130 135 140
 Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe
 145 150 155 160
 Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile
 165 170 175
 Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile

150 155 160 165
ggc act gtt gtc act gtg ttg cgt tct 622
Gly Thr Val Val Thr Val Leu Arg Ser
170

<210> 2016
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 2016
Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro
1 5 10 15
Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala
20 25 30
Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
35 40 45
Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
50 55 60
Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
65 70 75 80
Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
85 90 95
Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
100 105 110
Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
115 120 125
Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
130 135 140
Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
145 150 155 160
Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
165 170

<210> 2017
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXA01029

<400> 2017
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gtgtgggggtt ccttgccggc gtatgtccgg ggtgcttgct atg ctt caa acg att 115

	Met	Leu	Gln	Thr	Ile	
	1				5	
tca ttc aag aaa ctt aat tta tta aca act ctt aaa aga aaa gga gag						163
Ser Phe Lys Lys Leu Asn Leu Leu Thr Thr Leu Lys Arg Lys Gly Glu						
			10			20
ctg gtc atc atg atc act cgt cac gat gtt ccc tac atc atc gct ccg						211
Leu Val Ile Met Ile Thr Arg His Asp Val Pro Tyr Ile Ile Ala Pro						
			25			35
cct gtc tac gcg atc ttt gcg agc ctg atg acc acg cca cca tgg ttt						259
Pro Val Tyr Ala Ile Phe Ala Ser Leu Met Thr Thr Pro Pro Trp Phe						
			40			50
tat cga acc acc tac acc att gac ggt ttc gat ttt aag atc agc tgg						307
Tyr Arg Thr Thr Tyr Thr Ile Asp Gly Phe Asp Phe Lys Ile Ser Trp						
			55			65
gtc tac acc atc acc atc tac atc agc ctc atg atc ctc att atc ggg						355
Val Tyr Thr Ile Thr Ile Tyr Ile Ser Leu Met Ile Leu Ile Ile Gly						
			70			85
ttc tac caa gcc aat atg cgc aaa gcg tgc cct tat gag gaa gat cct						403
Phe Tyr Gln Ala Asn Met Arg Lys Ala Cys Pro Tyr Glu Glu Asp Pro						
			90			100
ttg gtc gat att tgg cac aag gtg tgg agc act gca ctc ttt atc cta						451
Leu Val Asp Ile Trp His Lys Val Trp Ser Thr Ala Leu Phe Ile Leu						
			105			115
cct atc gtt tta tcc atc gcg gtg tac tca ctg atc aca cag cgc ggg						499
Pro Ile Val Leu Ser Ile Ala Val Tyr Ser Leu Ile Thr Gln Arg Gly						
			120			130
ttt gac tgg tat gtc atg gtg ttt att ctc cct gta ggc ttg atg atc						547
Phe Asp Trp Tyr Val Met Val Phe Ile Leu Pro Val Gly Leu Met Ile						
			135			145
gct tat gga ttc ttc aag ccc tgt gat tgc gac aaa cac cgt						589
Ala Tyr Gly Phe Phe Lys Pro Cys Asp Cys Asp Lys His Arg						
			150			160
taaggatatac ttgtccaaga ctt						612

<210> 2018

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 2018

Met	Leu	Gln	Thr	Ile	Ser	Phe	Lys	Lys	Leu	Asn	Leu	Leu	Thr	Thr	Leu
1				5					10						15

Lys	Arg	Lys	Gly	Glu	Leu	Val	Ile	Met	Ile	Thr	Arg	His	Asp	Val	Pro
			20					25					30		

Tyr	Ile	Ile	Ala	Pro	Pro	Val	Tyr	Ala	Ile	Phe	Ala	Ser	Leu	Met	Thr
			35				40					45			

Thr Pro Pro Trp Phe Tyr Arg Thr Thr Tyr Thr Ile Asp Gly Phe Asp
 50 55 60
 Phe Lys Ile Ser Trp Val Tyr Thr Ile Thr Ile Tyr Ile Ser Leu Met
 65 70 75 80
 Ile Leu Ile Ile Gly Phe Tyr Gln Ala Asn Met Arg Lys Ala Cys Pro
 85 90 95
 Tyr Glu Glu Asp Pro Leu Val Asp Ile Trp His Lys Val Trp Ser Thr
 100 105 110
 Ala Leu Phe Ile Leu Pro Ile Val Leu Ser Ile Ala Val Tyr Ser Leu
 115 120 125
 Ile Thr Gln Arg Gly Phe Asp Trp Tyr Val Met Val Phe Ile Leu Pro
 130 135 140
 Val Gly Leu Met Ile Ala Tyr Gly Phe Phe Lys Pro Cys Asp Cys Asp
 145 150 155 160
 Lys His Arg

<210> 2019

<211> 789

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(766)

<223> RXA01031

<400> 2019

cagctgaact tgatcatttt gatgatctgc cagtacagcg ccaagaagat cttggcacct 60
 tagttgttat ctctgctggt cacgcaagcg actctgcggc atg aaa ctg ctg caa 115
 Met Lys Leu Leu Gln
 1 5
 tac gca ggt ggt gct gtc tat gtc gat cca gaa gat tct gcg cag tcc 163
 Tyr Ala Gly Gly Ala Val Tyr Val Asp Pro Glu Asp Ser Ala Gln Ser
 10 15 20
 caa gac ctg gat gcc agc act gca cgt gat gtt atc gac gct acc aac 211
 Gln Asp Leu Asp Ala Ser Thr Ala Arg Asp Val Ile Asp Ala Thr Asn
 25 30 35
 acc gcc atg acc act att acc tct cgc ccc acc atg att gtg cac ctg 259
 Thr Ala Met Thr Thr Ile Thr Ser Arg Pro Thr Met Ile Val His Leu
 40 45 50
 cac aag gtg cga aaa gtc att gag att tta tgc aac cct gca ctc ggc 307
 His Lys Val Arg Lys Val Ile Glu Ile Leu Cys Asn Pro Ala Leu Gly
 55 60 65
 ggt gaa cct gtc aat atc gac cag gac gag acc gga aaa cag gtg tac 355
 Gly Glu Pro Val Asn Ile Asp Gln Asp Glu Thr Gly Lys Gln Val Tyr
 70 75 80 85

aca ccc acc cca acg ctt gtc gcc tat cgc ttt atc tct gac aaa gaa 403
 Thr Pro Thr Pro Thr Leu Val Ala Tyr Arg Phe Ile Ser Asp Lys Glu
 90 95 100

atc ctg ctt cat tac ctg gcg cag gcg ggt gtg cag ggt gtg gag gtt 451
 Ile Leu Leu His Tyr Leu Ala Gln Ala Gly Val Gln Gly Val Glu Val
 105 110 115

ttt gac ggg tcg cct gac atg ctg agc cgt tgg aat gcg gga cgc att 499
 Phe Asp Gly Ser Pro Asp Met Leu Ser Arg Trp Asn Ala Gly Arg Ile
 120 125 130

ccg gtc tta ctt ttg cag cct gcg tct gct ggt cac ggc ttg aat ttc 547
 Pro Val Leu Leu Leu Gln Pro Ala Ser Ala Gly His Gly Leu Asn Phe
 135 140 145

cag cac ggc ggg cat cgc ttg gtg tgg tac aac ctg ccc gat aat aac 595
 Gln His Gly Gly His Arg Leu Val Trp Tyr Asn Leu Pro Asp Asn Asn
 150 155 160 165

gag cat tat atg caa gcg aat gct cgt cta cat cgc att ggt caa aag 643
 Glu His Tyr Met Gln Ala Asn Ala Arg Leu His Arg Ile Gly Gln Lys
 170 175 180

aat ccc gtg acc att cac cgc att att acc gct gat act tat gat gcg 691
 Asn Pro Val Thr Ile His Arg Ile Ile Thr Ala Asp Thr Tyr Asp Ala
 185 190 195

aat atg ccg gcg att ctg gcc ggt aaa gca aat aga cag caa cgt ctc 739
 Asn Met Pro Ala Ile Leu Ala Gly Lys Ala Asn Arg Gln Gln Arg Leu
 200 205 210

atc gac gcc gtg cgc cgt gat cca gtc taagaccggc acgatcgcac 786
 Ile Asp Ala Val Arg Arg Asp Pro Val
 215 220

cgt 789

<210> 2020

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 2020

Met Lys Leu Leu Gln Tyr Ala Gly Gly Ala Val Tyr Val Asp Pro Glu
 1 5 10 15

Asp Ser Ala Gln Ser Gln Asp Leu Asp Ala Ser Thr Ala Arg Asp Val
 20 25 30

Ile Asp Ala Thr Asn Thr Ala Met Thr Thr Ile Thr Ser Arg Pro Thr
 35 40 45

Met Ile Val His Leu His Lys Val Arg Lys Val Ile Glu Ile Leu Cys
 50 55 60

Asn Pro Ala Leu Gly Gly Glu Pro Val Asn Ile Asp Gln Asp Glu Thr
 65 70 75 80

<400> 2021															
agctaatacag caccacctac aacaccacaa acacacccca atcagcatga tcgtgccggt															60
tggggtgtgt cttatcccct aagaaagtga cacctttacc atg tca gac cac gac															115
Met Ser Asp His Asp															
1 5															
gcc cca caa aca ccg atc ccc aag ggg ttt tgg cag cag atc gac cac															163
Ala Pro Gln Thr Pro Ile Pro Lys Gly Phe Trp Gln Gln Ile Asp His															
10 15 20															
caa ctc gat cgc ctc ggc acg cag cgc cca gag acc ttc gca gca ctg															211
Gln Leu Asp Arg Leu Gly Thr Gln Arg Pro Glu Thr Phe Ala Ala Leu															
25 30 35															
cgt gac att ttg ctt gat cct gcc tac acc gcc att gtt cat gac cgt															259
Arg Asp Ile Leu Leu Asp Pro Ala Tyr Thr Ala Ile Val His Asp Arg															
40 45 50															
aat cgc tac ggc gtt gtc acc ttt gac acc aac tca gcc ttc ttc tca															307
Asn Arg Tyr Gly Val Val Thr Phe Asp Thr Asn Ser Ala Phe Phe Ser															
55 60 65															

ggc tct ggc gga gac aac ggc tta gcc gac gta ctc att aac tgt gat 355
Gly Ser Gly Gly Asp Asn Gly Leu Ala Asp Val Leu Ile Asn Cys Asp 85
70 75 80

tgg cgc atg act gac tac cgc gcc gag tac tac tac gtc atg aca cat 403
Trp Arg Met Thr Asp Tyr Arg Ala Glu Tyr Tyr Tyr Val Met Thr His 100
90 95

aaa tac acc aag gaa tcg ttt acc tat atc gag ggc gac gtg aaa cgc 451
Lys Tyr Thr Lys Glu Ser Phe Thr Tyr Ile Glu Gly Asp Val Lys Arg 115
105 110

ggc gac ctc atc ccg cct aat aat taaggacaac cgccatgact cag 498
Gly Asp Leu Ile Pro Pro Asn Asn 125
120

<210> 2022

<211> 125

<212> PRT

<213> Corynebacterium glutamicum

<400> 2022

Met Ser Asp His Asp Ala Pro Gln Thr Pro Ile Pro Lys Gly Phe Trp
1 5 10 15

Gln Gln Ile Asp His Gln Leu Asp Arg Leu Gly Thr Gln Arg Pro Glu
20 25 30

Thr Phe Ala Ala Leu Arg Asp Ile Leu Leu Asp Pro Ala Tyr Thr Ala
35 40 45

Ile Val His Asp Arg Asn Arg Tyr Gly Val Val Thr Phe Asp Thr Asn
50 55 60

Ser Ala Phe Phe Ser Gly Ser Gly Gly Asp Asn Gly Leu Ala Asp Val
65 70 75 80

Leu Ile Asn Cys Asp Trp Arg Met Thr Asp Tyr Arg Ala Glu Tyr Tyr
85 90 95

Tyr Val Met Thr His Lys Tyr Thr Lys Glu Ser Phe Thr Tyr Ile Glu
100 105 110

Gly Asp Val Lys Arg Gly Asp Leu Ile Pro Pro Asn Asn
115 120 125

<210> 2023

<211> 459

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(436)

<223> RXA01033

<400> 2023

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gcggcgacct catccgcct aataattaag gacaaccgcc atg act cag atc gcc 115
Met Thr Gln Ile Ala
1 5

atg tat ctc gca gga ccc atg aca ggt atc cct gaa tac aac tac ccc 163
Met Tyr Leu Ala Gly Pro Met Thr Gly Ile Pro Glu Tyr Asn Tyr Pro
10 15 20

acc ttc cat gca gcg gct aat aag ttc cgt gca gct ggc tac acc gta 211
Thr Phe His Ala Ala Ala Asn Lys Phe Arg Ala Ala Gly Tyr Thr Val
25 30 35

ctc tcc ccc gct gaa gac gaa tat gaa tcc cag ctc act gca cca ttg 259
Leu Ser Pro Ala Glu Asp Glu Tyr Glu Ser Gln Leu Thr Ala Pro Leu
40 45 50

cct gag aac gct gag cac aaa tac gac cac tac ttg cgt ctc ggt atc 307
Pro Glu Asn Ala Glu His Lys Tyr Asp His Tyr Leu Arg Leu Gly Ile
55 60 65

gaa aag ctg ctc aag gct gat gct gtc cac atg ctt cag gga tgg cag 355
Glu Lys Leu Leu Lys Ala Asp Ala Val His Met Leu Gln Gly Trp Gln
70 75 80 85

agt agc gcc ggt gcc act ctt gag cac gat att gca cag aaa ttg agg 403
Ser Ser Ala Gly Ala Thr Leu Glu His Asp Ile Ala Gln Lys Leu Arg
90 95 100

ctt gcc att acc tat gaa gaa cca cca gca tcc taaggcgcc cggcatagc 456
Leu Ala Ile Thr Tyr Glu Glu Pro Pro Ala Ser
105 110

gta 459

<210> 2024

<211> 112

<212> PRT

<213> Corynebacterium glutamicum

<400> 2024

Met Thr Gln Ile Ala Met Tyr Leu Ala Gly Pro Met Thr Gly Ile Pro
1 5 10 15

Glu Tyr Asn Tyr Pro Thr Phe His Ala Ala Ala Asn Lys Phe Arg Ala
20 25 30

Ala Gly Tyr Thr Val Leu Ser Pro Ala Glu Asp Glu Tyr Glu Ser Gln
35 40 45

Leu Thr Ala Pro Leu Pro Glu Asn Ala Glu His Lys Tyr Asp His Tyr
50 55 60

Leu Arg Leu Gly Ile Glu Lys Leu Leu Lys Ala Asp Ala Val His Met
65 70 75 80

Leu Gln Gly Trp Gln Ser Ser Ala Gly Ala Thr Leu Glu His Asp Ile
85 90 95

Ala Gln Lys Leu Arg Leu Ala Ile Thr Tyr Glu Glu Pro Pro Ala Ser
100 105 110

	90	95	100	
tcg gtg tgg ttg ggt gat aat gtc cgc atc atc agt ggc aat ttc cca				451
Ser Val Trp Leu Gly Asp Asn Val Arg Ile Ile Ser Gly Asn Phe Pro				
	105	110	115	
gaa gca gca gga tca ccc cag tac ccc ctc atc atg ggt gtg aag gct				499
Glu Ala Ala Gly Ser Pro Gln Tyr Pro Leu Ile Met Gly Val Lys Ala				
	120	125	130	
caa ccc gtt gtt atc cat gtg cag gaa ttc cct gta gat gct gtt tcg				547
Gln Pro Val Val Ile His Val Gln Glu Phe Pro Val Asp Ala Val Ser				
	135	140	145	
act att ccc ccg cga ttt aat cct att gtt atc act gca ccg ccg agc				595
Thr Ile Pro Pro Arg Phe Asn Pro Ile Val Ile Thr Ala Pro Pro Ser				
	150	155	160	165
att gat att gct gct ctt cga gct gaa cgc gaa cag ctc acc cga cgc				643
Ile Asp Ile Ala Ala Leu Arg Ala Glu Arg Glu Gln Leu Thr Arg Arg				
	170	175	180	
atc agc gaa att gac aag aaa atc gca cgt gct gtg cat cca acc att				691
Ile Ser Glu Ile Asp Lys Lys Ile Ala Arg Ala Val His Pro Thr Ile				
	185	190	195	
cag act gag gct gcc taataatgat gcagactctc aag				729
Gln Thr Glu Ala Ala				
	200			

<210> 2028

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 2028

Val	Leu	Ile	Arg	Ile	Ala	Glu	His	Gln	Gly	Arg	Leu	His	Val	His	Ser
1				5					10					15	

Pro	Tyr	Ser	Lys	Ala	Phe	Ala	Ala	Arg	Ala	Arg	Lys	Leu	Asn	Gly	Leu
			20					25					30		

Trp	Ser	Pro	Glu	Thr	Lys	Thr	Trp	His	Phe	Ser	Pro	Asp	Lys	Glu	Gln
		35					40					45			

Pro	Val	Arg	Arg	Ala	Leu	Lys	Asp	Val	Tyr	Gly	Trp	Asp	Glu	Phe	Thr
	50					55					60				

Thr	Pro	Glu	Leu	Cys	Thr	Val	Gln	Leu	Thr	Val	Thr	Pro	Glu	Ala	Val
65					70					75					80

Leu	Asn	Lys	His	Thr	Leu	Thr	Ile	Ala	Gly	Val	Thr	Leu	Leu	Ser	Arg
				85					90					95	

Leu	Arg	Arg	Asn	Tyr	Ser	Val	Trp	Leu	Gly	Asp	Asn	Val	Arg	Ile	Ile
			100					105					110		

Ser	Gly	Asn	Phe	Pro	Glu	Ala	Ala	Gly	Ser	Pro	Gln	Tyr	Pro	Leu	Ile
		115					120					125			

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Met Gly Val Lys Ala Gln Pro Val Val Ile His Val Gln Glu Phe Pro
130                      135                      140

Val Asp Ala Val Ser Thr Ile Pro Pro Arg Phe Asn Pro Ile Val Ile
145                      150                      155                      160

Thr Ala Pro Pro Ser Ile Asp Ile Ala Ala Leu Arg Ala Glu Arg Glu
                      165                      170                      175

Gln Leu Thr Arg Arg Ile Ser Glu Ile Asp Lys Lys Ile Ala Arg Ala
                      180                      185                      190

Val His Pro Thr Ile Gln Thr Glu Ala Ala
                      195                      200

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<210> 2029
<211> 576
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(553)
<223> RXA01036

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<400> 2029
ctgaggctgc ctaataatga tgcagactct caagcggaaa attccgctca tctcatgcaa 60

tgacctcaaa gaagtgcagt tactttttct taaaggctcag atg cac aca gtc ggc 115
                                         Met His Thr Val Gly
                                         1                      5

tac aag cta gat acc gat ctt cgc aag ctc act aat acc gat gtg ctt 163
Tyr Lys Leu Asp Thr Asp Leu Arg Lys Leu Thr Asn Thr Asp Val Leu
                      10                      15                      20

gat ctt att aac gcg ctc ttc ggc acc act gtg acc agc gca gat gac 211
Asp Leu Ile Asn Ala Leu Phe Gly Thr Thr Val Thr Ser Ala Asp Asp
                      25                      30                      35

gaa gca gca gat ttc att gac tct gat cct cag ttt gca gtg ctc gtt 259
Glu Ala Ala Asp Phe Ile Asp Ser Asp Pro Gln Phe Ala Val Leu Val
                      40                      45                      50

gag ctg gcc tac cac gac tgt gca cgc cgc gct gcc atg ggt cta tcc 307
Glu Leu Ala Tyr His Asp Cys Ala Arg Arg Ala Ala Met Gly Leu Ser
                      55                      60                      65

agg gta cag cag ctc atc tat gac aat gcg gct aaa tca acc tac tac 355
Arg Val Gln Gln Leu Ile Tyr Asp Asn Ala Ala Lys Ser Thr Tyr Tyr
                      70                      75                      80                      85

cgc agc gtc gca gct aga cat cgc aaa cac atc cgt gaa ctc cac gag 403
Arg Ser Val Ala Ala Arg His Arg Lys His Ile Arg Glu Leu His Glu
                      90                      95                      100

caa aca cag cga gat ggt att cac ttc gac aac ccg ttg tct cgt gca 451
Gln Thr Gln Arg Asp Gly Ile His Phe Asp Asn Pro Leu Ser Arg Ala
                      105                      110                      115

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gtc atc aac gat ctc agc atg tcc atg aac cgt gct cga cta aac cgc 499
 Val Ile Asn Asp Leu Ser Met Ser Met Asn Arg Ala Arg Leu Asn Arg
 120 125 130

atc gct tca tgg aaa tca gcc gcc gta cag cgc tat ctc aac ccc act 547
 Ile Ala Ser Trp Lys Ser Ala Gly Val Gln Arg Tyr Leu Asn Pro Thr
 135 140 145

atc tct tagaaccaca cacaaccaag aaa 576
 Ile Ser
 150

<210> 2030

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 2030

Met His Thr Val Gly Tyr Lys Leu Asp Thr Asp Leu Arg Lys Leu Thr
 1 5 10 15

Asn Thr Asp Val Leu Asp Leu Ile Asn Ala Leu Phe Gly Thr Thr Val
 20 25 30

Thr Ser Ala Asp Asp Glu Ala Ala Asp Phe Ile Asp Ser Asp Pro Gln
 35 40 45

Phe Ala Val Leu Val Glu Leu Ala Tyr His Asp Cys Ala Arg Arg Ala
 50 55 60

Ala Met Gly Leu Ser Arg Val Gln Gln Leu Ile Tyr Asp Asn Ala Ala
 65 70 75 80

Lys Ser Thr Tyr Tyr Arg Ser Val Ala Ala Arg His Arg Lys His Ile
 85 90 95

Arg Glu Leu His Glu Gln Thr Gln Arg Asp Gly Ile His Phe Asp Asn
 100 105 110

Pro Leu Ser Arg Ala Val Ile Asn Asp Leu Ser Met Ser Met Asn Arg
 115 120 125

Ala Arg Leu Asn Arg Ile Ala Ser Trp Lys Ser Ala Gly Val Gln Arg
 130 135 140

Tyr Leu Asn Pro Thr Ile Ser
 145 150

<210> 2031

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01037

<400> 2031

<400> 2032
Met Thr Thr Ser Ser Pro Leu Lys Ser Lys Asn Ser Leu Asn Gly Ala
1 5 10 15

Gln Thr Thr Phe Val Arg Asn Cys Val Ala Asp Gly Pro Thr Glu Val
 20 25 30
 Lys Ala Thr Ile Asp Ala Arg Gly Gly Ile Glu Gln Leu Arg Asp Asn
 35 40 45
 Glu Ile Ser Gln Leu Pro Asp Lys Leu Trp Phe Asn Ser Ala Thr Ser
 50 55 60
 Ala Ser Asn Asp Glu Phe Thr Thr Asp Asn Ile Arg Leu Gly Leu Leu
 65 70 75 80
 Tyr Asn Met Ala Leu Asn Lys Ala Ser Ala His Arg Tyr Glu Leu Ala
 85 90 95
 Ala Arg Trp Tyr Ala Ile Val Ser Pro Gln Pro Ser Gln Glu Ala Ser
 100 105 110
 His Lys Arg Ile Ala Ser Trp His Leu Thr Gln Leu His Ala Leu Val
 115 120 125
 Thr Leu Ser Arg Thr Leu Gly Val Ile Ile Pro Gly Asp Glu Ile Asp
 130 135 140
 Ala Leu Ala Gln Ser Met Glu Asn Ala Arg Gln Val Gly Thr Glu Asn
 145 150 155 160
 Trp Ser Thr Val Thr Met Arg Thr Tyr Val Thr Asn Arg Lys Ala Ser
 165 170 175

<210> 2033

<211> 870

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(847)

<223> RXA01038

<400> 2033

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 tcaccatgcg cacctacgtg accaaccgca aggcataccta atg act cgc gat att 115
 Met Thr Arg Asp Ile
 1 5
 ttc cac gag gct gca aaa ctc atc gca cac ctg ggg tgg agg gac gct 163
 Phe His Glu Ala Ala Lys Leu Ile Ala His Leu Gly Trp Arg Asp Ala
 10 15 20
 ttt cca gca cta cag cgc act gac cca gcg cca aca cat gct gtg ccg 211
 Phe Pro Ala Leu Gln Arg Thr Asp Pro Ala Pro Thr His Ala Val Pro
 25 30 35
 atc agg gcc ttt gat ctc aag gcg ggc gcc gtc atc acc gat gaa aat 259
 Ile Arg Ala Phe Asp Leu Lys Ala Gly Ala Val Ile Thr Asp Glu Asn
 40 45 50

cga agc aat gct tat atc tat gac acc ctt gtc atc acg cag cca tat 307
 Arg Ser Asn Ala Tyr Ile Tyr Asp Thr Leu Val Ile Thr Gln Pro Tyr
 55 60 65

aag cac gag tta cct cat caa aac acc cac cct ttt gag tgg gcc ctg 355
 Lys His Glu Leu Pro His Gln Asn Thr His Pro Phe Glu Trp Ala Leu
 70 75 80 85

gaa caa att gcc acg ctt gat ccg gcg ttc tcg atc aag ctc gat cgc 403
 Glu Gln Ile Ala Thr Leu Asp Pro Ala Phe Ser Ile Lys Leu Asp Arg
 90 95 100

tca gtg acc gtc cct gaa att gga ctc tac gcc cgc aca ctg cat gac 451
 Ser Val Thr Val Pro Glu Ile Gly Leu Tyr Ala Arg Thr Leu His Asp
 105 110 115

ctt aat act cgg cat caa gac ttc ttg gca cag cgc aac gcc atg ttg 499
 Leu Asn Thr Arg His Gln Asp Phe Leu Ala Gln Arg Asn Ala Met Leu
 120 125 130

ctt gtt gtt gcc cgt cgt ggt gtt gat cca aaa aat atc gca gac gta 547
 Leu Val Val Ala Arg Arg Gly Val Asp Pro Lys Asn Ile Ala Asp Val
 135 140 145

ctt ggt tta acc acc aat cag ata cat cgg att ctc agt gct act ccg 595
 Leu Gly Leu Thr Thr Asn Gln Ile His Arg Ile Leu Ser Ala Thr Pro
 150 155 160 165

gct gat tcc cct act gat tta ggc gtt aac ccc gcc aca aca atg ggt 643
 Ala Asp Ser Pro Thr Asp Leu Gly Val Asn Pro Ala Thr Thr Met Gly
 170 175 180

gat gta gtg agg ttt atc aag aaa cgt cgc acc act atg caa cta cgc 691
 Asp Val Val Arg Phe Ile Lys Lys Arg Arg Thr Thr Met Gln Leu Arg
 185 190 195

ggc acc gct gtc cgt gca ctg ctc tat cac ggc ctt acg ccg gca gtc 739
 Gly Thr Ala Val Arg Ala Leu Leu Tyr His Gly Leu Thr Pro Ala Val
 200 205 210

atc tcc cga cta agc ggc atg tcg cgt gcg ggt gtc atc aac gca gcc 787
 Ile Ser Arg Leu Ser Gly Met Ser Arg Ala Gly Val Ile Asn Ala Ala
 215 220 225

aag gca ttc ccc acc acc atc aac cac aag gtc aag aaa aga aag cag 835
 Lys Ala Phe Pro Thr Thr Ile Asn His Lys Val Lys Lys Arg Lys Gln
 230 235 240 245

cac ttc cat gtc taatctcggc acatactatg cag 870
 His Phe His Val

<210> 2034

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 2034

Met Thr Arg Asp Ile Phe His Glu Ala Ala Lys Leu Ile Ala His Leu
 1 5 10 15

Gly Trp Arg Asp Ala Phe Pro Ala Leu Gln Arg Thr Asp Pro Ala Pro
 20 25 30
 Thr His Ala Val Pro Ile Arg Ala Phe Asp Leu Lys Ala Gly Ala Val
 35 40 45
 Ile Thr Asp Glu Asn Arg Ser Asn Ala Tyr Ile Tyr Asp Thr Leu Val
 50 55 60
 Ile Thr Gln Pro Tyr Lys His Glu Leu Pro His Gln Asn Thr His Pro
 65 70 75 80
 Phe Glu Trp Ala Leu Glu Gln Ile Ala Thr Leu Asp Pro Ala Phe Ser
 85 90 95
 Ile Lys Leu Asp Arg Ser Val Thr Val Pro Glu Ile Gly Leu Tyr Ala
 100 105 110
 Arg Thr Leu His Asp Leu Asn Thr Arg His Gln Asp Phe Leu Ala Gln
 115 120 125
 Arg Asn Ala Met Leu Leu Val Val Ala Arg Arg Gly Val Asp Pro Lys
 130 135 140
 Asn Ile Ala Asp Val Leu Gly Leu Thr Thr Asn Gln Ile His Arg Ile
 145 150 155 160
 Leu Ser Ala Thr Pro Ala Asp Ser Pro Thr Asp Leu Gly Val Asn Pro
 165 170 175
 Ala Thr Thr Met Gly Asp Val Val Arg Phe Ile Lys Lys Arg Arg Thr
 180 185 190
 Thr Met Gln Leu Arg Gly Thr Ala Val Arg Ala Leu Leu Tyr His Gly
 195 200 205
 Leu Thr Pro Ala Val Ile Ser Arg Leu Ser Gly Met Ser Arg Ala Gly
 210 215 220
 Val Ile Asn Ala Ala Lys Ala Phe Pro Thr Thr Ile Asn His Lys Val
 225 230 235 240
 Lys Lys Arg Lys Gln His Phe His Val
 245

<210> 2035

<211> 699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(676)

<223> RXA01039

<400> 2035

aaacctatat gttaatagta acagaaatta ataagatact agagttaaatt ttgtagtatc 60

cagggaacat taaacgggta aaggtaaagg acaaacgaac atg gcg att aaa ggc 115

	Met	Ala	Ile	Lys	Gly	
	1				5	
gca atg ccg aaa aat cga gta cca ggt gtg gca gca ggt gcg ttt att						163
Ala Met Pro Lys Asn Arg Val Pro Gly Val Ala Ala Gly Ala Phe Ile						
gct gct gcc gtt att gca ggt gga tca ggc gtg acc ttt ctc gcc caa						211
Ala Ala Ala Val Ile Ala Gly Gly Ser Gly Val Thr Phe Leu Ala Gln						
ggc ggt ggt gat gtc aat aca gtg gcc gtc gtc gag cca cag gac gag						259
Gly Gly Gly Asp Val Asn Thr Val Ala Val Val Glu Pro Gln Asp Glu						
gta aaa aat cag gtc gtg aca gaa acc gaa att gtc acg aag gtt cac						307
Val Lys Asn Gln Val Val Thr Glu Thr Glu Ile Val Thr Lys Val His						
gat cct tct tca tct gac gcc agt gat gct gac agc aac aca ggc acc						355
Asp Pro Ser Ser Ser Asp Ala Ser Asp Ala Asp Ser Asn Thr Gly Thr						
gcc gaa ggc gca gac tca gat cac aaa gaa ccc cgt gag cac gac agt						403
Ala Glu Gly Ala Asp Ser Asp His Lys Glu Pro Arg Glu His Asp Ser						
gct caa gag cca acg gct ccg acc gac ccc acc ttg acc att acc ggc						451
Ala Gln Glu Pro Thr Ala Pro Thr Asp Pro Thr Leu Thr Ile Thr Gly						
aac ggt gac aca cca gta tca gca ctt gat gct gtc gca gga cct gcc						499
Asn Gly Asp Thr Pro Val Ser Ala Leu Asp Ala Val Ala Gly Pro Ala						
cgt cca ggt acg gtg cac gtc att gag aat ggc gaa acc ttg tcc tct						547
Arg Pro Gly Thr Val His Val Ile Glu Asn Gly Glu Thr Leu Ser Ser						
att tct cag gac agt ggt gtg ccg gtt ggg ttg atc att gat cgc aac						595
Ile Ser Gln Asp Ser Gly Val Pro Val Gly Leu Ile Ile Asp Arg Asn						
aag ctt gtt gat cca gac ctg atc tat gca ggc acg cca ttg gcg att						643
Lys Leu Val Asp Pro Asp Leu Ile Tyr Ala Gly Thr Pro Leu Ala Ile						
ccg act gag cag gaa ctt gct gct gcg ata cag taatgtagtg gtagagggtt						696
Pro Thr Glu Gln Glu Leu Ala Ala Ala Ile Gln						
aaa						699

<210> 2036

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 2036

Met Ala Ile Lys Gly Ala Met Pro Lys Asn Arg Val Pro Gly Val Ala

tac tcc cgc atc gca agc ttt att act ggt acc gag cgc gaa aac cgt	259
Tyr Ser Arg Ile Ala Ser Phe Ile Thr Gly Thr Glu Arg Glu Asn Arg	
40 45 50	
aat cgc gac agg ctt cac cca atc gaa ttc gac tac acc tcc ctg act	307
Asn Arg Asp Arg Leu His Pro Ile Glu Phe Asp Tyr Thr Ser Leu Thr	
55 60 65	
ttg agc cac cct gaa atc atc tac ggc aac ccg caa caa aag acc aat	355
Leu Ser His Pro Glu Ile Ile Tyr Gly Asn Pro Gln Gln Lys Thr Asn	
70 75 80 85	
gaa gaa ctc ttc ctt gag cag cga atc ttt gtc ggc aag aag cgt cct	403
Glu Glu Leu Phe Leu Glu Gln Arg Ile Phe Val Gly Lys Lys Arg Pro	
90 95 100	
gaa gag ggt cca aaa ttc tcc att gac aac aag agc aac cgt cta cca	451
Glu Glu Gly Pro Lys Phe Ser Ile Asp Asn Lys Ser Asn Arg Leu Pro	
105 110 115	
cag gtt tgg gtg cca tcc acc aat gct gat ggt act tat gag cag ctt	499
Gln Val Trp Val Pro Ser Thr Asn Ala Asp Gly Thr Tyr Glu Gln Leu	
120 125 130	
gaa ggt ctc gaa ggt gag ctc gac gca ggg ctc aac gtc att att ctc	547
Glu Gly Leu Glu Gly Glu Leu Asp Ala Gly Leu Asn Val Ile Ile Leu	
135 140 145	
atc gag ttc tat aag cca cgt aca cag gtt aat cgc ggc tcc cgc ctc	595
Ile Glu Phe Tyr Lys Pro Arg Thr Gln Val Asn Arg Gly Ser Arg Leu	
150 155 160 165	
aac gcc gtg ttc ctg cag gag ccc att cgt tac tac acc cct ggt tac	643
Asn Ala Val Phe Leu Gln Glu Pro Ile Arg Tyr Tyr Thr Pro Gly Tyr	
170 175 180	
aat gca gat aag ctc gct gcc ctc gga atc gta ctt aac gca ccg cca	691
Asn Ala Asp Lys Leu Ala Ala Leu Gly Ile Val Leu Asn Ala Pro Pro	
185 190 195	
aag gac act att cag ctc gtt cct aat gag gtc gct gca gga caa gac	739
Lys Asp Thr Ile Gln Leu Val Pro Asn Glu Val Ala Ala Gly Gln Asp	
200 205 210	
cag tcc acc acc gat gca tcc ggt ctc ccg ctt cca ggc cag gga tat	787
Gln Ser Thr Thr Asp Ala Ser Gly Leu Pro Leu Pro Gly Gln Gly Tyr	
215 220 225	
agc gca cct gat cag cca tat cag gcg cag cct cag tat cag cag gca	835
Ser Ala Pro Asp Gln Pro Tyr Gln Ala Gln Pro Gln Tyr Gln Gln Ala	
230 235 240 245	
acc cca gcg gct gca cct cag cag tac cag gcc cca cag ccc cag tac	883
Thr Pro Ala Ala Ala Pro Gln Gln Tyr Gln Ala Pro Gln Pro Gln Tyr	
250 255 260	
cag cag tca gct cca cag gca caa cct gca ccg gca cca gtt gcg cag	931
Gln Gln Ser Ala Pro Gln Ala Gln Pro Ala Pro Ala Pro Val Ala Gln	
265 270 275	
ttc cag cag gca agc gcc tca ggc acc tgc tca gcc agc aca gca gca	979

Phe Gln Gln Ala Ser Ala Ser Gly Thr Cys Ser Ala Ser Thr Ala Ala
 280 285 290

gta tca ggc acc act tcc tgc cgg taatcctctt gcagcaggtc agc 1026
 Val Ser Gly Thr Thr Ser Cys Arg
 295 300

<210> 2038

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 2038

Met Thr Tyr Pro Val Thr Pro Gln Pro Val Gln Pro Ala Pro Val Ala
 1 5 10 15

Glu Lys Ile Lys Ala Ser Ser Leu Lys Glu Gly Thr Gln Val Phe Ile
 20 25 30

Lys Gly Arg Val Asn Tyr Ser Arg Ile Ala Ser Phe Ile Thr Gly Thr
 35 40 45

Glu Arg Glu Asn Arg Asn Arg Asp Arg Leu His Pro Ile Glu Phe Asp
 50 55 60

Tyr Thr Ser Leu Thr Leu Ser His Pro Glu Ile Ile Tyr Gly Asn Pro
 65 70 75 80

Gln Gln Lys Thr Asn Glu Glu Leu Phe Leu Glu Gln Arg Ile Phe Val
 85 90 95

Gly Lys Lys Arg Pro Glu Glu Gly Pro Lys Phe Ser Ile Asp Asn Lys
 100 105 110

Ser Asn Arg Leu Pro Gln Val Trp Val Pro Ser Thr Asn Ala Asp Gly
 115 120 125

Thr Tyr Glu Gln Leu Glu Gly Leu Glu Gly Glu Leu Asp Ala Gly Leu
 130 135 140

Asn Val Ile Ile Leu Ile Glu Phe Tyr Lys Pro Arg Thr Gln Val Asn
 145 150 155 160

Arg Gly Ser Arg Leu Asn Ala Val Phe Leu Gln Glu Pro Ile Arg Tyr
 165 170 175

Tyr Thr Pro Gly Tyr Asn Ala Asp Lys Leu Ala Ala Leu Gly Ile Val
 180 185 190

Leu Asn Ala Pro Pro Lys Asp Thr Ile Gln Leu Val Pro Asn Glu Val
 195 200 205

Ala Ala Gly Gln Asp Gln Ser Thr Thr Asp Ala Ser Gly Leu Pro Leu
 210 215 220

Pro Gly Gln Gly Tyr Ser Ala Pro Asp Gln Pro Tyr Gln Ala Gln Pro
 225 230 235 240

Gln Tyr Gln Gln Ala Thr Pro Ala Ala Ala Pro Gln Gln Tyr Gln Ala
 245 250 255

Pro Gln Pro Gln Tyr Gln Gln Ser Ala Pro Gln Ala Gln Pro Ala Pro
 260 265 270

Ala Pro Val Ala Gln Phe Gln Gln Ala Ser Ala Ser Gly Thr Cys Ser
 275 280 285

Ala Ser Thr Ala Ala Val Ser Gly Thr Thr Ser Cys Arg
 290 295 300

<210> 2039

<211> 276

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(253)

<223> RXA01041

<400> 2039

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accacaagcc gggtctgcat ttaccgatgc tccgggtgct gtg cca cag gca cca 115
 Val Pro Gln Ala Pro
 1 5

gca gtt cag gct gct ccc gct gta gct cag gcg cct gtc gcg cca gta 163
 Ala Val Gln Ala Ala Pro Ala Val Ala Gln Ala Pro Val Ala Pro Val
 10 15 20

gtt gat atg acc gag cca gca tcc cca tgg gat ctt cca gct gca cct 211
 Val Asp Met Thr Glu Pro Ala Ser Pro Trp Asp Leu Pro Ala Ala Pro
 25 30 35

agt cag cca gcg cag cca gct cag ggc atc acc tac ccg gca 253
 Ser Gln Pro Ala Gln Pro Ala Gln Gly Ile Thr Tyr Pro Ala
 40 45 50

taacaaccag cacaaccctt aga 276

<210> 2040

<211> 51

<212> PRT

<213> Corynebacterium glutamicum

<400> 2040

Val Pro Gln Ala Pro Ala Val Gln Ala Ala Pro Ala Val Ala Gln Ala
 1 5 10 15

Pro Val Ala Pro Val Val Asp Met Thr Glu Pro Ala Ser Pro Trp Asp
 20 25 30

Leu Pro Ala Ala Pro Ser Gln Pro Ala Gln Pro Ala Gln Gly Ile Thr
 35 40 45

Tyr Pro Ala
 50

<210> 2041
 <211> 1401
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1378)
 <223> RXA01042

<400> 2041

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ttttttcacc agggtcgagg cgcggtctgt gtgcccacct cgacccactt ttcgcccacc 60

acttttctgtc aacctaccaa caacaaagcc caggtcactt atg gtc aac cct ttt 115
                                         Met Val Asn Pro Phe
                                         1 5

cac acg ctt gat aac tca ccg ttt gat ccg gtg gca cag ttt cct gcg 163
His Thr Leu Asp Asn Ser Pro Phe Asp Pro Val Ala Gln Phe Pro Ala
              10 15 20

ttt tat cac aac ccg ctt atc aat cac ttg ggc cgc cgt cgc gcc tgg 211
Phe Tyr His Asn Pro Leu Ile Asn His Leu Gly Arg Arg Arg Ala Trp
              25 30 35

aca atc tca gac atc aac aaa cgc ccc atc aat gtc caa cag atg ctg 259
Thr Ile Ser Asp Ile Asn Lys Arg Pro Ile Asn Val Gln Gln Met Leu
              40 45 50

acc acg gcc acc tac ggt agc ccc gtt att cat ggt gcc cgc att gaa 307
Thr Thr Ala Thr Tyr Gly Ser Pro Val Ile His Gly Ala Arg Ile Glu
              55 60 65

gac gca gca acc tcc cta ctt acc ctg gat gaa ctg cgt aca cag att 355
Asp Ala Ala Thr Ser Leu Leu Thr Leu Asp Glu Leu Arg Thr Gln Ile
              70 75 80 85

ccc acc gct gcc aac aat gcg ttt tat ctc gat gct gtc caa gat ggc 403
Pro Thr Ala Ala Asn Asn Ala Phe Tyr Leu Asp Ala Val Gln Asp Gly
              90 95 100

tgt ctt att tta gat att gaa aaa acc tgt ccc ccc gag gtc gca gcc 451
Cys Leu Ile Leu Asp Ile Glu Lys Thr Cys Pro Pro Glu Val Ala Ala
              105 110 115

aca cta ctc acg ctc tcc ccc acc gcc ttt tac aca gag gtg tcc atg 499
Thr Leu Leu Thr Leu Ser Pro Thr Ala Phe Tyr Thr Glu Val Ser Met
              120 125 130

agt ggt cgt ggc tat cac ctc gtt atg ccg ata cca gag aat ttt gca 547
Ser Gly Arg Gly Tyr His Leu Val Met Pro Ile Pro Glu Asn Phe Ala
              135 140 145

gcg ttt cct gcc gta cac aac aaa ccc agt atc aaa cac ccc aag cgc 595
Ala Phe Pro Ala Val His Asn Lys Pro Ser Ile Lys His Pro Lys Arg
              150 155 160 165

tgg ttc gaa att ctt acc tca cag tgg atc acc ttc acc cga caa cca 643
Trp Phe Glu Ile Leu Thr Ser Gln Trp Ile Thr Phe Thr Arg Gln Pro
              170 175 180

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atc cca gag cat gtt ctc cat cac agt gaa tct gct aac aca agt gct Ile Pro Glu His Val Leu His His Ser Glu Ser Ala Asn Thr Ser Ala 185 190 195	691
gtg cca tgg ttg aat gat caa cca ctt aca tgg gaa aac gtc ttt gca Val Pro Trp Leu Asn Asp Gln Pro Leu Thr Trp Glu Asn Val Phe Ala 200 205 210	739
gac tta gct aaa act gtt gca ccc aac tta aaa acc ggt gcc gga ctt Asp Leu Ala Lys Thr Val Ala Pro Asn Leu Lys Thr Gly Ala Gly Leu 215 220 225	787
acc atc aca ccc aat gca ctg atg cca cca gat ctc agc gat gct gag Thr Ile Thr Pro Asn Ala Leu Met Pro Pro Asp Leu Ser Asp Ala Glu 230 235 240 245	835
cgc att cgc gac gat gaa gtc atc gac tcg acc tgt cga tta ttt gcc Arg Ile Arg Asp Asp Glu Val Ile Asp Ser Thr Cys Arg Leu Phe Ala 250 255 260	883
gaa cat tac tcg aaa aca ctt gcg gac ttc tat gat gat gca tcc cgg Glu His Tyr Ser Lys Thr Leu Ala Asp Phe Tyr Asp Asp Ala Ser Arg 265 270 275	931
ttc gag ttc agc caa att ggt gtc att atc aat cta ctg ctc ccc act Phe Glu Phe Ser Gln Ile Gly Val Ile Ile Asn Leu Leu Leu Pro Thr 280 285 290	979
atg agg atg cat ccc acc acg atc agt ctc gac aaa ccc atc aac tcc Met Arg Met His Pro Thr Thr Ile Ser Leu Asp Lys Pro Ile Asn Ser 295 300 305	1027
gat cac atc atc aga ctt ctg ttc gct gtc gct act cgc gtg atc act Asp His Ile Ile Arg Leu Leu Phe Ala Val Ala Thr Arg Val Ile Thr 310 315 320 325	1075
cac cgc agc aaa cat gat gag gag cga tct ggc gtt ccg tat ctg atg His Arg Ser Lys His Asp Glu Glu Arg Ser Gly Val Pro Tyr Leu Met 330 335 340	1123
tat cag gtt att tcc tgc ctt gac atg cga gaa cac ccc gac aat ggc Tyr Gln Val Ile Ser Cys Leu Asp Met Arg Glu His Pro Asp Asn Gly 345 350 355	1171
gac tac cgt gtc gta ccc tcc cgg cat aat aga gac caa cac agc aac Asp Tyr Arg Val Val Pro Ser Arg His Asn Arg Asp Gln His Ser Asn 360 365 370	1219
aac ccc tca gct cat gtg gtc cac caa caa cca caa ccc cag ccc agc Asn Pro Ser Ala His Val Val His Gln Gln Pro Gln Pro Gln Pro Ser 375 380 385	1267
gca gca gat tcg cca cat cac tac cgt gca cta ccc caa gaa aac acg Ala Ala Asp Ser Pro His His Tyr Arg Ala Leu Pro Gln Glu Asn Thr 390 395 400 405	1315
gtg tcc gaa cac agt ttt aaa atc tat aac cca cca gcc aca ccc cct Val Ser Glu His Ser Phe Lys Ile Tyr Asn Pro Pro Ala Thr Pro Pro 410 415 420	1363

cta gga ggt gaa aat tagatttatt attaaaacac ttg
Leu Gly Gly Glu Asn
425

1401

<210> 2042

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 2042

Met Val Asn Pro Phe His Thr Leu Asp Asn Ser Pro Phe Asp Pro Val
1 5 10 15

Ala Gln Phe Pro Ala Phe Tyr His Asn Pro Leu Ile Asn His Leu Gly
20 25 30

Arg Arg Arg Ala Trp Thr Ile Ser Asp Ile Asn Lys Arg Pro Ile Asn
35 40 45

Val Gln Gln Met Leu Thr Thr Ala Thr Tyr Gly Ser Pro Val Ile His
50 55 60

Gly Ala Arg Ile Glu Asp Ala Ala Thr Ser Leu Leu Thr Leu Asp Glu
65 70 75 80

Leu Arg Thr Gln Ile Pro Thr Ala Ala Asn Asn Ala Phe Tyr Leu Asp
85 90 95

Ala Val Gln Asp Gly Cys Leu Ile Leu Asp Ile Glu Lys Thr Cys Pro
100 105 110

Pro Glu Val Ala Ala Thr Leu Leu Thr Leu Ser Pro Thr Ala Phe Tyr
115 120 125

Thr Glu Val Ser Met Ser Gly Arg Gly Tyr His Leu Val Met Pro Ile
130 135 140

Pro Glu Asn Phe Ala Ala Phe Pro Ala Val His Asn Lys Pro Ser Ile
145 150 155 160

Lys His Pro Lys Arg Trp Phe Glu Ile Leu Thr Ser Gln Trp Ile Thr
165 170 175

Phe Thr Arg Gln Pro Ile Pro Glu His Val Leu His His Ser Glu Ser
180 185 190

Ala Asn Thr Ser Ala Val Pro Trp Leu Asn Asp Gln Pro Leu Thr Trp
195 200 205

Glu Asn Val Phe Ala Asp Leu Ala Lys Thr Val Ala Pro Asn Leu Lys
210 215 220

Thr Gly Ala Gly Leu Thr Ile Thr Pro Asn Ala Leu Met Pro Pro Asp
225 230 235 240

Leu Ser Asp Ala Glu Arg Ile Arg Asp Asp Glu Val Ile Asp Ser Thr
245 250 255

Cys Arg Leu Phe Ala Glu His Tyr Ser Lys Thr Leu Ala Asp Phe Tyr
260 265 270

Asp Asp Ala Ser Arg Phe Glu Phe Ser Gln Ile Gly Val Ile Ile Asn
 275 280 285
 Leu Leu Leu Pro Thr Met Arg Met His Pro Thr Thr Ile Ser Leu Asp
 290 295 300
 Lys Pro Ile Asn Ser Asp His Ile Ile Arg Leu Leu Phe Ala Val Ala
 305 310 315 320
 Thr Arg Val Ile Thr His Arg Ser Lys His Asp Glu Glu Arg Ser Gly
 325 330 335
 Val Pro Tyr Leu Met Tyr Gln Val Ile Ser Cys Leu Asp Met Arg Glu
 340 345 350
 His Pro Asp Asn Gly Asp Tyr Arg Val Val Pro Ser Arg His Asn Arg
 355 360 365
 Asp Gln His Ser Asn Asn Pro Ser Ala His Val Val His Gln Gln Pro
 370 375 380
 Gln Pro Gln Pro Ser Ala Ala Asp Ser Pro His His Tyr Arg Ala Leu
 385 390 395 400
 Pro Gln Glu Asn Thr Val Ser Glu His Ser Phe Lys Ile Tyr Asn Pro
 405 410 415
 Pro Ala Thr Pro Pro Leu Gly Gly Glu Asn
 420 425

<210> 2043

<211> 696

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA01043

<400> 2043

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atcactacct attcaccact tgaacggagc gtttttcgcc atg ttg aaa ttc cgc 115
 Met Leu Lys Phe Arg
 1 5

atc atc tcc aca gtc act act gga tct cag cca act cca cga aaa agc 163
 Ile Ile Ser Thr Val Thr Thr Gly Ser Gln Pro Thr Pro Arg Lys Ser
 10 15 20

tgg agc cac ccc gac acc act ctc ctg gtc acc atg gtc act gca cca 211
 Trp Ser His Pro Asp Thr Thr Leu Leu Val Thr Met Val Thr Ala Pro
 25 30 35

tcg ctg tgc tca gcc atc aac gtg tgg aac gca act gag cgt att ccc 259
 Ser Leu Cys Ser Ala Ile Asn Val Trp Asn Ala Thr Glu Arg Ile Pro
 40 45 50

gct caa aaa atc ctt aat gtc gaa gaa gta cac gtt ctt ggt gag tgc 307
 Ala Gln Lys Ile Leu Asn Val Glu Glu Val His Val Leu Gly Glu Cys
 55 60 65
 agc gac gcc atc atc tct acg tca cta acc aaa aag gac aat ccg cac 355
 Ser Asp Ala Ile Ile Ser Thr Ser Leu Thr Lys Lys Asp Asn Pro His
 70 75 80 85
 gca ctt gtg ccc gat gat ttc gac caa atc ggc gat gtg ttt ggc tat 403
 Ala Leu Val Pro Asp Asp Phe Asp Gln Ile Gly Asp Val Phe Gly Tyr
 90 95 100
 gcg caa gac aat gta gct gtt ttt gat gtc att gtc gca gca ctg ggc 451
 Ala Gln Asp Asn Val Ala Val Phe Asp Val Ile Val Ala Ala Leu Gly
 105 110 115
 ggt gct ggt tat ggc ctg cta ccc gga ctg gtc atg cac cac att gat 499
 Gly Ala Gly Tyr Gly Leu Leu Pro Gly Leu Val Met His His Ile Asp
 120 125 130
 gag cac acc gtt gca ctt gtc ttt gat act gat tcc cct act ggg acg 547
 Glu His Thr Val Ala Leu Val Phe Asp Thr Asp Ser Pro Thr Gly Thr
 135 140 145
 cat atc ctc ggt gag cgc tgc gtg tac tcc gac atc att cac atg act 595
 His Ile Leu Gly Glu Arg Cys Val Tyr Ser Asp Ile Ile His Met Thr
 150 155 160 165
 gac gat aag tct gcc cgt ggc tgg ggt gca gtc att gcc ata gca cga 643
 Asp Asp Lys Ser Ala Arg Gly Trp Gly Ala Val Ile Ala Ile Ala Arg
 170 175 180
 gcc atc atc ctc aaa gtc gaa cag atc atg tagtacccca ccatgactca 693
 Ala Ile Ile Leu Lys Val Glu Gln Ile Met
 185 190
 ctt 696

<210> 2044

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 2044

Met Leu Lys Phe Arg Ile Ile Ser Thr Val Thr Thr Gly Ser Gln Pro
 1 5 10 15
 Thr Pro Arg Lys Ser Trp Ser His Pro Asp Thr Thr Leu Leu Val Thr
 20 25 30
 Met Val Thr Ala Pro Ser Leu Cys Ser Ala Ile Asn Val Trp Asn Ala
 35 40 45
 Thr Glu Arg Ile Pro Ala Gln Lys Ile Leu Asn Val Glu Glu Val His
 50 55 60
 Val Leu Gly Glu Cys Ser Asp Ala Ile Ile Ser Thr Ser Leu Thr Lys
 65 70 75 80
 Lys Asp Asn Pro His Ala Leu Val Pro Asp Asp Phe Asp Gln Ile Gly

85	90	95
Asp Val Phe Gly Tyr Ala Gln' Asp	Asn Val Ala Val Phe Asp Val Ile	
100	105	110
Val Ala Ala Leu Gly Gly Ala Gly Tyr Gly Leu Leu Pro Gly Leu Val		
115	120	125
Met His His Ile Asp Glu His Thr Val Ala Leu Val Phe Asp Thr Asp		
130	135	140
Ser Pro Thr Gly Thr His Ile Leu Gly Glu Arg Cys Val Tyr Ser Asp		
145	150	155
Ile Ile His Met Thr Asp Asp Lys Ser Ala Arg Gly Trp Gly Ala Val		
165	170	175
Ile Ala Ile Ala Arg Ala Ile Ile Leu Lys Val Glu Gln Ile Met		
180	185	190

<210> 2045
 <211> 1380
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1357)
 <223> RXA01044

<400> 2045
 cagatagcca ctacctacac gcatctgttg tgctgaaaca acagcgcgac actcactctt 60
 ctccattactc aacaacttac ttttaaggac tacataactt atg tct ctc tac ctt 115
 Met Ser Leu Tyr Leu
 1 5
 gac gac act ttg tct cgc atc gtt gaa ctt gat ctc aaa gac acc cgc 163
 Asp Asp Thr Leu Ser Arg Ile Val Glu Leu Asp Leu Lys Asp Thr Arg
 10 15 20
 att gtg ccg ttt ctt gct ggt gaa cca ggt atc ggt aaa acc tca ttc 211
 Ile Val Pro Phe Leu Ala Gly Glu Pro Gly Ile Gly Lys Thr Ser Phe
 25 30 35
 atc tac ggc atc ggc gaa cgt gca ggc tac aaa gtc ttc agt atc tcg 259
 Ile Tyr Gly Ile Gly Glu Arg Ala Gly Tyr Lys Val Phe Ser Ile Ser
 40 45 50
 gtt aac acc ctt gcc gat aag ggt gac ctc acg ggc gct cgc acc ctg 307
 Val Asn Thr Leu Ala Asp Lys Gly Asp Leu Thr Gly Ala Arg Thr Leu
 55 60 65
 cag gac cct gcc gat ggc aag tgg aag cag atg ttt ttc ccg cac gcg 355
 Gln Asp Pro Ala Asp Gly Lys Trp Lys Gln Met Phe Phe Pro His Ala
 70 75 80 85
 acc ttc gtc gaa gca aat gac tat gca cta gca aac cca aac gaa acg 403
 Thr Phe Val Glu Ala Asn Asp Tyr Ala Leu Ala Asn Pro Asn Glu Thr
 90 95 100

gtc gtc att ctt ctc gat gag att aac cga act gat tcg gat gtc acc	451
Val Val Ile Leu Leu Asp Glu Ile Asn Arg Thr Asp Ser Asp Val Thr	
105 110 115	
tct gcc tcg atg act atc tct act gag cgt cgc gtt ggt acc acc gat	499
Ser Ala Ser Met Thr Ile Ser Thr Glu Arg Arg Val Gly Thr Thr Asp	
120 125 130	
cta gca ccc aat gtc cgc ctt gct gtc acc gga aac ctc acc ggt aat	547
Leu Ala Pro Asn Val Arg Ser Leu Ala Val Thr Gly Asn Leu Thr Gly Asn	
135 140 145	
gtc acc cac ctt gat tca gca tct ctg acc agg ttc tcc ctc tat gag	595
Val Thr His Leu Asp Ser Ala Ser Leu Thr Arg Phe Ser Leu Tyr Glu	
150 155 160 165	
gtc aag cca tcc gca gag acc ttc atg aac atc atg ggc ggc cgc ctc	643
Val Lys Pro Ser Ala Glu Thr Phe Met Asn Ile Met Gly Gly Arg Leu	
170 175 180	
aac aag tac atc cgt acc gtg ctg acc aaa tac ccg gaa tac atc ttc	691
Asn Lys Tyr Ile Arg Thr Val Leu Thr Lys Tyr Pro Glu Tyr Ile Phe	
185 190 195	
atg aag cca act act gct act gct ctt att acc act ggc gat gat gat	739
Met Lys Pro Thr Thr Ala Thr Ala Leu Ile Thr Thr Gly Asp Asp Asp	
200 205 210	
gac gac cat aca acc aat gcg aag caa atg atg gac ttc aac gct gtg	787
Asp Asp His Thr Thr Asn Ala Lys Gln Met Met Asp Phe Asn Ala Val	
215 220 225	
ctc ggt tca gac caa gac atg gtt caa ttt acc gca cct aga act atc	835
Leu Gly Ser Asp Gln Asp Met Val Gln Phe Thr Ala Pro Arg Thr Ile	
230 235 240 245	
gaa ggt ttg tcc gtc tgg ctc aac aac gcc gat gat gac ttt ctt cgt	883
Glu Gly Leu Ser Val Trp Leu Asn Asn Ala Asp Asp Asp Phe Leu Arg	
250 255 260	
cta ctt cta caa gaa aag gtg gat ggt ctt gct cga tcc atg agc ttg	931
Leu Leu Leu Gln Glu Lys Val Asp Gly Leu Ala Arg Ser Met Ser Leu	
265 270 275	
ctg cag gct acg ctc gaa tct cac acc ggc gat acc gct ttt acc gca	979
Leu Gln Ala Thr Leu Glu Ser His Thr Gly Asp Thr Ala Phe Thr Ala	
280 285 290	
gaa gtc ctc agc gaa atg acc aat gat ctg ctg agc tcc gca tcg caa	1027
Glu Val Leu Ser Glu Met Thr Asn Asp Leu Leu Ser Ser Ala Ser Gln	
295 300 305	
gct cct agt ggt cca atc aaa cca ttt gtc tac gac cga ctc gct gct	1075
Ala Pro Ser Gly Pro Ile Lys Pro Phe Val Tyr Asp Arg Leu Ala Ala	
310 315 320 325	
gca cca agc aat act gta ctg gaa caa gag gtt cac aca ctc agt ctc	1123
Ala Pro Ser Asn Thr Val Leu Glu Gln Glu Val His Thr Leu Ser Leu	
330 335 340	

aat gac cgc gcc gat gtc ttg ttg ttt gcc ctc cat gac act gta aac 1171
 Asn Asp Arg Ala Asp Val Leu Leu Phe Ala Leu His Asp Thr Val Asn
 345 350 355
 aac gct gca cca agc atc atc gct cac ctt gca tct gaa ggc gta ctt 1219
 Asn Ala Ala Pro Ser Ile Ile Ala His Leu Ala Ser Glu Gly Val Leu
 360 365 370
 gat gaa ctg ccc aaa gac aga atc agc aaa att gtt tca ctc ggt cct 1267
 Asp Glu Leu Pro Lys Asp Arg Ile Ser Lys Ile Val Ser Leu Gly Pro
 375 380 385
 gta cca acg gca aac tat cac gcc ttg acc aga cag gat aca acg ttg 1315
 Val Pro Thr Ala Asn Tyr His Ala Leu Thr Arg Gln Asp Thr Thr Leu
 390 395 400 405
 act cga aat ctc ggt ccc gct gtc ttg ggc ttc ttg gaa agt 1357
 Thr Arg Asn Leu Gly Pro Ala Val Leu Gly Phe Leu Glu Ser
 410 415
 taaagcaatt tcctaagtac ctt 1380

<210> 2046

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 2046

Met Ser Leu Tyr Leu Asp Asp Thr Leu Ser Arg Ile Val Glu Leu Asp
 1 5 10 15
 Leu Lys Asp Thr Arg Ile Val Pro Phe Leu Ala Gly Glu Pro Gly Ile
 20 25 30
 Gly Lys Thr Ser Phe Ile Tyr Gly Ile Gly Glu Arg Ala Gly Tyr Lys
 35 40 45
 Val Phe Ser Ile Ser Val Asn Thr Leu Ala Asp Lys Gly Asp Leu Thr
 50 55 60
 Gly Ala Arg Thr Leu Gln Asp Pro Ala Asp Gly Lys Trp Lys Gln Met
 65 70 75 80
 Phe Phe Pro His Ala Thr Phe Val Glu Ala Asn Asp Tyr Ala Leu Ala
 85 90 95
 Asn Pro Asn Glu Thr Val Val Ile Leu Leu Asp Glu Ile Asn Arg Thr
 100 105 110
 Asp Ser Asp Val Thr Ser Ala Ser Met Thr Ile Ser Thr Glu Arg Arg
 115 120 125
 Val Gly Thr Thr Asp Leu Ala Pro Asn Val Arg Leu Ala Val Thr Gly
 130 135 140
 Asn Leu Thr Gly Asn Val Thr His Leu Asp Ser Ala Ser Leu Thr Arg
 145 150 155 160
 Phe Ser Leu Tyr Glu Val Lys Pro Ser Ala Glu Thr Phe Met Asn Ile
 165 170 175

Met Gly Gly Arg Leu Asn Lys Tyr Ile Arg Thr Val Leu Thr Lys Tyr
 180 185 190
 Pro Glu Tyr Ile Phe Met Lys Pro Thr Thr Ala Thr Ala Leu Ile Thr
 195 200 205
 Thr Gly Asp Asp Asp Asp Asp His Thr Thr Asn Ala Lys Gln Met Met
 210 215 220
 Asp Phe Asn Ala Val Leu Gly Ser Asp Gln Asp Met Val Gln Phe Thr
 225 230 235 240
 Ala Pro Arg Thr Ile Glu Gly Leu Ser Val Trp Leu Asn Asn Ala Asp
 245 250 255
 Asp Asp Phe Leu Arg Leu Leu Leu Gln Glu Lys Val Asp Gly Leu Ala
 260 265 270
 Arg Ser Met Ser Leu Leu Gln Ala Thr Leu Glu Ser His Thr Gly Asp
 275 280 285
 Thr Ala Phe Thr Ala Glu Val Leu Ser Glu Met Thr Asn Asp Leu Leu
 290 295 300
 Ser Ser Ala Ser Gln Ala Pro Ser Gly Pro Ile Lys Pro Phe Val Tyr
 305 310 315 320
 Asp Arg Leu Ala Ala Ala Pro Ser Asn Thr Val Leu Glu Gln Glu Val
 325 330 335
 His Thr Leu Ser Leu Asn Asp Arg Ala Asp Val Leu Leu Phe Ala Leu
 340 345 350
 His Asp Thr Val Asn Asn Ala Ala Pro Ser Ile Ile Ala His Leu Ala
 355 360 365
 Ser Glu Gly Val Leu Asp Glu Leu Pro Lys Asp Arg Ile Ser Lys Ile
 370 375 380
 Val Ser Leu Gly Pro Val Pro Thr Ala Asn Tyr His Ala Leu Thr Arg
 385 390 395 400
 Gln Asp Thr Thr Leu Thr Arg Asn Leu Gly Pro Ala Val Leu Gly Phe
 405 410 415
 Leu Glu Ser

<210> 2047

<211> 1947

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1924)

<223> RXA01045

<400> 2047

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cttacccttc	ttgacactag	taattgaaag	cgatcccctc	atg	gtt	acc	ttc	agc		115						
				Met	Val	Thr	Phe	Ser								
				1				5								
gtc	gca	aat	cac	gcg	cct	cat	act	ttt	agc	cca	ttc	gat	att	gaa	cca	163
Val	Ala	Asn	His	Ala	Pro	His	Thr	Phe	Ser	Pro	Phe	Asp	Ile	Glu	Pro	
				10				15						20		
cca	ctc	acc	ggg	aac	gcc	acc	acc	gac	gaa	cat	ggg	tac	gaa	cac	acc	211
Pro	Leu	Thr	Gly	Asn	Ala	Thr	Thr	Asp	Glu	His	Gly	Tyr	Glu	His	Thr	
			25					30					35			
tcâ	gtg	cta	gaa	aaa	cta	gcc	tcc	aac	cac	ctg	ttc	aat	cca	atc	aat	259
Ser	Val	Leu	Glu	Lys	Leu	Ala	Ser	Asn	His	Leu	Phe	Asn	Pro	Ile	Asn	
		40					45					50				
ccg	caa	cac	cca	gtc	act	atc	aca	gcc	acc	gaa	aac	gga	tca	acc	gtt	307
Pro	Gln	His	Pro	Val	Thr	Ile	Thr	Ala	Thr	Glu	Asn	Gly	Ser	Thr	Val	
	55					60					65					
gat	ctt	gat	gca	gca	gca	cta	gca	caa	cat	ctt	gct	cta	gcg	att	acc	355
Asp	Leu	Asp	Ala	Ala	Ala	Leu	Ala	Gln	His	Leu	Ala	Leu	Ala	Ile	Thr	
70					75					80					85	
cca	gac	tca	atg	ctg	gca	aat	cat	caa	ggc	tac	aac	cgt	gac	atg	atg	403
Pro	Asp	Ser	Met	Leu	Ala	Asn	His	Gln	Gly	Tyr	Asn	Arg	Asp	Met	Met	
				90					95					100		
ggg	cta	ctt	tcg	cag	ctt	act	aac	cat	gtt	ggc	ttt	gat	cgc	cga	ttc	451
Gly	Leu	Leu	Ser	Gln	Leu	Thr	Asn	His	Val	Gly	Phe	Asp	Arg	Arg	Phe	
			105					110					115			
att	gtt	gac	caa	ctc	ttt	atc	tcc	caa	gtg	ctc	aaa	gcg	aat	cgt	cta	499
Ile	Val	Asp	Gln	Leu	Phe	Ile	Ser	Gln	Val	Leu	Lys	Ala	Asn	Arg	Leu	
		120					125					130				
cca	gca	ccg	gca	aac	aac	gtt	att	tac	acc	gtg	ccc	aat	gac	gtt	atc	547
Pro	Ala	Pro	Ala	Asn	Asn	Val	Ile	Tyr	Thr	Val	Pro	Asn	Asp	Val	Ile	
	135					140					145					
cca	tct	gct	aaa	gac	atc	ttg	tcc	acc	act	gca	aaa	atg	aac	aat	cca	595
Pro	Ser	Ala	Lys	Asp	Ile	Leu	Ser	Thr	Thr	Ala	Lys	Met	Asn	Asn	Pro	
150					155					160					165	
ctg	aca	gtt	act	gca	agt	gcc	cca	att	act	gtt	gac	gac	att	cac	aca	643
Leu	Thr	Val	Thr	Ala	Ser	Ala	Pro	Ile	Thr	Val	Asp	Asp	Ile	His	Thr	
				170					175					180		
gcc	tat	gag	gta	ttt	ttc	gct	tct	ctt	gcc	tca	gtg	ttt	ttc	cct	tat	691
Ala	Tyr	Glu	Val	Phe	Phe	Ala	Ser	Leu	Ala	Ser	Val	Phe	Phe	Pro	Tyr	
		185						190					195			
acc	tac	ggg	gcg	gta	ttc	ctt										

tcc aac aac acc ttt aat agg ttc caa tca atg cgt aac atc tcc att	835
Ser Asn Asn Thr Phe Asn Arg Phe Gln Ser Met Arg Asn Ile Ser Ile	
230 235 240 245	
gat aat ctc acc gcc gag ttt ctc tta cgc aaa aat gaa gca gag aca	883
Asp Asn Leu Thr Ala Glu Phe Leu Leu Arg Lys Asn Glu Ala Glu Thr	
250 255 260	
act gat gat tat tca ttc ccc cgc gta ctt gtt tcc ctg ctg cat tct	931
Thr Asp Asp Tyr Ser Phe Pro Arg Val Leu Val Ser Leu Leu His Ser	
265 270 275	
tgg gtg aaa ctc aat cac gat gat gct cgt gct aac aat gat gca ccc	979
Trp Val Lys Leu Asn His Asp Asp Ala Arg Ala Asn Asn Asp Ala Pro	
280 285 290	
acc tgt gca cta gca ccg ttt agt gtg gct caa tgg atc atg ccg gag	1027
Thr Cys Ala Leu Ala Pro Phe Ser Val Ala Gln Trp Ile Met Pro Glu	
295 300 305	
acc att gtg ttt att aat gct gaa gct cat gct cat gca tcc tcc cag	1075
Thr Ile Val Phe Ile Asn Ala Glu Ala His Ala His Ala Ser Ser Gln	
310 315 320 325	
gac att gag aag aaa tgg aag gaa att aat gcg gcg tta aca ggg tct	1123
Asp Ile Glu Lys Lys Trp Lys Glu Ile Asn Ala Ala Leu Thr Gly Ser	
330 335 340	
att cgt att atg tcg cca aat gca att tcc aag ctg caa tct gct cag	1171
Ile Arg Ile Met Ser Pro Asn Ala Ile Ser Lys Leu Gln Ser Ala Gln	
345 350 355	
cat ctc ggg atg caa gca caa atg cag gcc atg cgt gct cga aaa gat	1219
His Leu Gly Met Gln Ala Gln Met Gln Ala Met Arg Ala Arg Lys Asp	
360 365 370	
cac cac aac atg cag aag cgt tcc tca caa gaa aac gac ttt tcc aag	1267
His His Asn Met Gln Lys Arg Ser Ser Gln Glu Asn Asp Phe Ser Lys	
375 380 385	
gca ctc ccc tca cca cag act atc gtg ctt tct gtc gca gag gtt ctg	1315
Ala Leu Pro Ser Pro Gln Thr Ile Val Leu Ser Val Ala Glu Val Leu	
390 395 400 405	
cgc aaa ctc act cac gta cgc caa tcg cac aac cct cag aaa tac cag	1363
Arg Lys Leu Thr His Val Arg Gln Ser His Asn Pro Gln Lys Tyr Gln	
410 415 420	
aag aag tct ctg acc aga gct tct cgc cga cac ccg gat aac cct aat	1411
Lys Lys Ser Leu Thr Arg Ala Ser Arg Arg His Pro Asp Asn Pro Asn	
425 430 435	
gtc cct ggc acc att aag agc aag ctc ttc tac cct gac ctg cat gtt	1459
Val Pro Gly Thr Ile Lys Ser Lys Leu Phe Tyr Pro Asp Leu His Val	
440 445 450	
tat gta gat act tct ggt tcg att agt gaa gaa agc tac cgc aac tct	1507
Tyr Val Asp Thr Ser Gly Ser Ile Ser Glu Glu Ser Tyr Arg Asn Ser	
455 460 465	

gtg gtt ctg ctc atg cag ctt gcc acc aaa ctg gac atc aac ctc tat 1555
Val Val Leu Leu Met Gln Leu Ala Thr Lys Leu Asp Ile Asn Leu Tyr
470 475 480 485

ttc tcc acc ttc tct cac gtg ctc tcc gaa gaa gta cta ttg ccg acc 1603
Phe Ser Thr Phe Ser His Val Leu Ser Glu Glu Val Leu Leu Pro Thr
490 495 500

aag ggt aaa aca cca cag caa ttg gca gct ctt att tcg gcc atc cca 1651
Lys Gly Lys Thr Pro Gln Gln Leu Ala Ala Leu Ile Ser Ala Ile Pro
505 510 515

aag gtc tct ggc ggt act gac tat cac cag att tgg gat tac atc cag 1699
Lys Val Ser Gly Gly Thr Asp Tyr His Gln Ile Trp Asp Tyr Ile Gln
520 525 530

atc aat ccg cag cgc caa gaa cgc atg aat ctt gtg tta act gac ttc 1747
Ile Asn Pro Gln Arg Gln Glu Arg Met Asn Leu Val Leu Thr Asp Phe
535 540 545

gga ttc atg ccg aat cgc ggc tta aac atc gac cac cca agt tct att 1795
Gly Phe Met Pro Asn Arg Gly Leu Asn Ile Asp His Pro Ser Ser Ile
550 555 560 565

ttc tac gtc cca atc ctg cct gac tac ggc agc tgg tca atg gtt cga 1843
Phe Tyr Val Pro Ile Leu Pro Asp Tyr Gly Ser Trp Ser Met Val Arg
570 575 580

aga gat atg tct cat ttc gca aat gaa atg gtt gac ttc gac ccc tat 1891
Arg Asp Met Ser His Phe Ala Asn Glu Met Val Asp Phe Asp Pro Tyr
585 590 595

atc cac agc cga cta ctc ggc gta cac gga aaa tagcagctga tccatctagg 1944
Ile His Ser Arg Leu Leu Gly Val His Gly Lys
600 605

gtc 1947

<210> 2048

<211> 608

<212> PRT

<213> Corynebacterium glutamicum

<400> 2048

Met Val Thr Phe Ser Val Ala Asn His Ala Pro His Thr Phe Ser Pro
1 5 10 15

Phe Asp Ile Glu Pro Pro Leu Thr Gly Asn Ala Thr Thr Asp Glu His
20 25 30

Gly Tyr Glu His Thr Ser Val Leu Glu Lys Leu Ala Ser Asn His Leu
35 40 45

Phe Asn Pro Ile Asn Pro Gln His Pro Val Thr Ile Thr Ala Thr Glu
50 55 60

Asn Gly Ser Thr Val Asp Leu Asp Ala Ala Ala Leu Ala Gln His Leu
65 70 75 80

Ala Leu Ala Ile Thr Pro Asp Ser Met Leu Ala Asn His Gln Gly Tyr

85										90					95						
Asn	Arg	Asp	Met	Met	Gly	Leu	Leu	Ser	Gln	Leu	Thr	Asn	His	Val	Gly						
			100					105					110								
Phe	Asp	Arg	Arg	Phe	Ile	Val	Asp	Gln	Leu	Phe	Ile	Ser	Gln	Val	Leu						
		115					120					125									
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Trp	Ile	Met	Pro	Glu	Thr	Ile	Val	Phe	Ile	Asn	Ala	Glu	Ala	His	Ala						
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His	Ala	Ser	Ser	Gln	Asp	Ile	Glu	Lys	Lys	Trp	Lys	Glu	Ile	Asn	Ala						
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Pro Gln Lys Tyr Gln Lys Lys Ser Leu Thr Arg Ala Ser Arg Arg His
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 Pro Asp Asn Pro Asn Val Pro Gly Thr Ile Lys Ser Lys Leu Phe Tyr
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 Pro Asp Leu His Val Tyr Val Asp Thr Ser Gly Ser Ile Ser Glu Glu
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 Ser Tyr Arg Asn Ser Val Val Leu Leu Met Gln Leu Ala Thr Lys Leu
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 Asp Ile Asn Leu Tyr Phe Ser Thr Phe Ser His Val Leu Ser Glu Glu
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 Val Leu Leu Pro Thr Lys Gly Lys Thr Pro Gln Gln Leu Ala Ala Leu
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 Ile Ser Ala Ile Pro Lys Val Ser Gly Gly Thr Asp Tyr His Gln Ile
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 Val Leu Thr Asp Phe Gly Phe Met Pro Asn Arg Gly Leu Asn Ile Asp
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 His Pro Ser Ser Ile Phe Tyr Val Pro Ile Leu Pro Asp Tyr Gly Ser
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1879)

<223> RXA01046

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 Met Ile Pro Phe Pro
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 Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp Glu Thr Arg Phe Ile
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 Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro Ala Leu Phe Arg Asp

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Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His Ile Ile Glu Pro Val	
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Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly Val Gly Lys Thr Glu	
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Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser Ile Thr Gly Leu Ile	
375 380 385	
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Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser Lys Arg Ala Lys Pro	
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Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val Ile Val Leu Asp Glu	
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ttt gag aag tct cac cct cat ttc cag caa ttg ttc atg gca gct ctt	1411
Phe Glu Lys Ser His Pro His Phe Gln Gln Leu Phe Met Ala Ala Leu	
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Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr Thr Leu Asn Phe Ser	
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Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala Arg Asp Lys Ile Gly	
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Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser Gly Val Leu Gly Ser	
470 475 480 485	
gct caa gca gca act gat ccg cgt gca cag gaa cgc ctc aag tca ctg	1603
Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu Arg Leu Lys Ser Leu	
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atg tcc aag gat ttc ctg ttg aac tgc tca acc gtt tcc aga ata tct	1651
Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr Val Ser Arg Ile Ser	
505 510 515	

ttg	cct	tca	acc	gca	ttg	atg	cag	gca	cct	acc	gtg	aga	ttc	tgg	aca	1699
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Ile	Ser	Thr	Ser	Val	Ala	Val	Thr	Pro	Cys	Cys	Leu	Ala	Thr	Pro	His	
		535				540					545					
tac	gca	gca	cag	atc	cct	gca	gat	att	gat	tca	gac	act	ctt	gat	cag	1795
Tyr	Ala	Ala	Gln	Ile	Pro	Ala	Asp	Ile	Asp	Ser	Asp	Thr	Leu	Asp	Gln	
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ctg	gtg	gaa	acc	acc	ttt	atc	tca	gat	ttt	ggT	gca	cgt	cct	gct	gca	1843
Leu	Val	Glu	Thr	Thr	Phe	Ile	Ser	Asp	Phe	Gly	Ala	Arg	Pro	Ala	Ala	
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Ala	Leu	Phe	Arg	Asp	Asp	Val	Ile	Asp	Gln	Thr	Leu	Ala	Ile	Leu	Ile	
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Ser	Lys	Asn	Lys	Pro	Asn	Ala	Leu	Leu	Val	Gly	Pro	Ala	Gly	Thr	Gly	
	50					55					60					
Lys	Ser	Arg	Ile	Ala	Glu	Asp	Ile	Ala	Arg	Arg	Leu	Ala	Asn	Asp	Asp	
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Val	Ser	Ile	Pro	Asp	Gln	Leu	Val	Gly	His	Arg	Ile	Leu	Asp	Val	Ser	
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Ile	Ala	Glu	Leu	Val	Ala	Gly	Ala	Gly	Val	Val	Gly	Gln	Leu	Lys	Lys	
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Arg	Ile	Leu	Asp	Leu	Ile	Lys	Tyr	Ala	Thr	Asp	Pro	Ser	Asn	Lys	Val	
		115					120					125				
Ile	Ile	Phe	Ile	Asp	Glu	Ile	His	Gln	Ile	Ala	Gly	Asp	Gln	Ser	Ser	
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His	Ser	Gly	Ser	Gln	Ala	Lys	Val	Ala	Gln	Ile	Leu	Lys	Pro	Tyr	Leu	
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Ala	Arg	Gly	Asp	Leu	Arg	Val	Ile	Gly	Ala	Thr	Thr	Thr	Gln	Glu	Ala	
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Arg Asp Phe Asp His Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val
 180 185 190
 Asn Val Asp Glu Phe Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala
 195 200 205
 Ala Arg Asp Gly Tyr Leu Lys His Phe Asn Asn Ala Val Thr Val Ser
 210 215 220
 Asp Asp Val Leu Gly Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro
 225 230 235 240
 Gly Asn Thr Ala Gln Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala
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 Leu Ala Ser Leu Thr Met Glu Lys Gln Arg Leu Ile Asn Asn His Val
 260 265 270
 Ile Ala Pro Ser Leu Lys Phe Pro Val Ser Glu Arg His Ile His Asn
 275 280 285
 Thr Ala Arg Lys Leu Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn
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 Thr Asp Asp Ala Arg Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His
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 Ile Ile Glu Pro Val Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile
 325 330 335
 Phe Pro Arg Thr Lys Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly
 340 345 350
 Val Gly Lys Thr Glu Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly
 355 360 365
 Gly Asp Pro Ile Ile Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser
 370 375 380
 Ile Thr Gly Leu Ile Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser
 385 390 395 400
 Lys Arg Ala Lys Pro Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val
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 Ile Val Leu Asp Glu Phe Glu Lys Ser His Pro His Phe Gln Gln Leu
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 Phe Met Ala Ala Leu Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr
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 Thr Leu Asn Phe Ser Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala
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 Arg Asp Lys Ile Gly Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser
 465 470 475 480
 Gly Val Leu Gly Ser Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu
 485 490 495

Arg Leu Lys Ser Leu Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr
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 Val Ser Arg Ile Ser Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr
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 Val Arg Phe Trp Thr Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys
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 Leu Ala Thr Pro His Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser
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Met

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 <222> (101)..(574)
 <223> RXA01047

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 Met Ile Asp Thr Thr
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 gct aac agc acc tca ggc acc cta cct aca ctc act gct gac caa gct 163
 Ala Asn Ser Thr Ser Gly Thr Leu Pro Thr Leu Thr Ala Asp Gln Ala
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 Ala Phe Ile Thr Gly Phe Cys Glu Ala Ala Ile Phe Thr Ala Thr Val
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 Thr Ile Asp Asn Glu Pro Ile Phe Leu Asp Glu Ala Phe Phe Leu Gly
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 Gln Glu Thr Tyr Thr Asp Ile Leu Met Asn Gln Leu Arg Thr Asn Glu
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 Ala Ile Val Lys Asp Cys Leu Asp Phe Phe Leu Asp Asn Tyr Thr Thr
 70 75 80 85
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 Met Asn Lys Leu Ile Val Asp Gly Leu Cys Pro Asp Trp Glu His His

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Gly His Asp Phe Leu Leu Thr Arg Asp His His Gly Ala Gly Phe Trp				
	105	110	115	
gat cgt ggc tac gac gaa tac ggt gcc caa ctc acc gac aat gcc gaa				499
Asp Arg Gly Tyr Asp Glu Tyr Gly Ala Gln Leu Thr Asp Asn Ala Glu				
	120	125	130	
aaa tat tca gaa aac tgt ctc aat ttc tgg att gag cct gat agt gac				547
Lys Tyr Ser Glu Asn Cys Leu Asn Phe Trp Ile Glu Pro Asp Ser Asp				
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Phe Thr Ala Thr Val Thr Ile Asp Asn Glu Pro Ile Phe Leu Asp Glu			
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Ala Phe Phe Leu Gly Gln Glu Thr Tyr Thr Asp Ile Leu Met Asn Gln			
50	55	60	

Leu Arg Thr Asn Glu Ala Ile Val Lys Asp Cys Leu Asp Phe Phe Leu			
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Asp Asn Tyr Thr Thr Met Asn Lys Leu Ile Val Asp Gly Leu Cys Pro			
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Asp Trp Glu His His Gly His Asp Phe Leu Leu Thr Arg Asp His His			
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Gly Ala Gly Phe Trp Asp Arg Gly Tyr Asp Glu Tyr Gly Ala Gln Leu			
115	120	125	

Thr Asp Asn Ala Glu Lys Tyr Ser Glu Asn Cys Leu Asn Phe Trp Ile			
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Glu Pro Asp Ser Asp Pro Leu Ile Ile Asn Phe Glu Tyr His			
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Thr Ala Ser Val Ala Leu Leu Thr Ala Gly Ala Leu Ala Leu Thr Ala	
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Thr Pro Ala Met Ala Gln Ser Thr Thr Gly Ser Ser Ala Ser Ser Gln	
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gtt ggc gac gca ctc ggt gct agc gac tac gag cgc gac atc tgg ggt	259
Val Gly Asp Ala Leu Gly Ala Ser Asp Tyr Glu Arg Asp Ile Trp Gly	
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tcc tct aag gac ttc gac gat gta acc cca ttc ggt tcc gct tgg tac	307
Ser Ser Lys Asp Phe Asp Asp Val Thr Pro Phe Gly Ser Ala Trp Tyr	
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ggc tac acc ctg gcc gca acc gca gtt gct atc tcc ggt ctt gtg tac	355
Gly Tyr Thr Leu Ala Ala Thr Ala Val Ala Ile Ser Gly Leu Val Tyr	
70 75 80 85	

gca aac ctt cct gca atc gag cag gct gct gca cag gcc ggc atc aag	403
Ala Asn Leu Pro Ala Ile Glu Gln Ala Ala Ala Gln Ala Gly Ile Lys	
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Leu Glu Ile Pro Arg Tyr	
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<211> 107

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<213> *Corynebacterium glutamicum*

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Arg Asp Ile Trp Gly Ser Ser Lys Asp Phe Asp Asp Val Thr Pro Phe	
50 55 60	

Gly Ser Ala Trp Tyr Gly Tyr Thr Leu Ala Ala Thr Ala Val Ala Ile
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Gln Ala Gly Ile Lys Leu Glu Ile Pro Arg Tyr
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<223> RXA01063

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Met Ala Asp Glu Lys
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Lys Val His Val Arg Ala Thr Leu Arg Phe Asp Ser Asp Thr His Gln
10 15 20

cgg gca att tat tgg gca gat cga aaa ggt atc tcg ctg agc gcg tat 211
Arg Ala Ile Tyr Trp Ala Asp Arg Lys Gly Ile Ser Leu Ser Ala Tyr
25 30 35

gca gaa gag gcg atc aga gag aag att gat cgt gat aac ggt gtg cac 259
Ala Glu Glu Ala Ile Arg Glu Lys Ile Asp Arg Asp Asn Gly Val His
40 45 50

gtt att ccg aat tca ctg ttg gat aac cgc atg aac caa atc att gat 307
Val Ile Pro Asn Ser Leu Leu Asp Asn Arg Met Asn Gln Ile Ile Asp
55 60 65

cag ctc agc tcg ttt ggt cgt gag ttg gcg aac aac acg aca gtt gta 355
Gln Leu Ser Ser Phe Gly Arg Glu Leu Ala Asn Asn Thr Thr Val Val
70 75 80 85

act agt ggt ttc aac acc att atc ggt atg act cgt ggc gac tcg tat 403
Thr Ser Gly Phe Asn Thr Ile Ile Gly Met Thr Arg Gly Asp Ser Tyr
90 95 100

ctc tct gat gat ctc gat gac ctg ggt taaacccgat gaacgagcag 450
Leu Ser Asp Asp Leu Asp Asp Leu Gly
105 110

gaa 453

<210> 2056

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 2056

Met Ala Asp Glu Lys Lys Val His Val Arg Ala Thr Leu Arg Phe Asp
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Ser Asp Thr His Gln Arg Ala Ile Tyr Trp Ala Asp Arg Lys Gly Ile
 20 25 30

Ser Leu Ser Ala Tyr Ala Glu Glu Ala Ile Arg Glu Lys Ile Asp Arg
 35 40 45

Asp Asn Gly Val His Val Ile Pro Asn Ser Leu Leu Asp Asn Arg Met
 50 55 60

Asn Gln Ile Ile Asp Gln Leu Ser Ser Phe Gly Arg Glu Leu Ala Asn
 65 70 75 80

Asn Thr Thr Val Val Thr Ser Gly Phe Asn Thr Ile Ile Gly Met Thr
 85 90 95

Arg Gly Asp Ser Tyr Leu Ser Asp Asp Leu Asp Asp Leu Gly
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<210> 2057

<211> 849

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(826)

<223> RXA01066

<400> 2057

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tttgaaccgc ctgggcttct agctttaagg gggtaggttc atg cgt agg gac agt 115
 Met Arg Arg Asp Ser
 1 5

ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc 163
 Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala
 10 15 20

gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga 211
 Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly
 25 30 35

gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259
 Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu
 40 45 50

cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg 307
 Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu
 55 60 65

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355
 Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile
 70 75 80 85

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<400> 2058
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  1          5          10          15
Asp Phe Gly Glu Ala Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His
          20          25          30
Gly Ile Val Arg Gly Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg
          35          40          45
Phe Gly Ser Arg Leu Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr
  50          55          60

```

Pro Gly Arg Lys Leu Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr
 65 70 75 80
 Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser
 85 90 95
 Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro
 100 105 110
 His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser
 115 120 125
 Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn
 130 135 140
 His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg
 145 150 155 160
 Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys
 165 170 175
 Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu
 180 185 190
 His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg
 195 200 205
 Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His
 210 215 220
 Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp
 225 230 235 240
 Gln Ala

<210> 2059
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1171)
 <223> RXA01068

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 Met Pro Thr Asn Gln
 1 5
 ccg acg cca gcc caa atc aaa cgc tgg cgc gga tac ctg gcc aat gag 163
 Pro Thr Pro Ala Gln Ile Lys Arg Trp Arg Gly Tyr Leu Ala Asn Glu
 10 15 20
 caa gca gag gcc gca gcc tac cgc gac ctg gcc aaa cga cgc gaa ggc 211
 Gln Ala Glu Ala Ala Ala Tyr Arg Asp Leu Ala Lys Arg Arg Glu Gly

25	30	35	
gaa gag cga gac atc ctc cta gcg ctc gcc gac gct gaa cac cga cac			259
Glu Glu Arg Asp Ile Leu Leu Ala Leu Ala Asp Ala Glu His Arg His			
40	45	50	
gcc gct tac tgg gtg gaa aag ctc ggc cct gat gcc gaa aac cca cca			307
Ala Ala Tyr Trp Val Glu Lys Leu Gly Pro Asp Ala Glu Asn Pro Pro			
55	60	65	
aaa gcc gac gtc aaa acc cgc ctg ctc ggt ttt cta gca cgc cga ttc			355
Lys Ala Asp Val Lys Thr Arg Leu Leu Gly Phe Leu Ala Arg Arg Phe			
70	75	80	85
ggc tcc gtg ttc acc ctg gca ctc atg cag tcc gcc gaa acg cgc agc			403
Gly Ser Val Phe Thr Leu Ala Leu Met Gln Ser Ala Glu Thr Arg Ser			
90	95	100	
ccc tac gac gac gat gcc gac gcc tcc cgc caa atc agc gcc gac gaa			451
Pro Tyr Asp Asp Asp Ala Asp Ala Ser Arg Gln Ile Ser Ala Asp Glu			
105	110	115	
cgc atc cac gcc gaa gtc gtt cga ggc cta gcc agc cgc ggc aga gaa			499
Arg Ile His Ala Glu Val Val Arg Gly Leu Ala Ser Arg Gly Arg Glu			
120	125	130	
cgc atg agc ggc aac ttc cgt gcc gcc gta ttc gga atc aac gac ggc			547
Arg Met Ser Gly Asn Phe Arg Ala Ala Val Phe Gly Ile Asn Asp Gly			
135	140	145	
ctg gtc tcc aac gtc gcc ctc gtc atg ggt gtc atg gcc acc ggc gtg			595
Leu Val Ser Asn Val Ala Leu Val Met Gly Val Met Ala Thr Gly Val			
150	155	160	165
ccc gcc caa att gtt ctc atc acc ggc att tcc ggt ctg ctc tcc ggc			643
Pro Ala Gln Ile Val Leu Ile Thr Gly Ile Ser Gly Leu Leu Ser Gly			
170	175	180	
gcg cta tcc atg gcc gcc ggc gaa tac atc tca gtg cgc tcc caa aca			691
Ala Leu Ser Met Ala Ala Gly Glu Tyr Ile Ser Val Arg Ser Gln Thr			
185	190	195	
gag ctt ctc gac gcc tcc ctc cca gac ccc aaa gcc cgc gaa gcc ctc			739
Glu Leu Leu Asp Ala Ser Leu Pro Asp Pro Lys Ala Arg Glu Ala Leu			
200	205	210	
cac gcc ctc gac gtc gaa tcc aac gaa ctg gaa ctc gtc tac cga gcc			787
His Ala Leu Asp Val Glu Ser Asn Glu Leu Glu Leu Val Tyr Arg Ala			
215	220	225	
cgc gga atg agc gaa gac gaa gcg cgg gca aaa gcg tca caa gtt ttc			835
Arg Gly Met Ser Glu Asp Glu Ala Arg Ala Lys Ala Ser Gln Val Phe			
230	235	240	245
caa aga atc agc gac caa aaa cgc atc agc gac aac gtc ctc ggc agc			883
Gln Arg Ile Ser Asp Gln Lys Arg Ile Ser Asp Asn Val Leu Gly Ser			
250	255	260	
acc gaa atc caa agc gcc ggc tcc gct cgt tcg gcc gcc aca ttc agc			931
Thr Glu Ile Gln Ser Ala Gly Ser Ala Arg Ser Ala Ala Thr Phe Ser			
265	270	275	

ttc ctg tcc ttt gcc atc ggc gca ttc ctc ccg atc gtc cca tac gtc 979
 Phe Leu Ser Phe Ala Ile Gly Ala Phe Leu Pro Ile Val Pro Tyr Val
 280 285 290

ttc ggc atg gaa ggc ctc gcc ggg gca gtg gtg tcc cta gtc ctc gtc 1027
 Phe Gly Met Glu Gly Leu Ala Gly Ala Val Val Ser Leu Val Leu Val
 295 300 305

gga cta tca ctg atg gca acg ggc gcg acc acc ggc ctg cta tcg gga 1075
 Gly Leu Ser Leu Met Ala Thr Gly Ala Thr Thr Gly Leu Leu Ser Gly
 310 315 320 325

aag cca ccg gga atc cgc gcg gtg cgt cag ctg tcg atc ggc tac ggc 1123
 Lys Pro Pro Gly Ile Arg Ala Val Arg Gln Leu Ser Ile Gly Tyr Gly
 330 335 340

gcg gcg ctg gtc acc tac gtg ctc gcc ctc ctg ttc ggc atg atc ctt 1171
 Ala Ala Leu Val Thr Tyr Val Leu Gly Leu Leu Phe Gly Met Ile Leu
 345 350 355

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<210> 2060

<211> 357

<212> PRT

<213> Corynebacterium glutamicum

<400> 2060

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Tyr Leu Ala Asn Glu Gln Ala Glu Ala Ala Tyr Arg Asp Leu Ala
 20 25 30

Lys Arg Arg Glu Gly Glu Glu Arg Asp Ile Leu Leu Ala Leu Ala Asp
 35 40 45

Ala Glu His Arg His Ala Ala Tyr Trp Val Glu Lys Leu Gly Pro Asp
 50 55 60

Ala Glu Asn Pro Pro Lys Ala Asp Val Lys Thr Arg Leu Leu Gly Phe
 65 70 75 80

Leu Ala Arg Arg Phe Gly Ser Val Phe Thr Leu Ala Leu Met Gln Ser
 85 90 95

Ala Glu Thr Arg Ser Pro Tyr Asp Asp Asp Ala Asp Ala Ser Arg Gln
 100 105 110

Ile Ser Ala Asp Glu Arg Ile His Ala Glu Val Val Arg Gly Leu Ala
 115 120 125

Ser Arg Gly Arg Glu Arg Met Ser Gly Asn Phe Arg Ala Ala Val Phe
 130 135 140

Gly Ile Asn Asp Gly Leu Val Ser Asn Val Ala Leu Val Met Gly Val
 145 150 155 160

Met Ala Thr Gly Val Pro Ala Gln Ile Val Leu Ile Thr Gly Ile Ser

165										170					175				
Gly	Leu	Leu	Ser	Gly	Ala	Leu	Ser	Met	Ala	Ala	Gly	Glu	Tyr	Ile	Ser				
			180					185					190						
Val	Arg	Ser	Gln	Thr	Glu	Leu	Leu	Asp	Ala	Ser	Leu	Pro	Asp	Pro	Lys				
		195					200					205							
Ala	Arg	Glu	Ala	Leu	His	Ala	Leu	Asp	Val	Glu	Ser	Asn	Glu	Leu	Glu				
	210					215					220								
Leu	Val	Tyr	Arg	Ala	Arg	Gly	Met	Ser	Glu	Asp	Glu	Ala	Arg	Ala	Lys				
225					230					235					240				
Ala	Ser	Gln	Val	Phe	Gln	Arg	Ile	Ser	Asp	Gln	Lys	Arg	Ile	Ser	Asp				
			245					250						255					
Asn	Val	Leu	Gly	Ser	Thr	Glu	Ile	Gln	Ser	Ala	Gly	Ser	Ala	Arg	Ser				
		260						265					270						
Ala	Ala	Thr	Phe	Ser	Phe	Leu	Ser	Phe	Ala	Ile	Gly	Ala	Phe	Leu	Pro				
		275					280					285							
Ile	Val	Pro	Tyr	Val	Phe	Gly	Met	Glu	Gly	Leu	Ala	Gly	Ala	Val	Val				
	290					295					300								
Ser	Leu	Val	Leu	Val	Gly	Leu	Ser	Leu	Met	Ala	Thr	Gly	Ala	Thr	Thr				
305					310					315					320				
Gly	Leu	Leu	Ser	Gly	Lys	Pro	Pro	Gly	Ile	Arg	Ala	Val	Arg	Gln	Leu				
			325					330						335					
Ser	Ile	Gly	Tyr	Gly	Ala	Ala	Leu	Val	Thr	Tyr	Val	Leu	Gly	Leu	Leu				
		340					345						350						
Phe	Gly	Met	Ile	Leu															
		355																	

<210> 2061

<211> 828

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(805)

<223> RXA01074

<400> 2061

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gccacatttc	actaaacgcc	ccgcacaacc	ccaagcagcc	ttg	gcg	gaa	gcc	gca		115
				Leu	Ala	Glu	Ala	Ala		
				1				5		

ggt	cta	cgc	tgg	ctc	gcc	gaa	gca	tct	tca	gct	gtg	gca	cag	gtt	gtt		163
Gly	Leu	Arg	Trp	Leu	Ala	Glu	Ala	Ser	Ser	Ala	Val	Ala	Gln	Val	Val		
			10					15					20				

agc	gcc	gac	gca	gag	cag	atc	acg	act	gtt	ggc	gtc	gaa	acg	caa	ttg		211
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Ser	Ala	Asp	Ala	Glu	Gln	Ile	Thr	Thr	Val	Gly	Val	Glu	Thr	Gln	Leu	
			25				30						35			
ccc	aca	ccc	gat	gcg	gcc	ttc	aag	gcc	ggc	gaa	gag	ctc	gcc	cgc	atc	259
Pro	Thr	Pro	Asp	Ala	Ala	Phe	Lys	Ala	Gly	Glu	Glu	Leu	Ala	Arg	Ile	
			40				45						50			
cac	ctt	gcc	ggc	gcc	cca	gcg	ttc	ggc	tgt	cca	cca	gcg	ggc	tgg	gcg	307
His	Leu	Ala	Gly	Ala	Pro	Ala	Phe	Gly	Cys	Pro	Pro	Ala	Gly	Trp	Ala	
			55				60						65			
ggg	tta	aac	tac	atc	ggc	acc	cag	gga	caa	gca	tgc	tta	tcg	acg	ccc	355
Gly	Leu	Asn	Tyr	Ile	Gly	Thr	Gln	Gly	Gln	Ala	Cys	Leu	Ser	Thr	Pro	
			70				75						80	85		
acc	tgg	ggt	gtt	ttt	tac	tcc	cag	caa	cgc	gta	ctc	ccg	ttt	gcg	cgc	403
Thr	Trp	Gly	Val	Phe	Tyr	Ser	Gln	Gln	Arg	Val	Leu	Pro	Phe	Ala	Arg	
			90				95						100			
cgg	gca	cgc	agg	cga	aat	cac	ctc	acc	gag	cac	gca	ctc	tgg	gtc	gtg	451
Arg	Ala	Arg	Arg	Arg	Asn	His	Leu	Thr	Glu	His	Ala	Leu	Trp	Val	Val	
			105				110						115			
gaa	gcc	gct	tgt	gat	ttg	att	agc	gaa	ctt	ccc	gat	gac	gtt	ccc	ccc	499
Glu	Ala	Ala	Cys	Asp	Leu	Ile	Ser	Glu	Leu	Pro	Asp	Asp	Val	Pro	Pro	
			120				125						130			
gcc	aga	atc	cac	ggc	gac	ttg	tgg	ttt	ggc	aac	cta	ctt	ttt	ggc	aca	547
Ala	Arg	Ile	His	Gly	Asp	Leu	Trp	Phe	Gly	Asn	Leu	Leu	Phe	Gly	Thr	
			135				140						145			
gac	ggg	cct	gtg	ttt	att	gac	ccc	gca	gct	cac	ggc	ggt	cat	ccc	gaa	595
Asp	Gly	Pro	Val	Phe	Ile	Asp	Pro	Ala	Ala	His	Gly	Gly	His	Pro	Glu	
			150				155						160	165		
act	gat	ctc	gcg	atg	ctt	gat	gta	ttt	ggc	gca	ccc	tat	ctc	gat	gaa	643
Thr	Asp	Leu	Ala	Met	Leu	Asp	Val	Phe	Gly	Ala	Pro	Tyr	Leu	Asp	Glu	
			170				175						180			
atc	cgg	gaa	ggt	tat	ctg	tct	atc	aac	ccg	ctg	cca	gac	ggg	tgg	cgt	691
Ile	Arg	Glu	Gly	Tyr	Leu	Ser	Ile	Asn	Pro	Leu	Pro	Asp	Gly	Trp	Arg	
			185				190						195			
gaa	cgc	acc	ccc	atg	cac	caa	ctc	cac	cct	ttg	gcc	gta	cat	gcg	gcg	739
Glu	Arg	Thr	Pro	Met	His	Gln	Leu	His	Pro	Leu	Ala	Val	His	Ala	Ala	
			200				205						210			
tct	cat	ggg	cca	agc	tac	ggc	gtg	gaa	cta	ctc	cac	gcc	gcc	aaa	gcg	787
Ser	His	Gly	Pro	Ser	Tyr	Gly	Val	Glu	Leu	Leu	His	Ala	Ala	Lys	Ala	
			215				220						225			
aca	ctc	aaa	ctg	ttg	gat	taacg	ccacc	aattttt	ctg	cgg						828
Thr	Leu	Lys	Leu	Leu	Asp											
			230				235									

<210> 2062

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 2062

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20 25 30
Val Glu Thr Gln Leu Pro Thr Pro Asp Ala Ala Phe Lys Ala Gly Glu
35 40 45
Glu Leu Ala Arg Ile His Leu Ala Gly Ala Pro Ala Phe Gly Cys Pro
50 55 60
Pro Ala Gly Trp Ala Gly Leu Asn Tyr Ile Gly Thr Gln Gly Gln Ala
65 70 75 80
Cys Leu Ser Thr Pro Thr Trp Gly Val Phe Tyr Ser Gln Gln Arg Val
85 90 95
Leu Pro Phe Ala Arg Arg Ala Arg Arg Arg Asn His Leu Thr Glu His
100 105 110
Ala Leu Trp Val Val Glu Ala Ala Cys Asp Leu Ile Ser Glu Leu Pro
115 120 125
Asp Asp Val Pro Pro Ala Arg Ile His Gly Asp Leu Trp Phe Gly Asn
130 135 140
Leu Leu Phe Gly Thr Asp Gly Pro Val Phe Ile Asp Pro Ala Ala His
145 150 155 160
Gly Gly His Pro Glu Thr Asp Leu Ala Met Leu Asp Val Phe Gly Ala
165 170 175
Pro Tyr Leu Asp Glu Ile Arg Glu Gly Tyr Leu Ser Ile Asn Pro Leu
180 185 190
Pro Asp Gly Trp Arg Glu Arg Thr Pro Met His Gln Leu His Pro Leu
195 200 205
Ala Val His Ala Ala Ser His Gly Pro Ser Tyr Gly Val Glu Leu Leu
210 215 220
His Ala Ala Lys Ala Thr Leu Lys Leu Leu Asp
225 230 235

<210> 2063

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1120)

<223> RXA01076

<400> 2063

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	Met	Thr	Pro	Ala	His	
	1				5	
ata ttt tct gaa ggt cca atc aat agt gtt gtt ctc agc cag gat gag						163
Ile Phe Ser Glu Gly Pro Ile Asn Ser Val Val Leu Ser Gln Asp Glu						
	10				20	
gat gga aat ttc acc acc tcc tac cag gac acg ttc tct gat cca tca						211
Asp Gly Asn Phe Thr Thr Ser Tyr Gln Asp Thr Phe Ser Asp Pro Ser						
	25				35	
ttt ttg ggg gaa ggt gac gtt cta att gag gtt ggt tgg tcc agc ttg						259
Phe Leu Gly Glu Gly Asp Val Leu Ile Glu Val Gly Trp Ser Ser Leu						
	40				50	
aat tac aag gac gca atg gct ctg aag ggt gat aag gga gtg gtg cgt						307
Asn Tyr Lys Asp Ala Met Ala Leu Lys Gly Asp Lys Gly Val Val Arg						
	55				65	
act gtg cca ctg att cca ggt atc gat gtg gtg ggc act gtg atc gag						355
Thr Val Pro Leu Ile Pro Gly Ile Asp Val Val Gly Thr Val Ile Glu						
	70				80	85
agc gct gat cct cgc ttt ggt cgt ggt gat gaa gtg gtg ctg aat ggc						403
Ser Ala Asp Pro Arg Phe Gly Arg Gly Asp Glu Val Val Leu Asn Gly						
	90				95	100
gct ggt ttg ggg gag aac cgg cat gga ggt ttc acg cag cgg ctg aaa						451
Ala Gly Leu Gly Glu Asn Arg His Gly Gly Phe Thr Gln Arg Leu Lys						
	105				110	115
gtg ccg tct gaa ccg ttg ctg cat att cca ttt aac ttc tcc gcg cag						499
Val Pro Ser Glu Pro Leu Leu His Ile Pro Phe Asn Phe Ser Ala Gln						
	120				125	130
cag gtg ggt gcg ttg ggt act gca ggt ttc acg gct gcg cta tcg gtg						547
Gln Val Gly Ala Leu Gly Thr Ala Gly Phe Thr Ala Ala Leu Ser Val						
	135				140	145
aat gct ctg gtc gat caa ggt atc aaa ccg gag gat ggg gag att ctg						595
Asn Ala Leu Val Asp Gln Gly Ile Lys Pro Glu Asp Gly Glu Ile Leu						
	150				155	160
gta act ggt tcg act ggt ggt gtg ggt tcg att gca ctt cac ctg ctg						643
Val Thr Gly Ser Thr Gly Gly Val Gly Ser Ile Ala Leu His Leu Leu						
	170				175	180
aat aag ttg gga tat acg acg gtc gcg gtg acg ggg cgt cga gaa gcg						691
Asn Lys Leu Gly Tyr Thr Thr Val Ala Val Thr Gly Arg Arg Glu Ala						
	185				190	195
cat gcc gaa tac ctg acc agc ctg ggc gca agc gac atc att gat cgc						739
His Ala Glu Tyr Leu Thr Ser Leu Gly Ala Ser Asp Ile Ile Asp Arg						
	200				205	210
gcg gag ctt tct gaa aag ggc cgg ccg ctg cag aag ggg cgt tgg gcg						787
Ala Glu Leu Ser Glu Lys Gly Arg Pro Leu Gln Lys Gly Arg Trp Ala						
	215				220	225
ggt gta gtg gat tca gtg gga tcc cac aca ctt gtc aat gcg att gct						835
Gly Val Val Asp Ser Val Gly Ser His Thr Leu Val Asn Ala Ile Ala						

230	235	240	245	
cag aca aaa tgg ggc gga att gtc acg gcg tgt ggc atg gct cag ggg				883
Gln Thr Lys Trp Gly Gly Ile Val Thr Ala Cys Gly Met Ala Gln Gly	250	255	260	
ccg gat ctg ccg gga acg gtg ttg ccg ttt att ctt cgt ggc gtg cat				931
Pro Asp Leu Pro Gly Thr Val Leu Pro Phe Ile Leu Arg Gly Val His	265	270	275	
ttg gtt ggc att aac tct gtc gat gca ccc cgt gag ctg cgt cga cgt				979
Leu Val Gly Ile Asn Ser Val Asp Ala Pro Arg Glu Leu Arg Arg Arg	280	285	290	
gcg tgg gcg ttg ctg tcc gag cat ctt gat acc gcg gtg cta gat gat				1027
Ala Trp Ala Leu Leu Ser Glu His Leu Asp Thr Ala Val Leu Asp Asp	295	300	305	
atg acc act gtg att gat gtc aag gat gtt gct caa gct ggc gaa gat				1075
Met Thr Thr Val Ile Asp Val Lys Asp Val Ala Gln Ala Gly Glu Asp	310	315	320	325
ttg atg gct ggc aag ctt cac gga cgt acc gcg gtg cgt gtt cat				1120
Leu Met Ala Gly Lys Leu His Gly Arg Thr Ala Val Arg Val His	330	335	340	
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<210> 2064

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 2064

Met Thr Pro Ala His Ile Phe Ser Glu Gly Pro Ile Asn Ser Val Val			
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Leu Ser Gln Asp Glu Asp Gly Asn Phe Thr Thr Ser Tyr Gln Asp Thr			
20 25 30			

Phe Ser Asp Pro Ser Phe Leu Gly Glu Gly Asp Val Leu Ile Glu Val			
35 40 45			

Gly Trp Ser Ser Leu Asn Tyr Lys Asp Ala Met Ala Leu Lys Gly Asp			
50 55 60			

Lys Gly Val Val Arg Thr Val Pro Leu Ile Pro Gly Ile Asp Val Val			
65 70 75 80			

Gly Thr Val Ile Glu Ser Ala Asp Pro Arg Phe Gly Arg Gly Asp Glu			
85 90 95			

Val Val Leu Asn Gly Ala Gly Leu Gly Glu Asn Arg His Gly Gly Phe			
100 105 110			

Thr Gln Arg Leu Lys Val Pro Ser Glu Pro Leu Leu His Ile Pro Phe			
115 120 125			

Asn Phe Ser Ala Gln Gln Val Gly Ala Leu Gly Thr Ala Gly Phe Thr			
130 135 140			

Ala Ala Leu Ser Val Asn Ala Leu Val Asp Gln Gly Ile Lys Pro Glu
 145 150 155 160
 Asp Gly Glu Ile Leu Val Thr Gly Ser Thr Gly Gly Val Gly Ser Ile
 165 170 175
 Ala Leu His Leu Leu Asn Lys Leu Gly Tyr Thr Thr Val Ala Val Thr
 180 185 190
 Gly Arg Arg Glu Ala His Ala Glu Tyr Leu Thr Ser Leu Gly Ala Ser
 195 200 205
 Asp Ile Ile Asp Arg Ala Glu Leu Ser Glu Lys Gly Arg Pro Leu Gln
 210 215 220
 Lys Gly Arg Trp Ala Gly Val Val Asp Ser Val Gly Ser His Thr Leu
 225 230 235 240
 Val Asn Ala Ile Ala Gln Thr Lys Trp Gly Gly Ile Val Thr Ala Cys
 245 250 255
 Gly Met Ala Gln Gly Pro Asp Leu Pro Gly Thr Val Leu Pro Phe Ile
 260 265 270
 Leu Arg Gly Val His Leu Val Gly Ile Asn Ser Val Asp Ala Pro Arg
 275 280 285
 Glu Leu Arg Arg Arg Ala Trp Ala Leu Leu Ser Glu His Leu Asp Thr
 290 295 300
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 Met Ser Asn Ala Val
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 Pro His Asn Val Ser Phe Asn Phe Val Pro Arg Ala Tyr Arg Pro Glu
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25 30 35	
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40 45 50	
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55 60 65	
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70 75 80 85	
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90 95 100	
gac gca gtt gat cat tac tta aag gaa gcc aag gaa gtc ggc ttc gat Asp Ala Val Asp His Tyr Leu Lys Glu Ala Lys Glu Val Gly Phe Asp	451
105 110 115	
gtt att gag att tcc acc gga ttc atc atg ctc aac act tca ggt ctt Val Ile Glu Ile Ser Thr Gly Phe Ile Met Leu Asn Thr Ser Gly Leu	499
120 125 130	
cag cgc ctg gta gaa aaa gtg gtc aag gca ggc ctc aaa gca aaa cct Gln Arg Leu Val Glu Lys Val Val Lys Ala Gly Leu Lys Ala Lys Pro	547
135 140 145	
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150 155 160 165	
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170 175 180	
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215 220 225	
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230 235 240 245	
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250 255 260	

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<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 2066

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 35 40 45

Asp Val Ala Gly Gln Trp Val Asp Gly Ile Lys Trp Ala Gly Gly Ser
 50 55 60

Phe Ser Leu Val Pro Thr Glu Gln Val Arg Ala Phe Ser Asp Ile Ala
 65 70 75 80

His Glu Asn Asn Ala Tyr Val Ser Ser Gly Gly Trp Ile Glu Thr Val
 85 90 95

Leu Arg Tyr Gly Asp Asp Ala Val Asp His Tyr Leu Lys Glu Ala Lys
 100 105 110

Glu Val Gly Phe Asp Val Ile Glu Ile Ser Thr Gly Phe Ile Met Leu
 115 120 125

Asn Thr Ser Gly Leu Gln Arg Leu Val Glu Lys Val Val Lys Ala Gly
 130 135 140

Leu Lys Ala Lys Pro Glu Leu Gly Leu Gln Ile Gly Ser Gly Gly Asp
 145 150 155 160

Ser Gly Glu Ala Glu Leu Ala Ala Glu Gly Lys Lys Asp Ile Gly Asp
 165 170 175

Leu Val Asp Arg Gly Lys Lys Ala Leu Asp Ala Gly Ala Ser Ile Ile
 180 185 190

Met Ile Glu Ser Glu Gly Ile Thr Glu Asn Val Thr Glu Trp Asp Thr
 195 200 205

Gly Ala Ala Ala Ser Ile Ile Asn Gly Leu Gly Leu Glu Asn Val Met
 210 215 220

Phe Glu Ala Ala Asp Gly Pro Val Phe Glu Trp Tyr Val Lys Asn Tyr
 225 230 235 240

Gly Asn Glu Cys Asn Leu Phe Val Asp His Ser Gln Ile Leu Gln Leu

245

250

255

Glu Gly Leu Arg Gln Asn Ile Trp Gly Asn Lys Ser Thr Trp Gly Arg
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 Met Phe Pro Arg Ile
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ccg ctg gca atg tgt gct gtc gca gca atc cct gct gtt gtg ctc agg 163
 Pro Leu Ala Met Cys Ala Val Ala Ala Ile Pro Ala Val Val Leu Arg
 10 15 20

ttt tct gag ctg tcg gcg tca cct gtg gcg acc atg ctg att ttt ggt 211
 Phe Ser Glu Leu Ser Ala Ser Pro Val Ala Thr Met Leu Ile Phe Gly
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acc gca gtg gtt gct gcc tct ttt gtg ttg gcg tgg gca gct gaa gct 259
 Thr Ala Val Val Ala Ala Ser Phe Val Leu Ala Trp Ala Ala Glu Ala
 40 45 50

gtg cgc aaa gat att tct ggt gcg ttg gca gtg gcc ttg ctt gcg tta 307
 Val Arg Lys Asp Ile Ser Gly Ala Leu Ala Val Ala Leu Leu Ala Leu
 55 60 65

gtt gca gtg ctt cct gaa tat gct tct gaa acg gtt gtc gag cac act 355
 Val Ala Val Leu Pro Glu Tyr Ala Ser Glu Thr Val Val Glu His Thr
 70 75 80 85

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<210> 2068

<211> 92

<212> PRT

<213> Corynebacterium glutamicum

<400> 2068

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Trp Ala Ala Glu Ala Val Arg Lys Asp Ile Ser Gly Ala Leu Ala Val		
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<212> DNA

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<222> (101)..(1282)

<223> RXA01088

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Met Gly Leu Trp Ile
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gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163
Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
10 15 20

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Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
25 30 35

atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259
Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
40 45 50

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Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
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70 75 80 85

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90 95 100

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883																	
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 35 40 45

 Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
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 His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
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 Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
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 Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
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 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
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 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
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 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
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 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
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 105 110 115
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 Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val Lys Ile Gly Lys Ser
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<212> PRT

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 35 40 45
 Pro His Thr Ile Glu Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln
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 Thr Val Phe His Ala Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu
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 Val Asp Val Val Lys Ala Ile Ser Asp Lys Met Val Leu Arg His Pro
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 His Val Phe Gly Ala Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val
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 Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala
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Met Lys Pro Arg Val																5
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Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser																
10 15 20																
tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt	211															
Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly																
25 30 35																
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Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met																
40 45 50																
gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc	307															
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120 125 130																
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Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu																
135 140 145																
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Lys Pro Gln Val Lys Ala Arg Val Trp His Pro Asp Phe Phe Arg His																
215 220 225																

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 Val Cys Ser Gly
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822

<210> 2078

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 2078

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Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe
 20 25 30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp
 35 40 45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala
 50 55 60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile
 65 70 75 80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu
 85 90 95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly
 100 105 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala
 115 120 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met
 130 135 140

Ile Gly Cys Ala Leu Ala Leu Val Gly Gly Val Val Leu Ala Met Arg
 145 150 155 160

Pro Ala Glu Asp Thr Ala Lys Ser Asn Gln Tyr Glu Arg Lys Gln Ala
 165 170 175

Arg Ala Glu Lys Ile His Thr Asp Leu Ala Gln Asp Pro Asp Ser Gly
 180 185 190

Arg Val Met Trp Thr His Ser Met Lys Thr Leu Thr Ser Pro Arg Arg
 195 200 205

Leu Arg Asn Pro Lys Lys Pro Gln Val Lys Ala Arg Val Trp His Pro
 210 215 220

Asp Phe Phe Arg His Val Cys Ser Gly
 225 230

<210> 2079

<211> 1368

<212> DNA

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gca gtg tct tca ttc ctt cca gct gca gtc att gag tta gat cca gga	787
Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile Glu Leu Asp Pro Gly	
215 220 225	
tta ggt gct gca tta gcg ggt att att tta tcc att acc ggt ggt tct	835
Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser Ile Thr Gly Gly Ser	
230 235 240 245	
tca atg gtg ttc cgc tac ctg tcc ggc gtt atc gct gac cgc cgc ggt	883
Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile Ala Asp Arg Arg Gly	
250 255 260	
gtg cct ggt acc acg atg att cct gct cag atc att ggg ttc tta ggt	931
Val Pro Gly Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly	
265 270 275	
gtc gtt tta atc acc gtc aca atc ttc caa ggc tgg tcc gtg tgg ctt	979
Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly Trp Ser Val Trp Leu	
280 285 290	
ttg att ata ggt gca gtg atg ttt ggt ggt gct ttt ggc atg gtg caa	1027
Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala Phe Gly Met Val Gln	
295 300 305	
aac gaa gcg ttg ctt tca atg ttt ttc cgg ctt cct cgc act aga gtc	1075
Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu Pro Arg Thr Arg Val	
310 315 320 325	
tcc gaa gcc tcc gcc atc tgg aat atc gcc ttt gat tcg gga aca gga	1123
Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe Asp Ser Gly Thr Gly	
330 335 340	
atc gga agc ttc ctc ctt ggc ata gtt gcc gca tcg ctt gct tac agt	1171
Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala Ser Leu Ala Tyr Ser	
345 350 355	
ggg gct ttt ggt tcc gga gcc gtg gtg att ttg ttt gga atc gtt ttg	1219
Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu Phe Gly Ile Val Leu	
360 365 370	
acc acc gcc gat cga atc att ggg cgg cac cgc att act gaa tac aac	1267
Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg Ile Thr Glu Tyr Asn	
375 380 385	
aac acc cgc gcg cgt ttg cgc cag gtg cca gtc gct cgg cgt gca gtg	1315
Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val Ala Arg Arg Ala Val	
390 395 400 405	
caa ggg ctg cgc aac agg cgc aaa gat cgc taaaacgctt ttcgacgcc	1365
Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg	
410 415	
ccc	1368

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 2080

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Ala Val Ala Gly Ala Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile
35 40 45
Thr Gln Ile Phe Thr Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro
50 55 60
Val Met Ala Phe Ala Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr
65 70 75 80
Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
85 90 95
Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
100 105 110
Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
115 120 125
Val Phe Ile Gly Leu Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala
130 135 140
Leu Gly Asp Gln Phe Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val
145 150 155 160
Ile Ala Leu Val Ala Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys
165 170 175
Ala Ala Ala Lys Gln Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val
180 185 190
Ser Thr Trp Lys Leu Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu
195 200 205
Ser Met Thr Phe Gly Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile
210 215 220
Glu Leu Asp Pro Gly Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser
225 230 235 240
Ile Thr Gly Gly Ser Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile
245 250 255
Ala Asp Arg Arg Gly Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile
260 265 270
Ile Gly Phe Leu Gly Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly
275 280 285
Trp Ser Val Trp Leu Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala
290 295 300

Phe Gly Met Val Gln Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu
 305 310 315 320
 Pro Arg Thr Arg Val Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe
 325 330 335
 Asp Ser Gly Thr Gly Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala
 340 345 350
 Ser Leu Ala Tyr Ser Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu
 355 360 365
 Phe Gly Ile Val Leu Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg
 370 375 380
 Ile Thr Glu Tyr Asn Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val
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 Ala Arg Arg Ala Val Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
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<210> 2081

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA01103

<400> 2081

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 Met Asn Ser Ser Pro
 1 5
 atc tct gat atg gtc act gcg gct gtg cag aac gaa cca gat gcg ggc 163
 Ile Ser Asp Met Val Thr Ala Ala Val Gln Asn Glu Pro Asp Ala Gly
 10 15 20
 gac cga tgg ttt att tat ggt ttg ttc ctc atc gcc ggg ctt ttc ttt 211
 Asp Arg Trp Phe Ile Tyr Gly Leu Phe Leu Ile Ala Gly Leu Phe Phe
 25 30 35
 ggc ggt gcc tgg tct gca tat aaa tca gaa aac aaa atc ctc atg gtt 259
 Gly Gly Ala Trp Ser Ala Tyr Lys Ser Glu Asn Lys Ile Leu Met Val
 40 45 50
 gca gcc ggc ctc atc gca gtg ctg gca gtg gct gga gga att cta tgg 307
 Ala Ala Gly Leu Ile Ala Val Leu Ala Val Ala Gly Gly Ile Leu Trp
 55 60 65
 ttg ttg gga gag atg act taatttgga tcacgggctt taa 348
 Leu Leu Gly Glu Met Thr
 70 75

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<400> 2082
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Glu Pro Asp Ala Gly Asp Arg Trp Phe Ile Tyr Gly Leu Phe Leu Ile
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Ala Gly Leu Phe Phe Gly Gly Ala Trp Ser Ala Tyr Lys Ser Glu Asn
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Lys Ile Leu Met Val Ala Ala Gly Leu Ile Ala Val Leu Ala Val Ala
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Gly Gly Ile Leu Trp Leu Leu Gly Glu Met Thr
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<222> (101)..(1300)
<223> RXA01107
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												atg	gat	ttc	acc	tct	115
												Met	Asp	Phe	Thr	Ser	
												1				5	
gtg	aat	gat	cga	aac	gtc	cct	gca	ccc	aac	acc	tcc	att	cct	ttc	cca	163	
Val	Asn	Asp	Arg	Asn	Val	Pro	Ala	Pro	Asn	Thr	Ser	Ile	Pro	Phe	Pro		
				10					15					20			
gtt	gac	ctg	aat	cga	gtg	acg	gag	gct	gtt	gat	tcc	ttg	ggc	tac	cac	211	
Val	Asp	Leu	Asn	Arg	Val	Thr	Glu	Ala	Val	Asp	Ser	Leu	Gly	Tyr	His		
				25					30					35			
tat	ttg	agc	tca	gaa	gat	cgc	atc	atc	gtg	ccg	tgg	caa	gat	cac	cgc	259	
Tyr	Leu	Ser	Ser	Glu	Asp	Arg	Ile	Ile	Val	Pro	Trp	Gln	Asp	His	Arg		
				40					45					50			
att	tcg	atg	tac	ttc	agc	cac	gaa	tca	ggg	caa	atg	ctc	acc	atc	ctt	307	
Ile	Ser	Met	Tyr	Phe	Ser	His	Glu	Ser	Gly	Gln	Met	Leu	Thr	Ile	Leu		
				55					60					65			
ggt	cgc	acg	cgc	ctt	aat	ttg	gac	atg	ttt	gcc	atc	aac	gat	gcg	gcg	355	
Gly	Arg	Thr	Arg	Leu	Asn	Leu	Asp	Met	Phe	Ala	Ile	Asn	Asp	Ala	Ala		
				70					75					80	85		
cga	gct	gtc	acc	gaa	tggt	aat	gcc	gaa	cgc	atc	ggg	cca	aca	gcc	ctc	403	
Arg	Ala	Val	Thr	Glu	Trp	Asn	Ala	Glu	Arg	Ile	Gly	Pro	Thr	Ala	Leu		

90										95										100																				
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Val	His	Leu	Gly	Asn	Asp	Gly	Glu	Val	Glu	Leu	Lys	Phe	Arg	Thr	Thr																									
105										110										115																				
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Ile	Cys	Ile	Asp	Glu	Gly	Leu	Ser	Thr	Gln	Gln	Leu	Arg	Gln	Phe	Ile																									
120										125										130																				
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Asn	Leu	Ser	Leu	Asp	Thr	Thr	Ala	Met	Ala	Val	Thr	Tyr	Ile	Leu	Glu																									
135										140										145																				
cgt	ttt	tca	gaa	ctt	aac	ttc	agc	gac	acc	gga	agc	cct	gac	gac	acg	595																								
Arg	Phe	Ser	Glu	Leu	Asn	Phe	Ser	Asp	Thr	Gly	Ser	Pro	Asp	Asp	Thr																									
150										155										160										165										
aac	aat	gcc	gat	gaa	ctc	agc	gac	gaa	caa	gac	caa	gca	gat	ctc	gta	643																								
Asn	Asn	Ala	Asp	Glu	Leu	Ser	Asp	Glu	Gln	Asp	Gln	Ala	Asp	Leu	Val																									
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Glu	Lys	Ile	Arg	Gly	Leu	Tyr	Val	Pro	Thr	Pro	Val	Glu	Glu	Leu	Ile																									
185										190										195																				
gaa	tcc	cta	gaa	gac	gca	gag	tgg	gaa	gaa	tca	gac	atg	gca	gac	gag	739																								
Glu	Ser	Leu	Glu	Asp	Ala	Glu	Trp	Glu	Glu	Ser	Asp	Met	Ala	Asp	Glu																									
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Asp	Ala	Glu	Asp	Asp	Tyr	Leu	Asp	Asp	Asp	Ser	Glu	Ile	Glu	Trp	Glu																									
215										220										225																				
aca	gac	gat	gac	tac	ttc	gaa	cct	gaa	gaa	gtc	gac	atg	gac	gaa	ctc	835																								
Thr	Asp	Asp	Asp	Tyr	Phe	Glu	Pro	Glu	Glu	Val	Asp	Met	Asp	Glu	Leu																									
230										235										240										245										
ctc	aac	ggt	ttc	ctc	gaa	gat	tct	gac	atc	ccc	cag	gaa	gtc	acc	ttg	883																								
Leu	Asn	Gly	Phe	Leu	Glu	Asp	Ser	Asp	Ile	Pro	Gln	Glu	Val	Thr	Leu																									
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Glu	Arg	Ile	Arg	Ala	Gln	Leu	His	Ala	Ile	Gly	Val	Val	Lys	Thr	Ser																									
265										270										275																				
ggc	gaa	gac	gat	ttc	atc	atc	gcg	tgg	atc	aac	gaa	gtg	ttt	tta	ggc	979																								
Gly	Glu	Asp	Asp	Phe	Ile	Ile	Ala	Trp	Ile	Asn	Glu	Val	Phe	Leu	Gly																									
280										285										290																				
ttc	ttc	gtt	gat	aat	ggc	ccc	act	ttc	ctg	gtg	aaa	ggt	cac	tgg	gat	1027																								
Phe	Phe	Val	Asp	Asn	Gly	Pro	Thr	Phe	Leu	Val	Lys	Gly	His	Trp	Asp																									
295										300										305																				
ccc	agc	atg	gac	ccc	aca	cgc	gac	ttc	atg	aaa	ctg	ttc	atg	atg	tgc	1075																								
Pro	Ser	Met	Asp	Pro	Thr	Arg	Asp	Phe	Met	Lys	Leu	Phe	Met	Met	Cys																									
310										315										320										325										
aat	cag	tgg	aac	gaa	aac	tct	ctg	act	acc	aaa	gct	ttt	tgc	cat	act	1123																								
Asn	Gln	Trp	Asn	Glu	Asn	Ser	Leu	Thr	Thr	Lys	Ala	Phe	Cys	His	Thr																									
330										335										340																				

Val Glu Glu Leu Ile Glu Ser Leu Glu Asp Ala Glu Trp Glu Glu Ser
 195 200 205

Asp Met Ala Asp Glu Asp Ala Glu Asp Asp Tyr Leu Asp Asp Asp Ser
 210 215 220

Glu Ile Glu Trp Glu Thr Asp Asp Asp Tyr Phe Glu Pro Glu Glu Val
 225 230 235 240

Asp Met Asp Glu Leu Leu Asn Gly Phe Leu Glu Asp Ser Asp Ile Pro
 245 250 255

Gln Glu Val Thr Leu Glu Arg Ile Arg Ala Gln Leu His Ala Ile Gly
 260 265 270

Val Val Lys Thr Ser Gly Glu Asp Asp Phe Ile Ile Ala Trp Ile Asn
 275 280 285

Glu Val Phe Leu Gly Phe Phe Val Asp Asn Gly Pro Thr Phe Leu Val
 290 295 300

Lys Gly His Trp Asp Pro Ser Met Asp Pro Thr Arg Asp Phe Met Lys
 305 310 315 320

Leu Phe Met Met Cys Asn Gln Trp Asn Glu Asn Ser Leu Thr Thr Lys
 325 330 335

Ala Phe Cys His Thr Asp Asp Lys Gly Leu Gln Val Arg Val Glu Phe
 340 345 350

Ala Val Ser Val Ala Glu Gly Leu Asn Asp Asp Gln Leu Gln His Asn
 355 360 365

Ile Ala Leu Ser Ile His His Ile Leu Gln Ala Ile Asp Ser Ile Ser
 370 375 380

Thr Glu Ala Thr Gly Ser Ser Thr Val Glu Trp Pro Glu Lys Asn Arg
 385 390 395 400

<210> 2085

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01108

<400> 2085

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 Met Thr Tyr Pro Gly
 1 5

atc acc tct gac cac aat cct tat gat gga tac aca ggc gat gac ggg 163
 Ile Thr Ser Asp His Asn Pro Tyr Asp Gly Tyr Thr Gly Asp Asp Gly
 10 15 20

gcc gga aac aag cgc aac ctc cca aac cga aag aaa ata aac aaa tcg 211
 Ala Gly Asn Lys Arg Asn Leu Pro Asn Arg Lys Lys Ile Asn Lys Ser
 25 30 35

gtg gga gtt tac gct ggt gtg ttt gcc cta aca ttg gct tta tac gcc 259
 Val Gly Val Tyr Ala Gly Val Phe Ala Leu Thr Leu Ala Leu Tyr Ala
 40 45 50

att ggg gga gcc gca tgg gga ctg ctc cga ccc act tat acc gct tat 307
 Ile Gly Gly Ala Ala Trp Gly Leu Leu Arg Pro Thr Tyr Thr Ala Tyr
 55 60 65

gtt gaa gac gct gaa aca gcc tcc ata gcg gtg gaa acc aac act tct 355
 Val Glu Asp Ala Glu Thr Ala Ser Ile Ala Val Glu Thr Asn Thr Ser
 70 75 80 85

ttt gcc ggc tat gcc tgg ttt gcg atc gcc acc ggt gtg ctt gca gca 403
 Phe Ala Gly Tyr Ala Trp Phe Ala Ile Ala Thr Gly Val Leu Ala Ala
 90 95 100

gca atc gca tta ttc gtt ttc ctg cgc acc cct caa cat cga ggc cca 451
 Ala Ile Ala Leu Phe Val Phe Leu Arg Thr Pro Gln His Arg Gly Pro
 105 110 115

gtt atg ctc cta tgg ctg gga att gta tct atc gca ggt tcc gtg gca 499
 Val Met Leu Leu Trp Leu Gly Ile Val Ser Ile Ala Gly Ser Val Ala
 120 125 130

ttc ctg gtg ttt gga aac gtg gcc tcg acg atg ctt cat ggt tca cca 547
 Phe Leu Val Phe Gly Asn Val Ala Ser Thr Met Leu His Gly Ser Pro
 135 140 145

tct gat tac gcc tca gcg atc ggt gcg tct ttc cag gta gca ccc act 595
 Ser Asp Tyr Ala Ser Ala Ile Gly Ala Ser Phe Gln Val Ala Pro Thr
 150 155 160 165

att acc cct ggt gtt gcg ttt ggg gtc gct cca ttt ttg agt gtg tgc 643
 Ile Thr Pro Gly Val Ala Phe Gly Val Ala Pro Phe Leu Ser Val Cys
 170 175 180

atg tat tgg tgc gcg gca ttt gtg aca cct gaa gaa gag ata gac cag 691
 Met Tyr Trp Cys Ala Ala Phe Val Thr Pro Glu Glu Glu Ile Asp Gln
 185 190 195

gac gac gca ggc cag ggg act tcg aaa gca tcg ggg tct gag atg act 739
 Asp Asp Ala Gly Gln Gly Thr Ser Lys Ala Ser Gly Ser Glu Met Thr
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 Gly Ala Ser Gly
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<210> 2086

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 2086

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Leu Thr Ala Cys Gly Ser Asp Ser Ser Asp Thr Glu Ala Ala Ser Ser			
25	30	35	
agc gca gcg acg acg aca aat tct tcc tca tcc agc gca gcg acc tcg			259
Ser Ala Ala Thr Thr Thr Asn Ser Ser Ser Ser Ser Ala Ala Thr Ser			
40	45	50	
gcg gaa gca gca gaa acc acc tcg tcc gaa tct gaa tct tcc gaa gca			307
Ala Glu Ala Ala Glu Thr Thr Ser Ser Glu Ser Glu Ser Ser Glu Ala			
55	60	65	
aca acc att aac gaa gag cag caa gca cag ctt gat gta ctg tct caa			355
Thr Thr Ile Asn Glu Glu Gln Gln Ala Gln Leu Asp Val Leu Ser Gln			
70	75	80	85
gag ctg tct gag aac cca att acc ttc gct gaa gct gcg cca gtt gaa			403
Glu Leu Ser Glu Asn Pro Ile Thr Phe Ala Glu Ala Ala Pro Val Glu			
90	95	100	
aac ggc gag acc gct tcc cca gaa gac aca gct gcc atc gag gct ctg			451
Asn Gly Glu Thr Ala Ser Pro Glu Asp Thr Ala Ala Ile Glu Ala Leu			
105	110	115	
gtt cgc gga tac act gac acc aac acc ttg cgt agc tcc ctt gcg tac			499
Val Arg Gly Tyr Thr Asp Thr Asn Thr Leu Arg Ser Ser Leu Ala Tyr			
120	125	130	
acc atc aac aac acc tgc acc cgc gtt ctt gaa gcc agc ggc gct gac			547
Thr Ile Asn Asn Thr Cys Thr Arg Val Leu Glu Ala Ser Gly Ala Asp			
135	140	145	
gct acc cag ctt gat ctc aac acc atc cct gat atc cca ctg ggt ggc			595
Ala Thr Gln Leu Asp Leu Asn Thr Ile Pro Asp Ile Pro Leu Gly Gly			
150	155	160	165
gaa ggc acc gga act gtt gat tcc atc acc gat gtt gtg gtc aac ggc			643
Glu Gly Thr Gly Thr Val Asp Ser Ile Thr Asp Val Val Val Asn Gly			
170	175	180	
cag gaa gca tcc gca tgg gtc gta gca acc gcc ggt gga acc acc gac			691
Gln Glu Ala Ser Ala Trp Val Val Ala Thr Ala Gly Thr Thr Asp			
185	190	195	
tct gca acc cag cgc ttc ttc aac gaa ggt ggc cag tgg aag ttc tgc			739
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Asp			

<210> 2088

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 2088

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 35 40 45
 Ser Ala Ala Thr Ser Ala Glu Ala Ala Glu Thr Thr Ser Ser Glu Ser
 50 55 60
 Glu Ser Ser Glu Ala Thr Thr Ile Asn Glu Glu Gln Gln Ala Gln Leu
 65 70 75 80
 Asp Val Leu Ser Gln Glu Leu Ser Glu Asn Pro Ile Thr Phe Ala Glu
 85 90 95
 Ala Ala Pro Val Glu Asn Gly Glu Thr Ala Ser Pro Glu Asp Thr Ala
 100 105 110
 Ala Ile Glu Ala Leu Val Arg Gly Tyr Thr Asp Thr Asn Thr Leu Arg
 115 120 125
 Ser Ser Leu Ala Tyr Thr Ile Asn Asn Thr Cys Thr Arg Val Leu Glu
 130 135 140
 Ala Ser Gly Ala Asp Ala Thr Gln Leu Asp Leu Asn Thr Ile Pro Asp
 145 150 155 160
 Ile Pro Leu Gly Gly Glu Gly Thr Gly Thr Val Asp Ser Ile Thr Asp
 165 170 175
 Val Val Val Asn Gly Gln Glu Ala Ser Ala Trp Val Val Ala Thr Ala
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 Gly Gly Thr Thr Asp Ser Ala Thr Gln Arg Phe Phe Asn Glu Gly Gly
 195 200 205
 Gln Trp Lys Phe Cys Asp
 210

<210> 2089

<211> 1053

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1030)

<223> RXA01119

<400> 2089

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 Leu Ala Gly Val Ile
 1 5

acc ggc ttt gcc atc atc ctg tcg gtt atc ggc gtt gga ttt ctt ctg 163

Thr	Gly	Phe	Ala	Ile	Ile	Leu	Ser	Val	Ile	Gly	Val	Gly	Phe	Leu	Leu		
				10					15					20			
gca	aag	ctg	ggg	gtc	atc	aat	gat	gac	aaa	cag	cgc	ttg	gtg	tta	aac	211	
Ala	Lys	Leu	Gly	Val	Ile	Asn	Asp	Asp	Lys	Gln	Arg	Leu	Val	Leu	Asn		
			25					30					35				
cgc	att	gct	ttt	tat	gcg	gca	act	cca	gcg	ctg	ctt	ttc	aat	gtc	gtt	259	
Arg	Ile	Ala	Phe	Tyr	Ala	Ala	Thr	Pro	Ala	Leu	Leu	Phe	Asn	Val	Val		
		40					45					50					
gcc	cga	tca	gat	ccc	agc	gcg	ttg	atc	tca	ccg	gtc	att	gtg	gtg	aca	307	
Ala	Arg	Ser	Asp	Pro	Ser	Ala	Leu	Ile	Ser	Pro	Val	Ile	Val	Val	Thr		
	55					60					65						
ttt	gtg	gcc	acg	atc	gtc	aca	gca	gct	gtg	tac	tgc	gtg	att	tcg	gcg	355	
Phe	Val	Ala	Thr	Ile	Val	Thr	Ala	Ala	Val	Tyr	Cys	Val	Ile	Ser	Ala		
	70				75				80						85		
att	ttc	ttt	aag	aag	gat	atc	gcc	act	acg	gcg	aca	gga	gct	gcg	gct	403	
Ile	Phe	Phe	Lys	Lys	Asp	Ile	Ala	Thr	Thr	Ala	Thr	Gly	Ala	Ala	Ala		
				90					95					100			
tct	gcc	tac	gtg	aac	tcc	aac	aac	att	ggc	ctg	ccg	gtg	tct	att	tat	451	
Ser	Ala	Tyr	Val	Asn	Ser	Asn	Asn	Ile	Gly	Leu	Pro	Val	Ser	Ile	Tyr		
			105					110					115				
gtg	ctg	gga	aca	ggc	gca	tat	gtg	gca	ccg	att	ctg	gtc	atg	cag	atg	499	
Val	Leu	Gly	Thr	Gly	Ala	Tyr	Val	Ala	Pro	Ile	Leu	Val	Met	Gln	Met		
		120					125					130					
gtg	att	ttc	gcg	ccc	atg	atc	ctg	gcc	gcg	ctg	acc	tct	ggt	gat	gtg	547	
Val	Ile	Phe	Ala	Pro	Met	Ile	Leu	Ala	Ala	Leu	Thr	Ser	Gly	Asp	Val		
	135					140					145						
aaa	ggc	tcg	cgc	ggg	caa	aaa	ata	tgg	gct	gcg	gtg	aaa	ggt	tca	ctg	595	
Lys	Gly	Ser	Arg	Gly	Gln	Lys	Ile	Trp	Ala	Ala	Val	Lys	Gly	Ser	Leu		
	150				155				160						165		
ctc	agc	cca	att	gtg	ttg	gcc	tct	atc	gcg	ggc	ctg	atc	gtg	tgt	ctg	643	
Leu	Ser	Pro	Ile	Val	Leu	Ala	Ser	Ile	Ala	Gly	Leu	Ile	Val	Cys	Leu		
				170					175					180			
tta	gaa	att	cag	ctg	cca	gcc	gca	gtc	atg	gaa	ccc	acc	atc	att	ttg	691	
Leu	Glu	Ile	Gln	Leu	Pro	Ala	Ala	Val	Met	Glu	Pro	Thr	Ile	Ile	Leu		
			185					190					195				
ggc	ggc	gca	tcc	att	ccg	ttg	att	ctg	atg	agc	ttc	ggc	gca	tca	ttg	739	
Gly	Gly	Ala	Ser	Ile	Pro	Leu	Ile	Leu	Met	Ser	Phe	Gly	Ala	Ser	Leu		
		200					205					210					
ccc	tca	acc	aac	gtg	ctg	gct	tcc	aag	gcg	gat	cgc	ccc	agc	ggt	ctt	787	
Pro	Ser	Thr	Asn	Val	Leu	Ala	Ser	Lys	Ala	Asp	Arg	Pro	Ser	Val	Leu		
		215				220					225						
act	gct	act	gcg	ata	aaa	att	gtg	ggt	atg	ccc	gcc	atc	act	tgg	ctg	835	
Thr	Ala	Thr	Ala	Ile	Lys	Ile	Val	Gly	Met	Pro	Ala	Ile	Thr	Trp	Leu		
	230				235				240						245		
atc	gcc	aag	gcg	ttt	ggt	ctg	gag	ggc	gat	tac	ctc	tac	gcc	gct	gtt	883	
Ile	Ala	Lys	Ala	Phe	Gly	Leu	Glu	Gly	Asp	Tyr	Leu	Tyr	Ala	Ala	Val		

250	255	260	
att ttg gcg gcg ctg ccc gcc gcg cag aat gtg tac aac tac gcg gcg			931
Ile Leu Ala Ala Leu Pro Ala Ala Gln Asn Val Tyr Asn Tyr Ala Ala			
265	270	275	
acg tac cgc aag ggc gag atc gtc gcc cgc gat acg gtc ttc ctc acc			979
Thr Tyr Arg Lys Gly Glu Ile Val Ala Arg Asp Thr Val Phe Leu Thr			
280	285	290	
acg ttc cta gcg ctg ctg ggc atg cta gga atc gcg gcc cta ttt ggt			1027
Thr Phe Leu Ala Leu Leu Gly Met Leu Gly Ile Ala Ala Leu Phe Gly			
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cgc tagggcttca ggctgctttt cga			1053
Arg			
310			
<210> 2090			
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<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2090			
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Val Gly Phe Leu Leu Ala Lys Leu Gly Val Ile Asn Asp Asp Lys Gln			
20	25	30	
Arg Leu Val Leu Asn Arg Ile Ala Phe Tyr Ala Ala Thr Pro Ala Leu			
35	40	45	
Leu Phe Asn Val Val Ala Arg Ser Asp Pro Ser Ala Leu Ile Ser Pro			
50	55	60	
Val Ile Val Val Thr Phe Val Ala Thr Ile Val Thr Ala Ala Val Tyr			
65	70	75	80
Cys Val Ile Ser Ala Ile Phe Phe Lys Lys Asp Ile Ala Thr Thr Ala			
85	90	95	
Thr Gly Ala Ala Ala Ser Ala Tyr Val Asn Ser Asn Asn Ile Gly Leu			
100	105	110	
Pro Val Ser Ile Tyr Val Leu Gly Thr Gly Ala Tyr Val Ala Pro Ile			
115	120	125	
Leu Val Met Gln Met Val Ile Phe Ala Pro Met Ile Leu Ala Ala Leu			
130	135	140	
Thr Ser Gly Asp Val Lys Gly Ser Arg Gly Gln Lys Ile Trp Ala Ala			
145	150	155	160
Val Lys Gly Ser Leu Leu Ser Pro Ile Val Leu Ala Ser Ile Ala Gly			
165	170	175	
Leu Ile Val Cys Leu Leu Glu Ile Gln Leu Pro Ala Ala Val Met Glu			
180	185	190	

Pro Thr Ile Ile Leu Gly Gly Ala Ser Ile Pro Leu Ile Leu Met Ser
 195 200 205

Phe Gly Ala Ser Leu Pro Ser Thr Asn Val Leu Ala Ser Lys Ala Asp
 210 215 220

Arg Pro Ser Val Leu Thr Ala Thr Ala Ile Lys Ile Val Gly Met Pro
 225 230 235 240

Ala Ile Thr Trp Leu Ile Ala Lys Ala Phe Gly Leu Glu Gly Asp Tyr
 245 250 255

Leu Tyr Ala Ala Val Ile Leu Ala Ala Leu Pro Ala Ala Gln Asn Val
 260 265 270

Tyr Asn Tyr Ala Ala Thr Tyr Arg Lys Gly Glu Ile Val Ala Arg Asp
 275 280 285

Thr Val Phe Leu Thr Thr Phe Leu Ala Leu Leu Gly Met Leu Gly Ile
 290 295 300

Ala Ala Leu Phe Gly Arg
 305 310

<210> 2091
 <211> 645
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(622)
 <223> RXA01122

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ggcctctact aagccccgaa gttgaaggga aactcccca atg ccg ttt cca gca 115
 Met Pro Phe Pro Ala
 1 5

ctg ttg ttg ccg ctg att ttc tgg aca gga att gca gct ttg tcc tct 163
 Leu Leu Leu Pro Leu Ile Phe Trp Thr Gly Ile Ala Ala Leu Ser Ser
 10 15 20

tgg gcg gtc agc cgt gca ctt ccg ctg cgc gcc gat aat tcc att gag 211
 Trp Ala Val Ser Arg Ala Leu Pro Leu Arg Ala Asp Asn Ser Ile Glu
 25 30 35

att gat gcg ccg gtg gaa aag gtc tgg gat ttc atc gag gag acc aac 259
 Ile Asp Ala Pro Val Glu Lys Val Trp Asp Phe Ile Glu Glu Thr Asn
 40 45 50

cgc gtg ccg gag tgg aat gag cac att ctg tac gtg cag gcg cct ggt 307
 Arg Val Pro Glu Trp Asn Glu His Ile Leu Tyr Val Gln Ala Pro Gly
 55 60 65

gag atc gag cag ggc atg aag ctc aag atg aaa aca agg cac cca gag 355
 Glu Ile Glu Gln Gly Met Lys Leu Lys Met Lys Thr Arg His Pro Glu
 70 75 80 85

acc aat cgc ctc act ttg aag ttt cgc ccc acc atc gac gtg ctg cgt 403
 Thr Asn Arg Leu Thr Leu Lys Phe Arg Pro Thr Ile Asp Val Leu Arg
 90 95 100
 cca cac cgt gaa ttg acg tgg tcc acc aaa att gtt gcg cgt tgg ctg 451
 Pro His Arg Glu Leu Thr Trp Ser Thr Lys Ile Val Ala Arg Trp Leu
 105 110 115
 ctc acc gtc acc gac acg atc gag ctg aag cct ttg gaa gat ggt cgc 499
 Leu Thr Val Thr Asp Thr Ile Glu Leu Lys Pro Leu Glu Asp Gly Arg
 120 125 130
 act gag gtg gat caa tca atg tcc ttt agt ggc gta cta tcc ccc gga 547
 Thr Glu Val Asp Gln Ser Met Ser Phe Ser Gly Val Leu Ser Pro Gly
 135 140 145
 gtg ccc ttt ttg gcc agc atc agc agg atc aaa gag aac tca aac cgc 595
 Val Pro Phe Leu Ala Ser Ile Ser Arg Ile Lys Glu Asn Ser Asn Arg
 150 155 160 165
 cag ttg aaa gca ctg atc gaa gcc gag taaacctcca acccctacat 642
 Gln Leu Lys Ala Leu Ile Glu Ala Glu
 170
 aac 645

<210> 2092

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 2092

Met Pro Phe Pro Ala Leu Leu Leu Pro Leu Ile Phe Trp Thr Gly Ile
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 Ala Ala Leu Ser Ser Trp Ala Val Ser Arg Ala Leu Pro Leu Arg Ala
 20 25 30
 Asp Asn Ser Ile Glu Ile Asp Ala Pro Val Glu Lys Val Trp Asp Phe
 35 40 45
 Ile Glu Glu Thr Asn Arg Val Pro Glu Trp Asn Glu His Ile Leu Tyr
 50 55 60
 Val Gln Ala Pro Gly Glu Ile Glu Gln Gly Met Lys Leu Lys Met Lys
 65 70 75 80
 Thr Arg His Pro Glu Thr Asn Arg Leu Thr Leu Lys Phe Arg Pro Thr
 85 90 95
 Ile Asp Val Leu Arg Pro His Arg Glu Leu Thr Trp Ser Thr Lys Ile
 100 105 110
 Val Ala Arg Trp Leu Leu Thr Val Thr Asp Thr Ile Glu Leu Lys Pro
 115 120 125
 Leu Glu Asp Gly Arg Thr Glu Val Asp Gln Ser Met Ser Phe Ser Gly
 130 135 140

Val Leu Ser Pro Gly Val Pro Phe Leu Ala Ser Ile Ser Arg Ile Lys
 145 150 155 160

Glu Asn Ser Asn Arg Gln Leu Lys Ala Leu Ile Glu Ala Glu
 165 170

<210> 2093

<211> 570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXA01123

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gtggcggttg gtggaaacac gtggctgggc gaatgtgagc atg cga acc ctg gcc 115
 Met Arg Thr Leu Ala
 1 5

gcg gag cta aat atc aag gcg ccg tcg ctg tac aag cat gta aaa acg 163
 Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr
 10 15 20

cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg 211
 Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu
 25 30 35

ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg 259
 Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala
 40 45 50

gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc 307
 Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu
 55 60 65

acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act 355
 Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr
 70 75 80 85

tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag 403
 Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys
 90 95 100

ggg caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc 451
 Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile
 105 110 115

gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg 499
 Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val
 120 125 130

tgg gag atc ggc gcg cgg gca ttt gac aca caa gta ttc gac caa ggc 547
 Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly
 135 140 145

tgagcaaaaa ggcgctaagc tgt 570

<210> 2094
 <211> 149
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2094
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 1 5 10 15
 Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys
 20 25 30
 Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val
 35 40 45
 Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn
 50 55 60
 Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro
 65 70 75 80
 Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly
 85 90 95
 His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met
 100 105 110
 Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser
 115 120 125
 Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln
 130 135 140
 Val Phe Asp Gln Gly
 145

<210> 2095
 <211> 302
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(279)
 <223> RXA01127

<400> 2095
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 Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly Thr Asn
 1 5 10 15
 cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc gca ggc 96
 Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile Ala Gly
 20 25 30
 cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg atg ctg 144
 Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala Met Leu
 35 40 45

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ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa aca gcc 192
Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu Thr Ala
   50                55                60

atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att tct acc 240
Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile Ser Thr
   65                70                75                80

act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc taaatttcaa 289
Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
           85                90

cgccgacccc ctt 302

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<210> 2096
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 2096
Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly Thr Asn
  1                5                10                15

Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile Ala Gly
          20                25                30

Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala Met Leu
   35                40                45

Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu Thr Ala
   50                55                60

Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile Ser Thr
   65                70                75                80

Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
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<210> 2097
 <211> 1989
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1966)
 <223> RXA01129

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cgaatgcagg atttcgagac aatgaggcag tttttctttt atg gtt aat ctc atg 115
                               Met Val Asn Leu Met
                               1                5

tcg gtc gaa ctc gaa gaa atc cgc gat ttc tta gca gga ttt gaa cct 163
Ser Val Glu Leu Glu Glu Ile Arg Asp Phe Leu Ala Gly Phe Glu Pro
           10                15                20

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ttc gcg cag cta cca gcc gag gaa cta gat cag tta cct gga aaa atg	211
Phe Ala Gln Leu Pro Ala Glu Glu Leu Asp Gln Leu Pro Gly Lys Met	
25 30 35	
agc ttg cgc tat ttt cgg cgt ggg gaa gag atc atc cca att ggt gtg	259
Ser Leu Arg Tyr Phe Arg Arg Gly Glu Glu Ile Ile Pro Ile Gly Val	
40 45 50	
ccc aat cat tac atg ggg gta atc aga tcg ggt gcc att gat gtt ctt	307
Pro Asn His Tyr Met Gly Val Ile Arg Ser Gly Ala Ile Asp Val Leu	
55 60 65	
gat cag gag ggc gta ctg ctg gat cgc cgt gac gcg ggg cgc tcg ttt	355
Asp Gln Glu Gly Val Leu Leu Asp Arg Arg Asp Ala Gly Arg Ser Phe	
70 75 80 85	
ggc tat tcc acg atg ggg cca gaa cga aat tct cgg tac cgt atg gtt	403
Gly Tyr Ser Thr Met Gly Pro Glu Arg Asn Ser Arg Tyr Arg Met Val	
90 95 100	
gcc gtg gaa gat tcc ttg gtg ttg cgt ctg ggg cgt gat gat ttt gat	451
Ala Val Glu Asp Ser Leu Val Leu Arg Leu Gly Arg Asp Asp Phe Asp	
105 110 115	
gag tta gcc aag cgc aac cct gat ctg aac cgt tac tac tcc agc tgg	499
Glu Leu Ala Lys Arg Asn Pro Asp Leu Asn Arg Tyr Tyr Ser Ser Trp	
120 125 130	
tcg aag cgt atc cgc gcc gct gct gat caa ttg cgc caa gaa tct agt	547
Ser Lys Arg Ile Arg Ala Ala Ala Asp Gln Leu Arg Gln Glu Ser Ser	
135 140 145	
tcg aag gtg ctg cgc acg aag ttg ggg gag ttc aag atc gcc aac ccg	595
Ser Lys Val Leu Arg Thr Lys Leu Gly Glu Phe Lys Ile Ala Asn Pro	
150 155 160 165	
att tcc tgc agc ccg gac acc acg atc atg gat gct gcc atc aag atg	643
Ile Ser Cys Ser Pro Asp Thr Thr Ile Met Asp Ala Ala Ile Lys Met	
170 175 180	
cat gag ttc ggg gtg tct tcg ttg ctg gtg cag atc gat ggg gaa ctc	691
His Glu Phe Gly Val Ser Ser Leu Leu Val Gln Ile Asp Gly Glu Leu	
185 190 195	
aaa ggc atc atc acc gat cac tat atg cgc agc agg gtg gtg gcg aag	739
Lys Gly Ile Ile Thr Asp His Tyr Met Arg Ser Arg Val Val Ala Lys	
200 205 210	
cat ttg gat att cag ctg ccg gtc tct gag gtc atg acg gtg gat ccg	787
His Leu Asp Ile Gln Leu Pro Val Ser Glu Val Met Thr Val Asp Pro	
215 220 225	
cgt tgc gcg acc tcg cag ggg ttg gct ttt gag gcc atg ttg ttg atg	835
Arg Cys Ala Thr Ser Gln Gly Leu Ala Phe Glu Ala Met Leu Leu Met	
230 235 240 245	
tcg gag ctg cgc att cac cac ttg ccg att gtg gat gat ggc caa atc	883
Ser Glu Leu Arg Ile His His Leu Pro Ile Val Asp Asp Gly Gln Ile	
250 255 260	

tcc ggc atc gtc act gca gct gac atc atg cgc ttg ctg cgc cac gat	931
Ser Gly Ile Val Thr Ala Ala Asp Ile Met Arg Leu Leu Arg His Asp	
265 270 275	
ccg att tac ctc act gcg gat ctg tcg cga aaa aat acc gtg gag gaa	979
Pro Ile Tyr Leu Thr Ala Asp Leu Ser Arg Lys Asn Thr Val Glu Glu	
280 285 290	
ttg gcc aac acc ttc cag tcg gca gcg gag gtg gct tcg aga ttt att	1027
Leu Ala Asn Thr Phe Gln Ser Ala Ala Glu Val Ala Ser Arg Phe Ile	
295 300 305	
gat cgg gga gct tct gcg gaa gaa gtc agt agc ttg ctc acc gtg gct	1075
Asp Arg Gly Ala Ser Ala Glu Glu Val Ser Ser Leu Leu Thr Val Ala	
310 315 320 325	
gcg gat tct ttg gca aga agg ctc ctt gtg ctg gcg gag cgg aaa ttt	1123
Ala Asp Ser Leu Ala Arg Arg Leu Leu Val Leu Ala Glu Arg Lys Phe	
330 335 340	
ggg gca ccg cca gtt ccg tat tgc ttt gtg gtg gtg ggc tcg cag ggc	1171
Gly Ala Pro Pro Val Pro Tyr Cys Phe Val Val Val Gly Ser Gln Gly	
345 350 355	
agg aaa gaa atg gga ctg gcc tct gat caa gac aat gcc ctt gtt ctg	1219
Arg Lys Glu Met Gly Leu Ala Ser Asp Gln Asp Asn Ala Leu Val Leu	
360 365 370	
gac aat tcc tac aat gac cgc gag cat gga cag tat ttt gca gcg ctg	1267
Asp Asn Ser Tyr Asn Asp Arg Glu His Gly Gln Tyr Phe Ala Ala Leu	
375 380 385	
agt gaa ttc gtg tgc cag ggc ctc gac cgc gca gga cag gtg ctg tgt	1315
Ser Glu Phe Val Cys Gln Gly Leu Asp Arg Ala Gly Gln Val Leu Cys	
390 395 400 405	
ccg ggt gac atg atg gca tcc aat ccg gag tgg cgg aaa act gct gac	1363
Pro Gly Asp Met Met Ala Ser Asn Pro Glu Trp Arg Lys Thr Ala Asp	
410 415 420	
cag tgg atc tcc acc ttc cat tcc tgg att act gcg ccg gag ccg gat	1411
Gln Trp Ile Ser Thr Phe His Ser Trp Ile Thr Ala Pro Glu Pro Asp	
425 430 435	
gcg ttg ctg cat gcc cag aca ttc ttt gat ttc agg gga att tac ggc	1459
Ala Leu Leu His Ala Gln Thr Phe Phe Asp Phe Arg Gly Ile Tyr Gly	
440 445 450	
gac acc gag atg gct aag gat gtc cac caa aat gcg gtg aat atg gcc	1507
Asp Thr Glu Met Ala Lys Asp Val His Gln Asn Ala Val Asn Met Ala	
455 460 465	
agg ggt gcg cgt cgc atg cat gca cac ttg gct agt ctt gcg gcc cgg	1555
Arg Gly Ala Arg Arg Met His Ala His Leu Ala Ser Leu Ala Ala Arg	
470 475 480 485	
cgc gat cct ccg ctg ggg ttt ttc cgt ggt ctt gtg gtg gag cgt tct	1603
Arg Asp Pro Pro Leu Gly Phe Phe Arg Gly Leu Val Val Glu Arg Ser	
490 495 500	
ggg gaa tac ggc gcg acg atg gat att aag aag ggt ggc acc gcg ggc	1651

Gly Glu Tyr Gly Ala Thr Met Asp Ile Lys Lys Gly Gly Thr Ala Gly
 505 510 515
 atc gtg cag atg gcg agg ctg tat gcg ctg gcc acg ggt agt gat gcg 1699
 Ile Val Gln Met Ala Arg Leu Tyr Ala Leu Ala Thr Gly Ser Asp Ala
 520 525 530
 att ggg act cgg gag cgg ttg att gct gcg tcg ggc cat ggt cag gtg 1747
 Ile Gly Thr Arg Glu Arg Leu Ile Ala Ala Ser Gly His Gly Gln Val
 535 540 545
 tcg cgt aag ggt gcg cag gat ttg ttg gat gcc ttt gat ttc tta gcg 1795
 Ser Arg Lys Gly Ala Gln Asp Leu Leu Asp Ala Phe Asp Phe Leu Ala
 550 555 560 565
 gcg atg gcg ttc cag cac cag gcg cgg ttg atc aag gtg ggg gag aag 1843
 Ala Met Ala Phe Gln His Gln Ala Arg Leu Ile Lys Val Gly Glu Lys
 570 575 580
 ccg aac tat cac att gat ccc aag acg ttg ggc aag atg gat cgg gag 1891
 Pro Asn Tyr His Ile Asp Pro Lys Thr Leu Gly Lys Met Asp Arg Glu
 585 590 595
 cat ttg cgc gat gca ttt tcc att att aaa gat atg cag tcg gcg tta 1939
 His Leu Arg Asp Ala Phe Ser Ile Ile Lys Asp Met Gln Ser Ala Leu
 600 605 610
 gct act aaa tat ccg gtg agg aac atc tagtggtggg.gcgtcgaaaa 1986
 Ala Thr Lys Tyr Pro Val Arg Asn Ile
 615 620
 gcg 1989

 <210> 2098
 <211> 622
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 2098
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 Leu Pro Gly Lys Met Ser Leu Arg Tyr Phe Arg Arg Gly Glu Glu Ile
 35 40 45
 Ile Pro Ile Gly Val Pro Asn His Tyr Met Gly Val Ile Arg Ser Gly
 50 55 60
 Ala Ile Asp Val Leu Asp Gln Glu Gly Val Leu Leu Asp Arg Arg Asp
 65 70 75 80
 Ala Gly Arg Ser Phe Gly Tyr Ser Thr Met Gly Pro Glu Arg Asn Ser
 85 90 95
 Arg Tyr Arg Met Val Ala Val Glu Asp Ser Leu Val Leu Arg Leu Gly
 100 105 110

Arg Asp Asp Phe Asp Glu Leu Ala Lys Arg Asn Pro Asp Leu Asn Arg
115 120 125

Tyr Tyr Ser Ser Trp Ser Lys Arg Ile Arg Ala Ala Ala Asp Gln Leu
130 135 140

Arg Gln Glu Ser Ser Ser Lys Val Leu Arg Thr Lys Leu Gly Glu Phe
145 150 155 160

Lys Ile Ala Asn Pro Ile Ser Cys Ser Pro Asp Thr Thr Ile Met Asp
165 170 175

Ala Ala Ile Lys Met His Glu Phe Gly Val Ser Ser Leu Leu Val Gln
180 185 190

Ile Asp Gly Glu Leu Lys Gly Ile Ile Thr Asp His Tyr Met Arg Ser
195 200 205

Arg Val Val Ala Lys His Leu Asp Ile Gln Leu Pro Val Ser Glu Val
210 215 220

Met Thr Val Asp Pro Arg Cys Ala Thr Ser Gln Gly Leu Ala Phe Glu
225 230 235 240

Ala Met Leu Leu Met Ser Glu Leu Arg Ile His His Leu Pro Ile Val
245 250 255

Asp Asp Gly Gln Ile Ser Gly Ile Val Thr Ala Ala Asp Ile Met Arg
260 265 270

Leu Leu Arg His Asp Pro Ile Tyr Leu Thr Ala Asp Leu Ser Arg Lys
275 280 285

Asn Thr Val Glu Glu Leu Ala Asn Thr Phe Gln Ser Ala Ala Glu Val
290 295 300

Ala Ser Arg Phe Ile Asp Arg Gly Ala Ser Ala Glu Glu Val Ser Ser
305 310 315 320

Leu Leu Thr Val Ala Ala Asp Ser Leu Ala Arg Arg Leu Leu Val Leu
325 330 335

Ala Glu Arg Lys Phe Gly Ala Pro Pro Val Pro Tyr Cys Phe Val Val
340 345 350

Val Gly Ser Gln Gly Arg Lys Glu Met Gly Leu Ala Ser Asp Gln Asp
355 360 365

Asn Ala Leu Val Leu Asp Asn Ser Tyr Asn Asp Arg Glu His Gly Gln
370 375 380

Tyr Phe Ala Ala Leu Ser Glu Phe Val Cys Gln Gly Leu Asp Arg Ala
385 390 395 400

Gly Gln Val Leu Cys Pro Gly Asp Met Met Ala Ser Asn Pro Glu Trp
405 410 415

Arg Lys Thr Ala Asp Gln Trp Ile Ser Thr Phe His Ser Trp Ile Thr
420 425 430

Ala Pro Glu Pro Asp Ala Leu Leu His Ala Gln Thr Phe Phe Asp Phe

435	440	445
Arg Gly Ile Tyr Gly Asp Thr Glu Met Ala Lys Asp Val His Gln Asn		
450	455	460
Ala Val Asn Met Ala Arg Gly Ala Arg Arg Met His Ala His Leu Ala		
465	470	475
Ser Leu Ala Ala Arg Arg Asp Pro Pro Leu Gly Phe Phe Arg Gly Leu		
	485	490
Val Val Glu Arg Ser Gly Glu Tyr Gly Ala Thr Met Asp Ile Lys Lys		
	500	505
Gly Gly Thr Ala Gly Ile Val Gln Met Ala Arg Leu Tyr Ala Leu Ala		
	515	520
Thr Gly Ser Asp Ala Ile Gly Thr Arg Glu Arg Leu Ile Ala Ala Ser		
	530	535
Gly His Gly Gln Val Ser Arg Lys Gly Ala Gln Asp Leu Leu Asp Ala		
545	550	555
Phe Asp Phe Leu Ala Ala Met Ala Phe Gln His Gln Ala Arg Leu Ile		
	565	570
Lys Val Gly Glu Lys Pro Asn Tyr His Ile Asp Pro Lys Thr Leu Gly		
	580	585
Lys Met Asp Arg Glu His Leu Arg Asp Ala Phe Ser Ile Ile Lys Asp		
	595	600
Met Gln Ser Ala Leu Ala Thr Lys Tyr Pro Val Arg Asn Ile		
610	615	620

<210> 2099

<211> 990

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXA01131

<400> 2099

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tgggagagaa gatttccctt aagaaagggtt cttaacaacc	atg ccg cct gcg acg	115
	Met Pro Pro Ala Thr	
	1 5	

ctg ttc aat gtt ttg act tca gct gga ctt gac cct cac cag tca ggt	163
Leu Phe Asn Val Leu Thr Ser Ala Gly Leu Asp Pro His Gln Ser Gly	
10 15 20	

gat gcc att gtt gtc gag tct gcc cat ttc aca ttg acg ttc acg tgg	211
Asp Ala Ile Val Val Glu Ser Ala His Phe Thr Leu Thr Phe Thr Trp	
25 30 35	

gat gag tgg ctg cga gct caa gcg acg tgg gtg ggg gag ttg agt gcg	259
Asp Glu Trp Leu Arg Ala Gln Ala Thr Trp Val Gly Glu Leu Ser Ala	
40 45 50	
tcg gat tat gtg cgt tct att gtg gcg att aac tct gcc cat gat gca	307
Ser Asp Tyr Val Arg Ser Ile Val Ala Ile Asn Ser Ala His Asp Ala	
55 60 65	
cgg gca acg ccg aag atg atg ttg gat gcc ccg act ggt ctg aca acg	355
Arg Ala Thr Pro Lys Met Met Leu Asp Ala Pro Thr Gly Leu Thr Thr	
70 75 80 85	
gtg ctt aag gcg gat aag ggt cag ttg cag gcg ttt gcc gtg gag gcg	403
Val Leu Lys Ala Asp Lys Gly Gln Leu Gln Ala Phe Ala Val Glu Ala	
90 95 100	
ctg ccg att ggc gat ggc ctc agc gag gct cag ttg gcg ggg ttt gtg	451
Leu Pro Ile Gly Asp Gly Leu Ser Glu Ala Gln Leu Ala Gly Phe Val	
105 110 115	
gct gcc gcg ttt gat ggc gcc atc gac ctc act cgt gag ttt cat gca	499
Ala Ala Ala Phe Asp Gly Ala Ile Asp Leu Thr Arg Glu Phe His Ala	
120 125 130	
ctt tac ccg gag cgc tcg ccg cag gag cgc ggc gca atg ctc aac att	547
Leu Tyr Pro Glu Arg Ser Pro Gln Glu Arg Gly Ala Met Leu Asn Ile	
135 140 145	
aag ctt gtc gac gcc tcc ccc tct caa aca gtt acg ccc gtg cga gta	595
Lys Leu Val Asp Ala Ser Pro Ser Gln Thr Val Thr Pro Val Arg Val	
150 155 160 165	
gct aac tgg ttc atg gat cag ggg gtg gag gaa gtt cct tat gat gca	643
Ala Asn Trp Phe Met Asp Gln Gly Val Glu Glu Val Pro Tyr Asp Ala	
170 175 180	
gct tct ggg cgc atc agc ttt gag ctg ggt gac acc cca gtg gat gtg	691
Ala Ser Gly Arg Ile Ser Phe Glu Leu Gly Asp Thr Pro Val Asp Val	
185 190 195	
att ttg gat gat ccc gag ttg ttg aag atc caa gcc gtg gtg gtt gct	739
Ile Leu Asp Asp Pro Glu Leu Leu Lys Ile Gln Ala Val Val Val Ala	
200 205 210	
gac cgc gat gtg gaa gcc act gaa gtt tta cat ttg tgt aat cga gcg	787
Asp Arg Asp Val Glu Ala Thr Glu Val Leu His Leu Cys Asn Arg Ala	
215 220 225	
aac ctg gat tct gat cac tcc acc att ttt atg cgt tcg gat ggg gat	835
Asn Leu Asp Ser Asp His Ser Thr Ile Phe Met Arg Ser Asp Gly Asp	
230 235 240 245	
gat gtg gat ttc gtc gcc acg gtt gcg gtg ccg att cgt gct ggt ctg	883
Asp Val Asp Phe Val Ala Thr Val Ala Val Pro Ile Arg Ala Gly Leu	
250 255 260	
aac gat ttc cag ttg agt caa gcc ctg cat gat ggg gta gtg ggg gtt	931
Asn Asp Phe Gln Leu Ser Gln Ala Leu His Asp Gly Val Val Gly Val	
265 270 275	
ggt ggg cag gta cga gct gtg atc aat cag cta cac tagtgaagtc	977

Val Gly Gln Val Arg Ala Val Ile Asn Gln Leu His
 280 285

catatagtga gaa

990

<210> 2100

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 2100

Met Pro Pro Ala Thr Leu Phe Asn Val Leu Thr Ser Ala Gly Leu Asp
 1 5 10 15

Pro His Gln Ser Gly Asp Ala Ile Val Val Glu Ser Ala His Phe Thr
 20 25 30

Leu Thr Phe Thr Trp Asp Glu Trp Leu Arg Ala Gln Ala Thr Trp Val
 35 40 45

Gly Glu Leu Ser Ala Ser Asp Tyr Val Arg Ser Ile Val Ala Ile Asn
 50 55 60

Ser Ala His Asp Ala Arg Ala Thr Pro Lys Met Met Leu Asp Ala Pro
 65 70 75 80

Thr Gly Leu Thr Thr Val Leu Lys Ala Asp Lys Gly Gln Leu Gln Ala
 85 90 95

Phe Ala Val Glu Ala Leu Pro Ile Gly Asp Gly Leu Ser Glu Ala Gln
 100 105 110

Leu Ala Gly Phe Val Ala Ala Ala Phe Asp Gly Ala Ile Asp Leu Thr
 115 120 125

Arg Glu Phe His Ala Leu Tyr Pro Glu Arg Ser Pro Gln Glu Arg Gly
 130 135 140

Ala Met Leu Asn Ile Lys Leu Val Asp Ala Ser Pro Ser Gln Thr Val
 145 150 155 160

Thr Pro Val Arg Val Ala Asn Trp Phe Met Asp Gln Gly Val Glu Glu
 165 170 175

Val Pro Tyr Asp Ala Ala Ser Gly Arg Ile Ser Phe Glu Leu Gly Asp
 180 185 190

Thr Pro Val Asp Val Ile Leu Asp Asp Pro Glu Leu Leu Lys Ile Gln
 195 200 205

Ala Val Val Val Ala Asp Arg Asp Val Glu Ala Thr Glu Val Leu His
 210 215 220

Leu Cys Asn Arg Ala Asn Leu Asp Ser Asp His Ser Thr Ile Phe Met
 225 230 235 240

Arg Ser Asp Gly Asp Asp Val Asp Phe Val Ala Thr Val Ala Val Pro
 245 250 255

Ile Arg Ala Gly Leu Asn Asp Phe Gln Leu Ser Gln Ala Leu His Asp

260 265 270
 Gly Val Val Gly Val Val Gly Gln Val Arg Ala Val Ile Asn Gln Leu
 275 280 285

His

<210> 2101
 <211> 483
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(460)
 <223> RXA01137

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 Val Arg Pro Thr Phe
 1 5
 gtg atc cta cgg atc tcc gaa tac ttc ggt gtc gct gaa gct gcg att 163
 Val Ile Leu Arg Ile Ser Glu Tyr Phe Gly Val Ala Glu Ala Ala Ile
 10 15 20
 aat gca gcc act gga cgt ctg acc agc ctc agc gaa gtg ttt atc gac 211
 Asn Ala Ala Thr Gly Arg Leu Thr Ser Leu Ser Glu Val Phe Ile Asp
 25 30 35
 aac gct gcc gag atc caa gac aac ctt tct tcg ctg gtc gcg ctt cag 259
 Asn Ala Ala Glu Ile Gln Asp Asn Leu Ser Ser Leu Val Ala Leu Gln
 40 45 50
 aaa gat ttg gca gag cga gtc aac gtt gaa gga gtc aat cct gtt act 307
 Lys Asp Leu Ala Glu Arg Val Asn Val Glu Gly Val Asn Pro Val Thr
 55 60 65
 cca gtt gat cta ctg gaa ctt cgc ctc ggt tcc gcg cag ctg gcc gtt 355
 Pro Val Asp Leu Leu Glu Leu Arg Leu Gly Ser Ala Gln Leu Ala Val
 70 75 80 85
 gct gca act gcc att gag gtt cgt gtt gct gga gga gca ggt tat gta 403
 Ala Ala Thr Ala Ile Glu Val Arg Val Ala Gly Gly Ala Gly Tyr Val
 90 95 100
 aag tct tca tca acg tct cgt cgt ttc cgt gtt gaa atg gga gct tgc 451
 Lys Ser Ser Ser Thr Ser Arg Arg Phe Arg Val Glu Met Gly Ala Cys
 105 110 115
 acg ggt ccg tgatctacag gccacgcaaa act 483
 Thr Gly Pro
 120

<210> 2102
 <211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 2102

Val Arg Pro Thr Phe Val Ile Leu Arg Ile Ser Glu Tyr Phe Gly Val
 1 5 10 15

Ala Glu Ala Ala Ile Asn Ala Ala Thr Gly Arg Leu Thr Ser Leu Ser
 20 25 30

Glu Val Phe Ile Asp Asn Ala Ala Glu Ile Gln Asp Asn Leu Ser Ser
 35 40 45

Leu Val Ala Leu Gln Lys Asp Leu Ala Glu Arg Val Asn Val Glu Gly
 50 55 60

Val Asn Pro Val Thr Pro Val Asp Leu Leu Glu Leu Arg Leu Gly Ser
 65 70 75 80

Ala Gln Leu Ala Val Ala Ala Thr Ala Ile Glu Val Arg Val Ala Gly
 85 90 95

Gly Ala Gly Tyr Val Lys Ser Ser Ser Thr Ser Arg Arg Phe Arg Val
 100 105 110

Glu Met Gly Ala Cys Thr Gly Pro
 115 120

<210> 2103

<211> 257

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (34)..(234)

<223> RXA01156

<400> 2103

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 Val Ser Val Val Asn Ala Lys
 1 5

caa acc caa att atg ggt ggc ggc gga cgt gac gag gac aac gcc gag 102
 Gln Thr Gln Ile Met Gly Gly Gly Gly Arg Asp Glu Asp Asn Ala Glu
 10 15 20

gat tcc gca cag gca tct gga cag gtt cag atc aac acc gaa ggt gtg 150
 Asp Ser Ala Gln Ala Ser Gly Gln Val Gln Ile Asn Thr Glu Gly Val
 25 30 35

gac agc ttg ctg gat gaa atc gac gga ctg ttg gaa aac aac gcc gag 198
 Asp Ser Leu Leu Asp Glu Ile Asp Gly Leu Leu Glu Asn Asn Ala Glu
 40 45 50 55

gaa ttc gtt cgt tcc tat gta caa aag ggt ggc gaa tagtcactgt 244
 Glu Phe Val Arg Ser Tyr Val Gln Lys Gly Gly Glu
 60 65

gagtaccgtg gaa 257

<210> 2104

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 2104

Val Ser Val Val Asn Ala Lys Gln Thr Gln Ile Met Gly Gly Gly Gly
1 5 10 15

Arg Asp Glu Asp Asn Ala Glu Asp Ser Ala Gln Ala Ser Gly Gln Val
20 25 30

Gln Ile Asn Thr Glu Gly Val Asp Ser Leu Leu Asp Glu Ile Asp Gly
35 40 45

Leu Leu Glu Asn Asn Ala Glu Glu Phe Val Arg Ser Tyr Val Gln Lys
50 55 60

Gly Gly Glu
65

<210> 2105

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA01158

<400> 2105

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agttatctca aaaaagaaga agaagtctcc tacgggagag atg tcc att gtt gag 115
Met Ser Ile Val Glu
1 5

cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163
His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
10 15 20

ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211
Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
25 30 35

cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259
Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu
40 45 50

cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307
Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg 355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala
70 75 80 85

gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tggtggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150 155 160 165	
ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
295 300 305	
ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta	1065
Phe Gly Asp Val Leu	
310	

<210> 2106

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 2106

Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
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Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
 20 25 30

Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
 35 40 45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
 50 55 60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65 70 75 80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
 85 90 95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
 100 105 110

Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
 115 120 125

Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
 130 135 140

Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
 145 150 155 160

Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
 165 170 175

Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
 180 185 190

Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
 195 200 205

Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
 210 215 220

Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
 225 230 235 240

Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
 245 250 255

Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala
 260 265 270

Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu
 275 280 285

Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys

290

295

300

Pro Gly Arg Ala Asp Phe Gly Asp Val Leu
305 310

<210> 2107

<211> 438

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(415)

<223> RXA01159

<400> 2107

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catgaacaag cttgtttaat gtgaatttgg agtagaccac atg tcc ctc gga cca 115
Met Ser Leu Gly Pro
1 5

tgg gaa att gga atc att gtc ctg ctg atc atc gtg ctg ttc ggc gcg 163
Trp Glu Ile Gly Ile Ile Val Leu Leu Ile Ile Val Leu Phe Gly Ala
10 15 20

aag aag ctg cct gat gca gct cgt tcc atc ggc cgt tcc atg cgc atc 211
Lys Lys Leu Pro Asp Ala Ala Arg Ser Ile Gly Arg Ser Met Arg Ile
25 30 35

ttc aag tct gaa gtc aaa gaa atg aac aag gac ggc gat acc cca gaa 259
Phe Lys Ser Glu Val Lys Glu Met Asn Lys Asp Gly Asp Thr Pro Glu
40 45 50

caa cag cag cag cct cag cag cag att gcg ccc aac cag atc gag gct 307
Gln Gln Gln Gln Pro Gln Gln Gln Ile Ala Pro Asn Gln Ile Glu Ala
55 60 65

cct cag cca aac ttt gag cag cac tac cag gga cag cag gtt cag cag 355
Pro Gln Pro Asn Phe Glu Gln His Tyr Gln Gly Gln Gln Val Gln Gln
70 75 80 85

cct cag aac cct cag acc cct gac tac cgt cag aac tac gag gat cca 403
Pro Gln Asn Pro Gln Thr Pro Asp Tyr Arg Gln Asn Tyr Glu Asp Pro
90 95 100

aac cgc acc tct taaagttggg cagtttgcac cta 438
Asn Arg Thr Ser
105

<210> 2108

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 2108

Met Ser Leu Gly Pro Trp Glu Ile Gly Ile Ile Val Leu Leu Ile Ile
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<400>	2109																
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Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu																	
1				5					10					15			
ccg tat ttc acc agg tat aaa ggc cgt acc gtc atg gaa gca gcg cgc																	96
Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg																	
			20					25						30			
gat ctt ggc caa ccc tcc tcc caa atc atg gaa gac ctc aac aga tta																	144
Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu																	
		35					40					45					
tgg atg tgt ggt ctg cca gga ctt ctt cca ggt gac ttg gtg gag ctt																	192
Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu																	
	50						55				60						
gat cat tcc ttt aag gaa gta aaa atc cac aat gct caa ggc atg gat																	240
Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp																	
65					70				75							80	
aaa ccc ttg cgc ctc aca cca act gaa gcc ggt gtt ttg ctg cta																	288
Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr																	
				85					90						95		
ctt gaa tcc ctg gaa tcc ctc ccc ggt att gcg aaa cag gaa gcg gtc																	336
Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val																	
			100					105					110				
gta tct gct gcg aac aag cta cgc gcc atc atg ggg gag tat tcc tcg																	384
Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser																	
		115					120					125					

act gtt ttc gac tcc act gga gaa gac ctc gat gct gaa gtt cta gag 432
 Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
 130 135 140

atc atc cgc gac gcc atg gat tta cac cag cag gtc agt ttt gaa tac 480
 Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
 145 150 155 160

cac tcg cac aga tca gac aac acc agc ctg agg caa gtc agc cct gct 528
 His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
 165 170 175

cat atc ttc acc cat gaa ggc gaa acc tac atc aaa gcc tgg gaa gaa 576
 His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
 180 185 190

gct gtg aac caa tgg cgg acg ttt agg ctt gat cgc atc cga agc att 624
 Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
 195 200 205

gtg ctt ctt gac agc aaa gca gtg cac ccg gcg cga ggg gtt tca gta 672
 Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
 210 215 220

tcc acg gac gat cct ttt gag ttc gca aaa tct tcc gat att gcc acg 720
 Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
 225 230 235 240

tta ttg ctg cgt gag gac gca atg tgg tta ggc aat tac atg gcc atg 768
 Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
 245 250 255

gag gtg gat gaa acg gtg gaa ccg att cgc gat agc gac gga ttc agc 816
 Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
 260 265 270

tgg cac aca gtc cac ttt ccg ctg ctt tct agg gat tgg ttc gtc cga 864
 Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
 275 280 285

ttc gcg att ggc cat gct gag cat ttg aaa gta act agt ccc gaa gat 912
 Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
 290 295 300

ctt cgg aaa tgc ata aag caa aag gct ttt agt ggt ttg tca gcg tat 960
 Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
 305 310 315 320

gat cat cac gta gag taacacccaa gagtaagacg caa 998
 Asp His His Val Glu
 325

<210> 2110

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 2110

Lys Ser Ser Asn Lys Ile Ser Asp Leu Ala Arg Gln Leu Asn Leu Leu

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Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg	20	25	30
Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu	35	40	45
Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu	50	55	60
Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp	65	70	75
Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr	85	90	95
Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val	100	105	110
Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser	115	120	125
Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu	130	135	140
Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr	145	150	155
His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala	165	170	175
His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu	180	185	190
Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile	195	200	205
Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val	210	215	220
Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr	225	230	235
Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met	245	250	255
Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser	260	265	270
Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg	275	280	285
Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp	290	295	300
Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr	305	310	315
Asp His His Val Glu	325		

	170	175	180	
ttc atc gat tac ccc cgc gac ccc gca acc ggc gtc caa tac tat tgc				691
Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly Val Gln Tyr Tyr Cys				
	185	190	195	
gat tcc atc gct gca gct aaa tcg ctt ctc gac gcc gtc ctc gcc tcc				739
Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp Ala Val Leu Ala Ser				
	200	205	210	
aga caa ctc ggc ctt tca ccg gaa gca ccg ctt ggc ctg tgg gga ttc				787
Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu Gly Leu Trp Gly Phe				
	215	220	225	
tcc caa gga ggc ggc gcc				805
Ser Gln Gly Gly Gly Ala				
230	235			

<210> 2112

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 2112

Met Gly Tyr Thr Asn Leu Asn Asp Thr Arg Val Leu Arg Ala Gly Ser				
1	5	10	15	
Cys Asp Ala Trp Trp Arg Thr Met Ser Pro Leu Val Gln Gln Gly Ser				
20	25	30		
Glu Ala Val Phe Arg Arg Ile Met Gly Leu Ser Arg Arg Pro Asp Arg				
35	40	45		
Lys Pro Gly Phe Asp Asp Val Pro His Phe Gly Ala Ala Val Arg Val				
50	55	60		
Pro Gly Leu Lys His Gly Thr Leu Val Asn Ala Ala Pro Leu Lys Val				
65	70	75	80	
Leu Gly Ala Arg Gly Glu Pro Asn Pro Ala Ser Ser Tyr Arg Phe Glu				
85	90	95		
Tyr Ile Thr Gly Asp Ser Ala Gly Arg Ala Ile Thr Ala Thr Gly Ala				
100	105	110		
Val Leu Phe Ser Thr Arg Pro Trp Thr Thr Gly Pro Arg Pro Ala Ile				
115	120	125		
Ala Met Ala Pro Ser Thr Gln Gly Val Ala Gln His Cys Asp Pro Ser				
130	135	140		
His Thr Cys Ala Ile Gly Leu Asn Ala Phe Tyr Asp Lys Pro Phe Asp				
145	150	155	160	
Ala Ile Ile Ala Tyr Glu Leu Pro Val Ile Leu Trp Phe Leu Ala His				
165	170	175		
Gly Leu Asp Val Val Phe Ile Asp Tyr Pro Arg Asp Pro Ala Thr Gly				
180	185	190		

Val Gln Tyr Tyr Cys Asp Ser Ile Ala Ala Ala Lys Ser Leu Leu Asp
 195 200 205

Ala Val Leu Ala Ser Arg Gln Leu Gly Leu Ser Pro Glu Ala Pro Leu
 210 215 220

Gly Leu Trp Gly Phe Ser Gln Gly Gly Gly Ala
 225 230 235

<210> 2113
 <211> 696
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(673)
 <223> RXA01165

<400> 2113
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tcacagggat ccattagcca tttggtcctt gtcgaaaggt atg gtg ggg cat gtg 115
 Met Val Gly His Val
 1 5

cct gca gca ata gca atc cca tat ttc att att gag atc ctc gcc ttc 163
 Pro Ala Ala Ile Ala Ile Pro Tyr Phe Ile Ile Glu Ile Leu Ala Phe
 10 15 20

att ggt gtc gtc atg tgg ctc ggt ttc ggc tgg gct ttg ggt ctc ctc 211
 Ile Gly Val Val Met Trp Leu Gly Phe Gly Trp Ala Leu Gly Leu Leu
 25 30 35

gta ttg ttc ttc gtc ggt gga ctt ctt cta gcc ggc gtg gag ctt cgt 259
 Val Leu Phe Phe Val Gly Gly Leu Leu Leu Ala Gly Val Glu Leu Arg
 40 45 50

cgc att agt aag agt gcc gcc att cat cag gct tcg ggc cag gga agt 307
 Arg Ile Ser Lys Ser Ala Ala Ile His Gln Ala Ser Gly Gln Gly Ser
 55 60 65

gcg gga gcg atc gcc gga aac att ggg ctg acc gca gct ggt gcc att 355
 Ala Gly Ala Ile Ala Gly Asn Ile Gly Leu Thr Ala Ala Gly Ala Ile
 70 75 80 85

ttg gtg gcc atg ccg ggg ttt gtg tct tcg att atc ggt ttg ttg ttc 403
 Leu Val Ala Met Pro Gly Phe Val Ser Ser Ile Ile Gly Leu Leu Phe
 90 95 100

att ttt gca cca acc agg gcg ctg ttc cgc aag gtt ttg gcc aag cgc 451
 Ile Phe Ala Pro Thr Arg Ala Leu Phe Arg Lys Val Leu Ala Lys Arg
 105 110 115

atg cgc agt gcc atc gag aac cta ggt gtg cgt ggt ttt gaa gcc gtt 499
 Met Arg Ser Ala Ile Glu Asn Leu Gly Val Arg Gly Phe Glu Ala Val
 120 125 130

aat ggt tac cgc acc cag gca tcc tac gga aac ttc gga gcg gca ttc 547
 Asn Gly Tyr Arg Thr Gln Ala Ser Tyr Gly Asn Phe Gly Ala Ala Phe

135	140	145	
aat ggt ggt gcg caa caa cca tca aat gag ccg atc gtg att gat gaa			595
Asn Gly Gly Ala Gln Gln Pro Ser Asn Glu Pro Ile Val Ile Asp Glu			
150	155	160	165
gac gag atc caa gcc tgg act tct gat ctc aaa cct gaa gat ttc acc			643
Asp Glu Ile Gln Ala Trp Thr Ser Asp Leu Lys Pro Glu Asp Phe Thr			
	170	175	180
aaa ggt aaa gat gaa tcc gac ggt gag aaa taagtgcac tgtttggtcg			693
Lys Gly Lys Asp Glu Ser Asp Gly Glu Lys			
	185	190	
gct			696

<210> 2114

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 2114

Met Val Gly His Val Pro Ala Ala Ile Ala Ile Pro Tyr Phe Ile Ile
1 5 10 15

Glu Ile Leu Ala Phe Ile Gly Val Val Met Trp Leu Gly Phe Gly Trp
20 25 30

Ala Leu Gly Leu Leu Val Leu Phe Phe Val Gly Gly Leu Leu Leu Ala
35 40 45

Gly Val Glu Leu Arg Arg Ile Ser Lys Ser Ala Ala Ile His Gln Ala
50 55 60

Ser Gly Gln Gly Ser Ala Gly Ala Ile Ala Gly Asn Ile Gly Leu Thr
65 70 75 80

Ala Ala Gly Ala Ile Leu Val Ala Met Pro Gly Phe Val Ser Ser Ile
85 90 95

Ile Gly Leu Leu Phe Ile Phe Ala Pro Thr Arg Ala Leu Phe Arg Lys
100 105 110

Val Leu Ala Lys Arg Met Arg Ser Ala Ile Glu Asn Leu Gly Val Arg
115 120 125

Gly Phe Glu Ala Val Asn Gly Tyr Arg Thr Gln Ala Ser Tyr Gly Asn
130 135 140

Phe Gly Ala Ala Phe Asn Gly Gly Ala Gln Gln Pro Ser Asn Glu Pro
145 150 155 160

Ile Val Ile Asp Glu Asp Glu Ile Gln Ala Trp Thr Ser Asp Leu Lys
165 170 175

Pro Glu Asp Phe Thr Lys Gly Lys Asp Glu Ser Asp Gly Glu Lys
180 185 190

<210> 2115

<211> 506
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(483)
 <223> RXA01166

<400> 2115
 ctc acc gga gtg att gcc tac gcc atc gcg gga ctt gca gtg aac tct 48
 Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser
 1 5 10 15

 tca gag atg ttt gag gaa atc atg tcg gtg tta aat gaa cgc gga gtc 96
 Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val
 20 25 30

 agt gat gtg ctg aaa aat atc acc agc tgc gcg gga ggt tcc ttg ttg 144
 Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu
 35 40 45

 gcc agt ggc tac tcg tct tcc cgc ggg tgg aca cat cag ggc acg ccg 192
 Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro
 50 55 60

 ctg gca gac att ctg gac gat ctg cca ctt gtt gtc gct gag ttt ggg 240
 Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly
 65 70 75 80

 aag caa aag ctg ggt cgt gtg gcg cca gaa atc cca gtg ctg ttg tgg 288
 Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp
 85 90 95

 ggc tct aaa aat gat gat gtc att ccc att gat ccc att agg gaa ttg 336
 Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu
 100 105 110

 cgt gat agc tgg gcg gac aag ggt acg cca ttg acc tgg cat gaa tcc 384
 Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser
 115 120 125

 caa gcg ccg cgt gtg cca gga cgc aca ggt ctc aac cat ttc ggg ccc 432
 Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro
 130 135 140

 tat ttt aga aac ctg gaa aag tac tcg gga tgg ctc ata gat cat ctt 480
 Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu
 145 150 155 160

 gtc tgagtgccgt tttaaaggct cgg 506
 Val

<210> 2116
 <211> 161
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2116

Leu Thr Gly Val Ile Ala Tyr Ala Ile Ala Gly Leu Ala Val Asn Ser
 1 5 10 15
 Ser Glu Met Phe Glu Glu Ile Met Ser Val Leu Asn Glu Arg Gly Val
 20 25 30
 Ser Asp Val Leu Lys Asn Ile Thr Ser Cys Ala Gly Gly Ser Leu Leu
 35 40 45
 Ala Ser Gly Tyr Ser Ser Ser Arg Gly Trp Thr His Gln Gly Thr Pro
 50 55 60
 Leu Ala Asp Ile Leu Asp Asp Leu Pro Leu Val Val Ala Glu Phe Gly
 65 70 75 80
 Lys Gln Lys Leu Gly Arg Val Ala Pro Glu Ile Pro Val Leu Leu Trp
 85 90 95
 Gly Ser Lys Asn Asp Asp Val Ile Pro Ile Asp Pro Ile Arg Glu Leu
 100 105 110
 Arg Asp Ser Trp Ala Asp Lys Gly Thr Pro Leu Thr Trp His Glu Ser
 115 120 125
 Gln Ala Pro Arg Val Pro Gly Arg Thr Gly Leu Asn His Phe Gly Pro
 130 135 140
 Tyr Phe Arg Asn Leu Glu Lys Tyr Ser Gly Trp Leu Ile Asp His Leu
 145 150 155 160

Val

<210> 2117
 <211> 606
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(583)
 <223> RXA01170

<400> 2117
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 gtcacttaaa ctaaacaaga aggggtggagg acccaagcac gtg agt ctt tca aac 115
 Val Ser Leu Ser Asn 5
 aaa gct aaa gga atc gtt gca gta atc atc gtc gcc tgg atc gtc gcg 163
 Lys Ala Lys Gly Ile Val Ala Val Ile Ile Val Ala Trp Ile Val Ala 20
 10 15
 atg gct ggc atg gtc gca tac gcg tca agc aat aat gct gat aag aca 211
 Met Ala Gly Met Val Ala Tyr Ala Ser Ser Asn Asn Ala Asp Lys Thr 35
 25 30
 ttt cca act gca ggt gcg cta gaa caa acc gtc gca gca ttt gat agg 259
 Phe Pro Thr Ala Gly Ala Leu Glu Gln Thr Val Ala Ala Phe Asp Arg

40	45	50	
caa ggc ctt cag gtc tct gca gtc gca ctg gca gac atc tac ggc gat			307
Gln Gly Leu Gln Val Ser Ala Val Ala Leu Ala Asp Ile Tyr Gly Asp			
55	60	65	
gaa tac gtc tcc gcg gcg att ctg tgc gaa gga act cca acc gca aca			355
Glu Tyr Val Ser Ala Ala Ile Leu Cys Glu Gly Thr Pro Thr Ala Thr			
70	75	80	85
ctc gag cag tca ctg ggc gta gac ctg tct gag ctg aac ctg gac gag			403
Leu Glu Gln Ser Leu Gly Val Asp Leu Ser Glu Leu Asn Leu Asp Glu			
90	95	100	
tct ggt gtt cct tcg ggc gtg tcc tac ttg gct ctg tcc aat cag gat			451
Ser Gly Val Pro Ser Gly Val Ser Tyr Leu Ala Leu Ser Asn Gln Asp			
105	110	115	
ggg gaa gtt gtc tac gac aag att gat cgt gcc aac gtt gat ctc tgc			499
Gly Glu Val Val Tyr Asp Lys Ile Asp Arg Ala Asn Val Asp Leu Cys			
120	125	130	
gca acg cca ctc aat ggt gct ttc agc gct tat tca ttg atg cca gtt			547
Ala Thr Pro Leu Asn Gly Ala Phe Ser Ala Tyr Ser Leu Met Pro Val			
135	140	145	
gcc aag gtt ggc gag aac tcc tgg gcg atc gcc gct taggggtttta			593
Ala Lys Val Gly Glu Asn Ser Trp Ala Ile Ala Ala			
150	155	160	
agggtcaatc cgc			606
<210> 2118			
<211> 161			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2118			
Val Ser Leu Ser Asn Lys Ala Lys Gly Ile Val Ala Val Ile Ile Val			
1	5	10	15
Ala Trp Ile Val Ala Met Ala Gly Met Val Ala Tyr Ala Ser Ser Asn			
20	25	30	
Asn Ala Asp Lys Thr Phe Pro Thr Ala Gly Ala Leu Glu Gln Thr Val			
35	40	45	
Ala Ala Phe Asp Arg Gln Gly Leu Gln Val Ser Ala Val Ala Leu Ala			
50	55	60	
Asp Ile Tyr Gly Asp Glu Tyr Val Ser Ala Ala Ile Leu Cys Glu Gly			
65	70	75	80
Thr Pro Thr Ala Thr Leu Glu Gln Ser Leu Gly Val Asp Leu Ser Glu			
85	90	95	
Leu Asn Leu Asp Glu Ser Gly Val Pro Ser Gly Val Ser Tyr Leu Ala			
100	105	110	
Leu Ser Asn Gln Asp Gly Glu Val Val Tyr Asp Lys Ile Asp Arg Ala			

115	120	125
Asn Val Asp Leu Cys Ala Thr Pro Leu Asn Gly Ala Phe Ser Ala Tyr		
130	135	140
Ser Leu Met Pro Val Ala Lys Val Gly Glu Asn Ser Trp Ala Ile Ala		
145	150	155
		160
Ala		

<210> 2119
 <211> 816
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(793)
 <223> RXA01171

<400> 2119
 gtagaaattt tccatgcaga ggaaagccga taatggggca gaaccccttc ccgccaaaat 60

gacataatgt acattatcgg acaattatcc atatctggcc atg tcg cag gcc gct 115
 Met Ser Gln Ala Ala
 1 5

ggt aag ttt aag ccc atg act tca acg ctc gcc gaa tca aca ctt aca 163
 Gly Lys Phe Lys Pro Met Thr Ser Thr Leu Ala Glu Ser Thr Leu Thr
 10 15 20

tcc ctt aaa gaa ctt gag gat cca aag atc ctt tcc gtc aat gaa cgc 211
 Ser Leu Lys Glu Leu Glu Asp Pro Lys Ile Leu Ser Val Asn Glu Arg
 25 30 35

cac ggc gat gat cac gca gtg aac ctc acc aag ctt cgc gcc gtt gcc 259
 His Gly Asp Asp His Ala Val Asn Leu Thr Lys Leu Arg Ala Val Ala
 40 45 50

aaa gag ctg aaa aag aac cag ccg ctg gct cgt gag ctt tgg gca acc 307
 Lys Glu Leu Lys Lys Asn Gln Pro Leu Ala Arg Glu Leu Trp Ala Thr
 55 60 65

gac gat aca gcc gca cgt ttg gtg gcg ttg ctt att tgc cga ccc aag 355
 Asp Asp Thr Ala Ala Arg Leu Val Ala Leu Leu Ile Cys Arg Pro Lys
 70 75 80 85

gaa ttt gat cag tct gaa ctc gac tcg atg atc cat gag gct cgc acg 403
 Glu Phe Asp Gln Ser Glu Leu Asp Ser Met Ile His Glu Ala Arg Thr
 90 95 100

ccg aag gtt ctt gat tgg ttg atc aat tat gtg gtc aag aag aat cct 451
 Pro Lys Val Leu Asp Trp Leu Ile Asn Tyr Val Val Lys Lys Asn Pro
 105 110 115

cat tgg aac gat ctc cgt gtg ctc tgg ctt gaa gat ccc gcc gag aat 499
 His Trp Asn Asp Leu Arg Val Leu Trp Leu Glu Asp Pro Ala Glu Asn
 120 125 130

gtt gcg gcc gcc ggc tgg gct ctc aac act cat gcc gtt atc aca aag 547
Val Ala Ala Ala Gly Trp Ala Leu Asn Thr His Ala Val Ile Thr Lys
135 140 145

ccg gac gca ttg gac gat tcc gaa atc ctt gac acc att gaa gct cag 595
Pro Asp Ala Leu Asp Asp Ser Glu Ile Leu Asp Thr Ile Glu Ala Gln
150 155 160 165

atg aaa act gcc gag cct cgc gta cag tgg tca atg aat gaa tgt ttg 643
Met Lys Thr Ala Glu Pro Arg Val Gln Trp Ser Met Asn Glu Cys Leu
170 175 180

gcg caa atc ggc atc cat cgt cca gag ctt cgt gat cgt gcc att gcc 691
Ala Gln Ile Gly Ile His Arg Pro Glu Leu Arg Asp Arg Ala Ile Ala
185 190 195

att ggt gag cgc ctg gaa gtt ctc aaa gat tat ccg acc cct cca aat 739
Ile Gly Glu Arg Leu Glu Val Leu Lys Asp Tyr Pro Thr Pro Pro Asn
200 205 210

tgc acc tcg cct ttt gct ccg att tgg atc gaa gag atg gtt cgc agg 787
Cys Thr Ser Pro Phe Ala Pro Ile Trp Ile Glu Glu Met Val Arg Arg
215 220 225

aaa aaa taaccgacct gttccctatc ttt 816
Lys Lys
230

<210> 2120

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 2120

Met Ser Gln Ala Ala Gly Lys Phe Lys Pro Met Thr Ser Thr Leu Ala
1 5 10 15

Glu Ser Thr Leu Thr Ser Leu Lys Glu Leu Glu Asp Pro Lys Ile Leu
20 25 30

Ser Val Asn Glu Arg His Gly Asp Asp His Ala Val Asn Leu Thr Lys
35 40 45

Leu Arg Ala Val Ala Lys Glu Leu Lys Lys Asn Gln Pro Leu Ala Arg
50 55 60

Glu Leu Trp Ala Thr Asp Asp Thr Ala Ala Arg Leu Val Ala Leu Leu
65 70 75 80

Ile Cys Arg Pro Lys Glu Phe Asp Gln Ser Glu Leu Asp Ser Met Ile
85 90 95

His Glu Ala Arg Thr Pro Lys Val Leu Asp Trp Leu Ile Asn Tyr Val
100 105 110

Val Lys Lys Asn Pro His Trp Asn Asp Leu Arg Val Leu Trp Leu Glu
115 120 125

Asp Pro Ala Glu Asn Val Ala Ala Ala Gly Trp Ala Leu Asn Thr His
130 135 140

Ala Val Ile Thr Lys Pro Asp Ala Leu Asp Asp Ser Glu Ile Leu Asp
 145 150 155 160

Thr Ile Glu Ala Gln Met Lys Thr Ala Glu Pro Arg Val Gln Trp Ser
 165 170 175

Met Asn Glu Cys Leu Ala Gln Ile Gly Ile His Arg Pro Glu Leu Arg
 180 185 190

Asp Arg Ala Ile Ala Ile Gly Glu Arg Leu Glu Val Leu Lys Asp Tyr
 195 200 205

Pro Thr Pro Pro Asn Cys Thr Ser Pro Phe Ala Pro Ile Trp Ile Glu
 210 215 220

Glu Met Val Arg Arg Lys Lys
 225 230

<210> 2121
 <211> 627
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(604)
 <223> RXA01176

<400> 2121
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acaaaccgac gttttcgacg ctgtgaagga ctaattgcta gtg cgt tat ttt tac 115
 Val Arg Tyr Phe Tyr
 1 5

gat act gag ttc att gaa gat ggg cgc acg atc gaa ttg gtc tct att 163
 Asp Thr Glu Phe Ile Glu Asp Gly Arg Thr Ile Glu Leu Val Ser Ile
 10 15 20

gga atc gtc gca gaa gac ggt cgc gag tat tac gca gtt agc aca cag 211
 Gly Ile Val Ala Glu Asp Gly Arg Glu Tyr Tyr Ala Val Ser Thr Gln
 25 30 35

ttt gat tcc tcc aag gcg aac gct tgg gtg cgc gcc aac gtg ttg gac 259
 Phe Asp Ser Ser Lys Ala Asn Ala Trp Val Arg Ala Asn Val Leu Asp
 40 45 50

aaa ttg cct aat cct tcc tcc aaa gtg tgg aaa tct gca gac act ata 307
 Lys Leu Pro Asn Pro Ser Ser Lys Val Trp Lys Ser Ala Asp Thr Ile
 55 60 65

aag cgc gaa gtt tat gag ttt ctc acc tcc acc gga cca acc cct gaa 355
 Lys Arg Glu Val Tyr Glu Phe Leu Thr Ser Thr Gly Pro Thr Pro Glu
 70 75 80 85

ctg tgg gcc tgg gtg ggc gca tat gac cac gtg ttg ttg gca caa atg 403
 Leu Trp Ala Trp Val Gly Ala Tyr Asp His Val Leu Leu Ala Gln Met
 90 95 100

tgg ggc gat atg gcg ggg ctt cct cgg gag atc cct cgt ttt acc cgc 451
 Trp Gly Asp Met Ala Gly Leu Pro Arg Glu Ile Pro Arg Phe Thr Arg
 105 110 115

gag ctt cgc cag tat tgg gac atg gct ggc cgc cca acg ctg cca gag 499
 Glu Leu Arg Gln Tyr Trp Asp Met Ala Gly Arg Pro Thr Leu Pro Glu
 120 125 130

ctg ccg aac ggc aac cac gat gcg ttg att gat gcg cgt cat aat tta 547
 Leu Pro Asn Gly Asn His Asp Ala Leu Ile Asp Ala Arg His Asn Leu
 135 140 145

gcc aag ttc aaa gtg tgc atg gca gcg ctg cct ttg ggt aaa agg gat 595
 Ala Lys Phe Lys Val Cys Met Ala Ala Leu Pro Leu Gly Lys Arg Asp
 150 155 160 165

cgc gtc tct tagtcgatct gctcccatc cat 627
 Arg Val Ser

<210> 2122

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 2122

Val Arg Tyr Phe Tyr Asp Thr Glu Phe Ile Glu Asp Gly Arg Thr Ile
 1 5 10 15

Glu Leu Val Ser Ile Gly Ile Val Ala Glu Asp Gly Arg Glu Tyr Tyr
 20 25 30

Ala Val Ser Thr Gln Phe Asp Ser Ser Lys Ala Asn Ala Trp Val Arg
 35 40 45

Ala Asn Val Leu Asp Lys Leu Pro Asn Pro Ser Ser Lys Val Trp Lys
 50 55 60

Ser Ala Asp Thr Ile Lys Arg Glu Val Tyr Glu Phe Leu Thr Ser Thr
 65 70 75 80

Gly Pro Thr Pro Glu Leu Trp Ala Trp Val Gly Ala Tyr Asp His Val
 85 90 95

Leu Leu Ala Gln Met Trp Gly Asp Met Ala Gly Leu Pro Arg Glu Ile
 100 105 110

Pro Arg Phe Thr Arg Glu Leu Arg Gln Tyr Trp Asp Met Ala Gly Arg
 115 120 125

Pro Thr Leu Pro Glu Leu Pro Asn Gly Asn His Asp Ala Leu Ile Asp
 130 135 140

Ala Arg His Asn Leu Ala Lys Phe Lys Val Cys Met Ala Ala Leu Pro
 145 150 155 160

Leu Gly Lys Arg Asp Arg Val Ser
 165

gtt ctc atg gat acc ttc acc aaa aag ccc tgg ttg cca cgt ggt ttt Val Leu Met Asp Thr Phe Thr Lys Lys Pro Trp Leu Pro Arg Gly Phe 185 190 195	691
tgg att ggt ttg gcg gca tcc atc aag ctg acc ccc gca gtc ttt ggc Trp Ile Gly Leu Ala Ala Ser Ile Lys Leu Thr Pro Ala Val Phe Gly 200 205 210	739
ctt tac ttc cta gtg aag aag gac tgg aag ggc gct gga gta gca att Leu Tyr Phe Leu Val Lys Lys Asp Trp Lys Gly Ala Gly Val Ala Ile 215 220 225	787
gct tct ggc gta ggt ttt tcc gcc ttg gcg ttt atc ctc tca cct tca Ala Ser Gly Val Gly Phe Ser Ala Leu Ala Phe Ile Leu Ser Pro Ser 230 235 240 245	835
agt tcc aag att tac tgg act gaa aca ctc aac gac cct tct cgc atc Ser Ser Lys Ile Tyr Trp Thr Glu Thr Leu Asn Asp Pro Ser Arg Ile 250 255 260	883
ggc aac cta tct tat att gct aac caa tct gtg cgt gga acg ctc agc Gly Asn Leu Ser Tyr Ile Ala Asn Gln Ser Val Arg Gly Thr Leu Ser 265 270 275	931
cga atg atg cat gaa cag cag gat ctc gtc gaa aag ctt tgg ctt gtg Arg Met Met His Glu Gln Gln Asp Leu Val Glu Lys Leu Trp Leu Val 280 285 290	979
gca gtt gtc ttg tgc ctt gcc gct gtc gcc gtc gcc atg tgg cgc gtg Ala Val Val Leu Cys Leu Ala Ala Val Ala Val Ala Met Trp Arg Val 295 300 305	1027
gta cgc gcc ggc aac ccg tac ggc gcc gtc atg ctc aac tcg ttg att Val Arg Ala Gly Asn Pro Tyr Gly Ala Val Met Leu Asn Ser Leu Ile 310 315 320 325	1075
gct ctg ctg tgc tcc cct gtt tca tgg tct cac cac tgg gta tgg ctg Ala Leu Leu Cys Ser Pro Val Ser Trp Ser His His Trp Val Trp Leu 330 335 340	1123
att cca atc gct att ggt ttg ggg gca agt gcg tgg aac cag cgg cgg Ile Pro Ile Ala Ile Gly Leu Gly Ala Ser Ala Trp Asn Gln Arg Arg 345 350 355	1171
act gct cca gga att gcc gcg acg gct gga gtc ttg gcg ctt ctg acc Thr Ala Pro Gly Ile Ala Ala Thr Ala Gly Val Leu Ala Leu Leu Thr 360 365 370	1219
acg att ccg atg ttc atc aca aca ttt tgg aac atg cca tac gat tca Thr Ile Pro Met Phe Ile Thr Thr Phe Trp Asn Met Pro Tyr Asp Ser 375 380 385	1267
gag tct tac cca ttt tgg cca ttg att ctg cag ccg tcg ggc aac gcg Glu Ser Tyr Pro Phe Trp Pro Leu Ile Leu Gln Pro Ser Gly Asn Ala 390 395 400 405	1315
tat gta gta gtg gtc atc gct att ttg atc gtc gcg att gtg aat cca Tyr Val Val Val Val Ile Ala Ile Leu Ile Val Ala Ile Val Asn Pro 410 415 420	1363
aca gtt ttg ggc agt ggc aat aaa gct gtt tca ggc cag gca gag aag	1411

Thr Val Leu Gly Ser Gly Asn Lys Ala Val Ser Gly Gln Ala Glu Lys	
425 430 435	
aag tcc tcc cct gcg ttg ctt gtt gtt tta gcg att gcc att ttc tac	1459
Lys Ser Ser Pro Ala Leu Leu Val Val Leu Ala Ile Ala Ile Phe Tyr	
440 445 450	
ctc ttt gcc aat att tgg ttt aag gga aac aat caa aac aaa gcg ctc	1507
Leu Phe Ala Asn Ile Trp Phe Lys Gly Asn Asn Gln Asn Lys Ala Leu	
455 460 465	
att cag tac cca ctg cag act atg gaa ggt cgc ggt ctc act gac ttc	1555
Ile Gln Tyr Pro Leu Gln Thr Met Glu Gly Arg Gly Leu Thr Asp Phe	
470 475 480 485	
ggc gag ctt att ttt gaa ttc gcg gct tcc tcc aac cag ctt gtt tcc	1603
Gly Glu Leu Ile Phe Glu Phe Ala Ala Ser Ser Asn Gln Leu Val Ser	
490 495 500	
ctc tgg ata atc ggc gcc ctc aac gcc atc gca ttg gct att acc ctg	1651
Leu Trp Ile Ile Gly Ala Leu Asn Ala Ile Ala Leu Ala Ile Thr Leu	
505 510 515	
tgg ttc ctc ctt cag cgt ttt gct ggg aag aag agc tcc tgg ctg att	1699
Trp Phe Leu Leu Gln Arg Phe Ala Gly Lys Lys Ser Ser Trp Leu Ile	
520 525 530	
tat ctc agc acc gtg gct gtt gcg ctg atg atg ttc tca gtg cag gat	1747
Tyr Leu Ser Thr Val Ala Val Ala Leu Met Met Phe Ser Val Gln Asp	
535 540 545	
gcc ttg cag ttt ggt tcg ctg act ctc gtt gca ctc gca ttg atc act	1795
Ala Leu Gln Phe Gly Ser Leu Thr Leu Val Ala Leu Ala Leu Ile Thr	
550 555 560 565	
gtt gat gtg ttg agt gtc aga gag att ggc cgc cgc ggg ctg ctc aca	1843
Val Asp Val Leu Ser Val Arg Glu Ile Gly Arg Arg Gly Leu Leu Thr	
570 575 580	
gga ctt gca gca gcc ctg ttt gga tgg cca att ctg att gtt atc gga	1891
Gly Leu Ala Ala Ala Leu Phe Gly Trp Pro Ile Leu Ile Val Ile Gly	
585 590 595	
ttc ctc att cac cga cgt tat gca gca aca atc aca acc act gtc acc	1939
Phe Leu Ile His Arg Arg Tyr Ala Ala Thr Ile Thr Thr Val Thr	
600 605 610	
gca gct gtg ctg tgg atc tta gga att ctg ctc aat cca gac gcc ttc	1987
Ala Ala Val Leu Trp Ile Leu Gly Ile Leu Leu Asn Pro Asp Ala Phe	
615 620 625	
aac ctc aac ctg ctg cgt caa tgg ttc aac ggg cgc gat ggt cgg gac	2035
Asn Leu Asn Leu Leu Arg Gln Trp Phe Asn Gly Arg Asp Gly Arg Asp	
630 635 640 645	
aat ttg tcc ttc tat gct ttc ctt gcc agg tgg gtc agc gaa tcc cca	2083
Asn Leu Ser Phe Tyr Ala Phe Leu Ala Arg Trp Val Ser Glu Ser Pro	
650 655 660	
gca tgatgttcgt atggttcacg gtc	2109
Ala	

<210> 2124

<211> 662

<212> PRT

<213> Corynebacterium glutamicum

<400> 2124

Met His Gly Glu Lys Leu Val Asp Gly Thr Glu Gly Asn Leu Ser Gln
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Phe Gln Trp Arg Asp Met Ala Thr Asn Gln Thr Leu Arg Lys Ala Leu
20 25 30

Leu Val Leu Ser Thr Ile Ala Leu Leu Thr Leu Trp Pro Ser Ile
35 40 45

Phe Asn Val Arg Ala Ile Glu Ser Phe Val Phe Phe Phe His Ile Asp
50 55 60

Thr Asp Val Tyr Arg Ala Gly Ala Asn Ala Phe Leu His Gly Glu Asn
65 70 75 80

Leu Tyr Thr Gln Asp Tyr Gln Val Gly Ser Ile Gln Leu Pro Phe Thr
85 90 95

Tyr Pro Pro Ile Ser Ala Ala Leu Phe Val Pro Leu Ala Ile Leu Ala
100 105 110

Ser Ser Val Ala Gly Ile Ala Leu Thr Leu Ile Ser Thr Val Leu Leu
115 120 125

Trp Trp Ser Val Ala Ile Val Leu Arg Arg Val Leu Lys Gly Leu Thr
130 135 140

Asp Ala Asp Ser Arg Phe Val Ser Tyr Leu Ile Leu Pro Met Ala Leu
145 150 155 160

Ser Thr Glu Pro Val Phe Gln Thr Leu Gln Phe Gly Gln Val Asn Ile
165 170 175

Ile Leu Met Ala Leu Val Leu Met Asp Thr Phe Thr Lys Lys Pro Trp
180 185 190

Leu Pro Arg Gly Phe Trp Ile Gly Leu Ala Ala Ser Ile Lys Leu Thr
195 200 205

Pro Ala Val Phe Gly Leu Tyr Phe Leu Val Lys Lys Asp Trp Lys Gly
210 215 220

Ala Gly Val Ala Ile Ala Ser Gly Val Gly Phe Ser Ala Leu Ala Phe
225 230 235 240

Ile Leu Ser Pro Ser Ser Ser Lys Ile Tyr Trp Thr Glu Thr Leu Asn
245 250 255

Asp Pro Ser Arg Ile Gly Asn Leu Ser Tyr Ile Ala Asn Gln Ser Val
260 265 270

Arg Gly Thr Leu Ser Arg Met Met His Glu Gln Gln Asp Leu Val Glu

275	280	285
Lys Leu Trp Leu Val Ala Val Val Leu Cys Leu Ala Ala Val Ala Val 290 295 300		
Ala Met Trp Arg Val Val Arg Ala Gly Asn Pro Tyr Gly Ala Val Met 305 310 315 320		
Leu Asn Ser Leu Ile Ala Leu Leu Cys Ser Pro Val Ser Trp Ser His 325 330 335		
His Trp Val Trp Leu Ile Pro Ile Ala Ile Gly Leu Gly Ala Ser Ala 340 345 350		
Trp Asn Gln Arg Arg Thr Ala Pro Gly Ile Ala Ala Thr Ala Gly Val 355 360 365		
Leu Ala Leu Leu Thr Thr Ile Pro Met Phe Ile Thr Thr Phe Trp Asn 370 375 380		
Met Pro Tyr Asp Ser Glu Ser Tyr Pro Phe Trp Pro Leu Ile Leu Gln 385 390 395 400		
Pro Ser Gly Asn Ala Tyr Val Val Val Val Ile Ala Ile Leu Ile Val 405 410 415		
Ala Ile Val Asn Pro Thr Val Leu Gly Ser Gly Asn Lys Ala Val Ser 420 425 430		
Gly Gln Ala Glu Lys Lys Ser Ser Pro Ala Leu Leu Val Val Leu Ala 435 440 445		
Ile Ala Ile Phe Tyr Leu Phe Ala Asn Ile Trp Phe Lys Gly Asn Asn 450 455 460		
Gln Asn Lys Ala Leu Ile Gln Tyr Pro Leu Gln Thr Met Glu Gly Arg 465 470 475 480		
Gly Leu Thr Asp Phe Gly Glu Leu Ile Phe Glu Phe Ala Ala Ser Ser 485 490 495		
Asn Gln Leu Val Ser Leu Trp Ile Ile Gly Ala Leu Asn Ala Ile Ala 500 505 510		
Leu Ala Ile Thr Leu Trp Phe Leu Leu Gln Arg Phe Ala Gly Lys Lys 515 520 525		
Ser Ser Trp Leu Ile Tyr Leu Ser Thr Val Ala Val Ala Leu Met Met 530 535 540		
Phe Ser Val Gln Asp Ala Leu Gln Phe Gly Ser Leu Thr Leu Val Ala 545 550 555 560		
Leu Ala Leu Ile Thr Val Asp Val Leu Ser Val Arg Glu Ile Gly Arg 565 570 575		
Arg Gly Leu Leu Thr Gly Leu Ala Ala Ala Leu Phe Gly Trp Pro Ile 580 585 590		
Leu Ile Val Ile Gly Phe Leu Ile His Arg Arg Tyr Ala Ala Thr Ile 595 600 605		

Thr Thr Thr Val Thr Ala Ala Val Leu Trp Ile Leu Gly Ile Leu Leu
 610 615 620

Asn Pro Asp Ala Phe Asn Leu Asn Leu Leu Arg Gln Trp Phe Asn Gly
 625 630 635 640

Arg Asp Gly Arg Asp Asn Leu Ser Phe Tyr Ala Phe Leu Ala Arg Trp
 645 650 655

Val Ser Glu Ser Pro Ala
 660

<210> 2125
 <211> 573
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(550)
 <223> RXA01178

<400> 2125
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tctatgcttt ccttgccagg tgggtcagcg aatccccagc atg atg ttc gta tgg 115
 Met Met Phe Val Trp
 1 5

ttc atc gtc gcc cta gga ctt ggt gcc tgg gca atc cac cgc acc tgg 163
 Phe Ile Val Ala Leu Gly Leu Gly Ala Trp Ala Ile His Arg Thr Trp
 10 15 20

tca cat gga ttc aag gac ctc tcc gtt gca ctg agc atc gca cta cca 211
 Ser His Gly Phe Lys Asp Leu Ser Val Ala Leu Ser Ile Ala Leu Pro
 25 30 35

acc ttg gtg ctc ccc ata gtg gaa ctc cac cac ctc gtg cta ctt ctt 259
 Thr Leu Val Leu Pro Ile Val Glu Leu His His Leu Val Leu Leu Leu
 40 45 50

cca ctg atc gca gtg ttg ctt cgt caa gga cgc gtg gca att tcc tac 307
 Pro Leu Ile Ala Val Leu Leu Arg Gln Gly Arg Val Ala Ile Ser Tyr
 55 60 65

ctc atc gga ttt atc tac cta gtc tca tgg act ccg caa cac ctg tcc 355
 Leu Ile Gly Phe Ile Tyr Leu Val Ser Trp Thr Pro Gln His Leu Ser
 70 75 80 85

tac tcc acg gta ttc cca ctt aat gat cca gca cca gaa ggg tac gtc 403
 Tyr Ser Thr Val Phe Pro Leu Asn Asp Pro Ala Pro Glu Gly Tyr Val
 90 95 100

gcc cac ttt gga tgg tat tta ctc gtt gaa cca atg gcg gta gca ccg 451
 Ala His Phe Gly Trp Tyr Leu Leu Val Glu Pro Met Ala Val Ala Pro
 105 110 115

gca gct ata atc ctc gga gca ttt att gcc tgt gct gca acc aca cct 499
 Ala Ala Ile Ile Leu Gly Ala Phe Ile Ala Cys Ala Ala Thr Thr Pro

120 125 130
aaa aca agt cag ctc gtg cag gtc gac aag tca agc gcg gaa aac acc 547
Lys Thr Ser Gln Leu Val Gln Val Asp Lys Ser Ser Ala Glu Asn Thr
135 140 145

aag taagccttac agtccgacag cct 573
Lys
150

<210> 2126
<211> 150
<212> PRT
<213> Corynebacterium glutamicum

<400> 2126
Met Met Phe Val Trp Phe Ile Val Ala Leu Gly Leu Gly Ala Trp Ala
1 5 10 15

Ile His Arg Thr Trp Ser His Gly Phe Lys Asp Leu Ser Val Ala Leu
20 25 30

Ser Ile Ala Leu Pro Thr Leu Val Leu Pro Ile Val Glu Leu His His
35 40 45

Leu Val Leu Leu Leu Pro Leu Ile Ala Val Leu Leu Arg Gln Gly Arg
50 55 60

Val Ala Ile Ser Tyr Leu Ile Gly Phe Ile Tyr Leu Val Ser Trp Thr
65 70 75 80

Pro Gln His Leu Ser Tyr Ser Thr Val Phe Pro Leu Asn Asp Pro Ala
85 90 95

Pro Glu Gly Tyr Val Ala His Phe Gly Trp Tyr Leu Leu Val Glu Pro
100 105 110

Met Ala Val Ala Pro Ala Ala Ile Ile Leu Gly Ala Phe Ile Ala Cys
115 120 125

Ala Ala Thr Thr Pro Lys Thr Ser Gln Leu Val Gln Val Asp Lys Ser
130 135 140

Ser Ala Glu Asn Thr Lys
145 150

<210> 2127
<211> 1589
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1573)
<223> RXA01184

<400> 2127
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cca	ggt	att	cct	tgg	tca	ggt	gga	ggt	gcc	att	ttc	tcg	agg	tcg	ctg	883
Pro	Gly	Ile	Pro	Trp	Ser	Val	Gly	Gly	Ala	Ile	Phe	Ser	Arg	Ser	Leu	
				250					255					260		
cgt	tat	atg	ttc	agg	gac	tcc	agg	ttg	ttg	gga	tca	atg	att	gtg	ttc	931
Arg	Tyr	Met	Phe	Arg	Asp	Ser	Arg	Leu	Leu	Gly	Ser	Met	Ile	Val	Phe	
			265					270					275			
ccg	ctt	ctt	ggc	gtg	ctg	ttt	att	ttc	cag	agc	ttc	acc	gtt	gag	ttt	979
Pro	Leu	Leu	Gly	Val	Leu	Phe	Ile	Phe	Gln	Ser	Phe	Thr	Val	Glu	Phe	
			280				285					290				
ttc	atg	atc	tat	gtt	ggg	ttg	atc	atg	atg	gca	gtg	ttc	gca	gga	tcc	1027
Phe	Met	Ile	Tyr	Val	Gly	Leu	Ile	Met	Met	Ala	Val	Phe	Ala	Gly	Ser	
	295					300					305					
gtt	gct	acc	aat	gat	ttt	ggc	tat	gac	ggc	cct	tcg	ttg	tgg	cta	aat	1075
Val	Ala	Thr	Asn	Asp	Phe	Gly	Tyr	Asp	Gly	Pro	Ser	Leu	Trp	Leu	Asn	
310					315					320					325	
atc	gtt	gct	ggc	gtc	aaa	gcc	cga	acg	ttg	ttg	atg	ccc	agg	cac	tgg	1123
Ile	Val	Ala	Gly	Val	Lys	Ala	Arg	Thr	Leu	Leu	Met	Pro	Arg	His	Trp	
				330					335					340		
gca	tca	atg	ctg	ccg	gga	agt	gtg	tca	att	gtg	gtg	ttt	atg	atc	atc	1171
Ala	Ser	Met	Leu	Pro	Gly	Ser	Val	Ser	Ile	Val	Val	Phe	Met	Ile	Ile	
			345					350					355			
acc	att	gtg	ctc	gcg	gag	aat	aag	acc	acc	gct	gtg	ctg	atc	tgt	ttt	1219
Thr	Ile	Val	Leu	Ala	Glu	Asn	Lys	Thr	Thr	Ala	Val	Leu	Ile	Cys	Phe	
		360					365					370				
att	ggc	ctg	ggg	atc	ttt	atc	tcc	agt	gcg	gct	gta	gcg	ttg	ttg	gtc	1267
Ile	Gly	Leu	Gly	Ile	Phe	Ile	Ser	Ser	Ala	Ala	Val	Ala	Leu	Leu	Val	
	375					380					385					
acc	aca	ttt	aat	ccg	tat	ccg	act	tct	aag	cca	ggc	acg	agt	cct	tgg	1315
Thr	Thr	Phe	Asn	Pro	Tyr	Pro	Thr	Ser	Lys	Pro	Gly	Thr	Ser	Pro	Trp	
390					395				400						405	
ggc	gat	cga	agt	ggc	tat	tcc	ggt	gct	gcg	ttc	gtg	gga	gca	ttt	gcc	1363
Gly	Asp	Arg	Ser	Gly	Tyr	Ser	Gly	Ala	Ala	Phe	Val	Gly	Ala	Phe	Ala	
				410				415						420		
gca	ctg	tta	ctg	gga	tgg	atc	ccg	acg	att	cct	act	atc	gca	ttg	ggt	1411
Ala	Leu	Leu	Leu	Gly	Trp	Ile	Pro	Thr	Ile	Pro	Thr	Ile	Ala	Leu	Gly	
			425					430					435			
atc	ttt	ggt	ctg	gtt	acc	gat	cag	atg	tgg	atg	atc	atc	ctc	gcg	gag	1459
Ile	Phe	Gly	Leu	Val	Thr	Asp	Gln	Met	Trp	Met	Ile	Ile	Leu	Ala	Glu	
		440					445					450				
gtg	ctg	gcc	att	att	ctc	cca	gta	gct	gtg	tac	atc	ggc	gtt	gct	aag	1507
Val	Leu	Ala	Ile	Ile	Leu	Pro	Val	Ala	Val	Tyr	Ile	Gly	Val	Ala	Lys	
	455					460					465					
gtg	tgt	att	cgc	aag	gtg	gag	aag	gat	ctt	ccg	gag	atc	ttc	gac	aag	1555
Val	Cys	Ile	Arg	Lys	Val	Glu	Lys	Asp	Leu	Pro	Glu	Ile	Phe	Asp	Lys	

470

475

480

485

gtg aaa act cac gtg aaa tagaaaaatg cggggt
 Val Lys Thr His Val Lys
 490

1589

<210> 2128

<211> 491

<212> PRT

<213> Corynebacterium glutamicum

<400> 2128

Met Gly Leu Phe Gly Phe Gly Ile Phe Leu Ala Leu Gly Leu Gly Gln
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Asp His Met Gly Ile Leu Ala Gly Val Val Ser Val Gly Met Val Ala
 20 25 30

Tyr Cys Ile Ala Ala Phe Met Trp Pro Ser Gly Glu Gly Gln Leu Asp
 35 40 45

Pro Thr Ala Phe Ser Thr Met Pro Leu Ser Ala Lys Gln Leu Leu Pro
 50 55 60

Gly Phe Ala Ile Gly Thr Leu Leu Gln Ser Arg Gly Ile Ile Ala Val
 65 70 75 80

Ile Cys Thr Val Ala Thr Ser Ile Ile Ala Ala Val Phe Leu Pro Val
 85 90 95

Gly Ser Trp Pro Met Ile Val Phe Met Met Ala Val Ser Leu Val Thr
 100 105 110

Thr Leu Leu Leu Gly Glu Leu Leu Gly Ala Leu Thr Ser Gly Ser Ser
 115 120 125

Ser Arg Val Ser Asn Asp Arg Arg Thr Val Leu Thr Ser Val Val Phe
 130 135 140

Met Val Phe Val Val Gly Tyr Asn Met Leu Ile Gly Ala Asp Gly Met
 145 150 155 160

Ser Arg Ile Asp Ala Ile Gly Ala Tyr Thr Lys Trp Thr Pro Phe Gly
 165 170 175

Ala Gly Ala Gly Ala Ile Glu Ala Phe Ala Val Gly Leu Trp Gly Glu
 180 185 190

Ala Gly Leu Leu Thr Leu Leu Ala Phe Val Tyr Val Ala Ala Gly Phe
 195 200 205

Trp Leu Trp Ser Gln Leu Ile Asn Arg Ala Leu Thr Ala Pro Leu Asp
 210 215 220

Gln Gly Gly Gln Gly Gln Ser Ala Lys Asp Ser Ala Gly Glu Gly Lys
 225 230 235 240

Lys Val Leu Phe Leu Pro Gly Ile Pro Trp Ser Val Gly Gly Ala Ile
 245 250 255

Phe Ser Arg Ser Leu Arg Tyr Met Phe Arg Asp Ser Arg Leu Leu Gly
 260 265 270
 Ser Met Ile Val Phe Pro Leu Leu Gly Val Leu Phe Ile Phe Gln Ser
 275 280 285
 Phe Thr Val Glu Phe Phe Met Ile Tyr Val Gly Leu Ile Met Met Ala
 290 295 300
 Val Phe Ala Gly Ser Val Ala Thr Asn Asp Phe Gly Tyr Asp Gly Pro
 305 310 315 320
 Ser Leu Trp Leu Asn Ile Val Ala Gly Val Lys Ala Arg Thr Leu Leu
 325 330 335
 Met Pro Arg His Trp Ala Ser Met Leu Pro Gly Ser Val Ser Ile Val
 340 345 350
 Val Phe Met Ile Ile Thr Ile Val Leu Ala Glu Asn Lys Thr Thr Ala
 355 360 365
 Val Leu Ile Cys Phe Ile Gly Leu Gly Ile Phe Ile Ser Ser Ala Ala
 370 375 380
 Val Ala Leu Leu Val Thr Thr Phe Asn Pro Tyr Pro Thr Ser Lys Pro
 385 390 395 400
 Gly Thr Ser Pro Trp Gly Asp Arg Ser Gly Tyr Ser Gly Ala Ala Phe
 405 410 415
 Val Gly Ala Phe Ala Ala Leu Leu Leu Gly Trp Ile Pro Thr Ile Pro
 420 425 430
 Thr Ile Ala Leu Gly Ile Phe Gly Leu Val Thr Asp Gln Met Trp Met
 435 440 445
 Ile Ile Leu Ala Glu Val Leu Ala Ile Ile Leu Pro Val Ala Val Tyr
 450 455 460
 Ile Gly Val Ala Lys Val Cys Ile Arg Lys Val Glu Lys Asp Leu Pro
 465 470 475 480
 Glu Ile Phe Asp Lys Val Lys Thr His Val Lys
 485 490

<210> 2129

<211> 1221

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1198)

<223> RXA01186

<400> 2129

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 agttcaacaa ttacataaca tctgaaagaa tagggacatt atg gct aca cct gta 115
 Met Ala Thr Pro Val

1

5

cca ctg gtt ttt aac gca cct aag cgt ggc atg ccc cca acc cac ttt	163
Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met Pro Pro Thr His Phe	
10 15 20	
gcg gat ctt aat gat gag gct cgc att gag gct ctt aaa gag ctc ggc	211
Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala Leu Lys Glu Leu Gly	
25 30 35	
ttg ccc aaa ttc cga ctc aat cag atc gct cga cac tac tat ggt cgc	259
Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg His Tyr Tyr Gly Arg	
40 45 50	
ctc gag gct gac cca ctc act atg acg gac ctg cct gaa ggt gct cgt	307
Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu Pro Glu Gly Ala Arg	
55 60 65	
caa gaa gtc aag gat gct ctt ttt cca acg ttg atg tct cct ctg cgc	355
Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu Met Ser Pro Leu Arg	
70 75 80 85	
gtc gtc gaa acc gat gac gat aca act cag aag acg tta tgg aag ctc	403
Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys Thr Leu Trp Lys Leu	
90 95 100	
cat gat ggc act ttg ctt gag tct gtt ctc atg cgc tat tca gat cgc	451
His Asp Gly Thr Leu Leu Glu Ser Val Leu Met Arg Tyr Ser Asp Arg	
105 110 115	
tcc acg ctg tgt att tct tcg cag gct ggt tgc ggc atg gcg tgc cca	499
Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys Gly Met Ala Cys Pro	
120 125 130	
ttc tgt gca act ggt cag ggc ggt ttg gac cgt aac ctt tca atc ggt	547
Phe Cys Ala Thr Gly Gln Gly Leu Asp Arg Asn Leu Ser Ile Gly	
135 140 145	
gag atc gtg gat cag gtt cgt aat gct gct gca acg atg cag tca gag	595
Glu Ile Val Asp Gln Val Arg Asn Ala Ala Thr Met Gln Ser Glu	
150 155 160 165	
ggc ggt cgt ctg tcc aac att gtg ttc atg gga atg ggc gag cct ctc	643
Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu	
170 175 180	
gct aac tac aag cgc gtg gtg tcg gct gtt cgt cag atc acg cag cca	691
Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg Gln Ile Thr Gln Pro	
185 190 195	
agc cct gcg ggc ttc ggc att tcc cag cgc agt gtg act gtc tcc acc	739
Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser Val Thr Val Ser Thr	
200 205 210	
gtg ggc ctc gct cca gct atc agg aag ctt gcc gac gaa gag atg tcc	787
Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala Asp Glu Glu Met Ser	
215 220 225	
gta act ttg gca gtt tcc ttg cac act cca gac gat gag ttg cgt gac	835
Val Thr Leu Ala Val Ser Leu His Thr Pro Asp Asp Glu Leu Arg Asp	
230 235 240 245	

act ctc gtg cca gtc aac aat cgt tgg cct gtc gct gag gta ctg gac 883
 Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val Ala Glu Val Leu Asp
 250 255 260

gct gct cgt tac tac gca gat aag tct ggc cgt cgc gtc tcc atc gag 931
 Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg Arg Val Ser Ile Glu
 265 270 275

tat gcg ctc att cgc gat gtg aat gac cag gat tgg cgc gca gat atg 979
 Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp Trp Arg Ala Asp Met
 280 285 290

ctg ggc gag aag ctg cat aag gct ttg ggc tcc cgt gtg cac gtc aac 1027
 Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser Arg Val His Val Asn
 295 300 305

ttg att cca ttg aac cca act cct ggt tct aag tgg gat gct gca cca 1075
 Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys Trp Asp Ala Ala Pro
 310 315 320 325

aag gct cgt cag gat gag ttt gtg cgt cgt gtg atc gcc aag ggt gtt 1123
 Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val Ile Ala Lys Gly Val
 330 335 340

cca tgc act gtg cgt gat acc aag gga caa gaa atc gct gcg gct tgt 1171
 Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu Ile Ala Ala Ala Cys
 345 350 355

gga cag ctt gct gcg gag gaa tct gct taagccctca aagctcaaaa 1218
 Gly Gln Leu Ala Ala Glu Glu Ser Ala
 360 365

gcc 1221

<210> 2130

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 2130

Met Ala Thr Pro Val Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met
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Pro Pro Thr His Phe Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala
 20 25 30

Leu Lys Glu Leu Gly Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg
 35 40 45

His Tyr Tyr Gly Arg Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu
 50 55 60

Pro Glu Gly Ala Arg Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu
 65 70 75 80

Met Ser Pro Leu Arg Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys
 85 90 95

Thr Leu Trp Lys Leu His Asp Gly Thr Leu Leu Glu Ser Val Leu Met

100					105					110					
Arg	Tyr	Ser	Asp	Arg	Ser	Thr	Leu	Cys	Ile	Ser	Ser	Gln	Ala	Gly	Cys
		115					120					125			
Gly	Met	Ala	Cys	Pro	Phe	Cys	Ala	Thr	Gly	Gln	Gly	Gly	Leu	Asp	Arg
	130					135					140				
Asn	Leu	Ser	Ile	Gly	Glu	Ile	Val	Asp	Gln	Val	Arg	Asn	Ala	Ala	Ala
	145					150					155				160
Thr	Met	Gln	Ser	Glu	Gly	Gly	Arg	Leu	Ser	Asn	Ile	Val	Phe	Met	Gly
				165					170					175	
Met	Gly	Glu	Pro	Leu	Ala	Asn	Tyr	Lys	Arg	Val	Val	Ser	Ala	Val	Arg
			180					185					190		
Gln	Ile	Thr	Gln	Pro	Ser	Pro	Ala	Gly	Phe	Gly	Ile	Ser	Gln	Arg	Ser
	195						200					205			
Val	Thr	Val	Ser	Thr	Val	Gly	Leu	Ala	Pro	Ala	Ile	Arg	Lys	Leu	Ala
	210					215					220				
Asp	Glu	Glu	Met	Ser	Val	Thr	Leu	Ala	Val	Ser	Leu	His	Thr	Pro	Asp
	225					230					235				240
Asp	Glu	Leu	Arg	Asp	Thr	Leu	Val	Pro	Val	Asn	Asn	Arg	Trp	Pro	Val
				245					250					255	
Ala	Glu	Val	Leu	Asp	Ala	Ala	Arg	Tyr	Tyr	Ala	Asp	Lys	Ser	Gly	Arg
			260					265					270		
Arg	Val	Ser	Ile	Glu	Tyr	Ala	Leu	Ile	Arg	Asp	Val	Asn	Asp	Gln	Asp
		275					280					285			
Trp	Arg	Ala	Asp	Met	Leu	Gly	Glu	Lys	Leu	His	Lys	Ala	Leu	Gly	Ser
	290					295					300				
Arg	Val	His	Val	Asn	Leu	Ile	Pro	Leu	Asn	Pro	Thr	Pro	Gly	Ser	Lys
	305					310					315				320
Trp	Asp	Ala	Ala	Pro	Lys	Ala	Arg	Gln	Asp	Glu	Phe	Val	Arg	Arg	Val
				325					330					335	
Ile	Ala	Lys	Gly	Val	Pro	Cys	Thr	Val	Arg	Asp	Thr	Lys	Gly	Gln	Glu
			340					345					350		
Ile	Ala	Ala	Ala	Cys	Gly	Gln	Leu	Ala	Ala	Glu	Glu	Ser	Ala		
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<210> 2131

<211> 1221

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1198)

<223> RXA01186

<400> 2131

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agttcaacaa ttacataaca tctgaaagaa tagggacatt atg gct aca cct gta 115
                                         Met Ala Thr Pro Val
                                         1 5

cca ctg gtt ttt aac gca cct aag cgt ggc atg ccc cca acc cac ttt 163
Pro Leu Val Phe Asn Ala Pro Lys Arg Gly Met Pro Pro Thr His Phe
                        10 15 20

gcg gat ctt aat gat gag gct cgc att gag gct ctt aaa gag ctc ggc 211
Ala Asp Leu Asn Asp Glu Ala Arg Ile Glu Ala Leu Lys Glu Leu Gly
                        25 30 35

ttg ccc aaa ttc cga ctc aat cag atc gct cga cac tac tat ggt cgc 259
Leu Pro Lys Phe Arg Leu Asn Gln Ile Ala Arg His Tyr Tyr Gly Arg
                        40 45 50

ctc gag gct gac cca ctc act atg acg gac ctg cct gaa ggt gct cgt 307
Leu Glu Ala Asp Pro Leu Thr Met Thr Asp Leu Pro Glu Gly Ala Arg
                        55 60 65

caa gaa gtc aag gat gct ctt ttt cca acg ttg atg tct cct ctg cgc 355
Gln Glu Val Lys Asp Ala Leu Phe Pro Thr Leu Met Ser Pro Leu Arg
                        70 75 80 85

gtc gtc gaa acc gat gac gat aca act cag aag acg tta tgg aag ctc 403
Val Val Glu Thr Asp Asp Thr Thr Gln Lys Thr Leu Trp Lys Leu
                        90 95 100

cat gat ggc act ttg ctt gag tct gtt ctc atg cgc tat tca gat cgc 451
His Asp Gly Thr Leu Leu Glu Ser Val Leu Met Arg Tyr Ser Asp Arg
                        105 110 115

tcc acg ctg tgt att tct tcg cag gct ggt tgc ggc atg gcg tgc cca 499
Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys Gly Met Ala Cys Pro
                        120 125 130

ttc tgt gca act ggt cag ggc ggt ttg gac cgt aac ctt tca atc ggt 547
Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg Asn Leu Ser Ile Gly
                        135 140 145

gag atc gtg gat cag gtt cgt aat gct gct gca acg atg cag tca gag 595
Glu Ile Val Asp Gln Val Arg Asn Ala Ala Thr Met Gln Ser Glu
                        150 155 160 165

ggc ggt cgt ctg tcc aac att gtg ttc atg gga atg ggc gag cct ctc 643
Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu
                        170 175 180

gct aac tac aag cgc gtg gtg tcg gct gtt cgt cag atc acg cag cca 691
Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg Gln Ile Thr Gln Pro
                        185 190 195

agc cct gcg ggc ttc ggc att tcc cag cgc agt gtg act gtc tcc acc 739
Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser Val Thr Val Ser Thr
                        200 205 210

gtg ggc ctc gct cca gct atc agg aag ctt gcc gac gaa gag atg tcc 787
Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala Asp Glu Glu Met Ser

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215	220	225	
gta act ttg gca gtt tcc ttg cac act cca gac gat gag ttg cgt gac			835
Val Thr Leu Ala Val Ser Leu His Thr Pro Asp Asp Glu Leu Arg Asp			
230	235	240	245
act ctc gtg cca gtc aac aat cgt tgg cct gtc gct gag gta ctg gac			883
Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val Ala Glu Val Leu Asp			
	250	255	260
gct gct cgt tac tac gca gat aag tct ggc cgt cgc gtc tcc atc gag			931
Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg Arg Val Ser Ile Glu			
	265	270	275
tat gcg ctc att cgc gat gtg aat gac cag gat tgg cgc gca gat atg			979
Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp Trp Arg Ala Asp Met			
	280	285	290
ctg ggc gag aag ctg cat aag gct ttg ggc tcc cgt gtg cac gtc aac			1027
Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser Arg Val His Val Asn			
	295	300	305
ttg att cca ttg aac cca act cct ggt tct aag tgg gat gct gca cca			1075
Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys Trp Asp Ala Ala Pro			
	310	315	320
aag gct cgt cag gat gag ttt gtg cgt cgt gtg atc gcc aag ggt gtt			1123
Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val Ile Ala Lys Gly Val			
	330	335	340
cca tgc act gtg cgt gat acc aag gga caa gaa atc gct gcg gct tgt			1171
Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu Ile Ala Ala Ala Cys			
	345	350	355
gga cag ctt gct gcg gag gaa tct gct taagccctca aagctcaaaa			1218
Gly Gln Leu Ala Ala Glu Glu Ser Ala			
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gcc			1221

<210> 2132

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 2132

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Pro	Pro	Thr	His	Phe	Ala	Asp	Leu	Asn	Asp	Glu	Ala	Arg	Ile	Glu	Ala
			20					25					30		

Leu	Lys	Glu	Leu	Gly	Leu	Pro	Lys	Phe	Arg	Leu	Asn	Gln	Ile	Ala	Arg
		35					40					45			

His	Tyr	Tyr	Gly	Arg	Leu	Glu	Ala	Asp	Pro	Leu	Thr	Met	Thr	Asp	Leu
	50					55					60				

Pro	Glu	Gly	Ala	Arg	Gln	Glu	Val	Lys	Asp	Ala	Leu	Phe	Pro	Thr	Leu
65					70					75					80

Met Ser Pro Leu Arg Val Val Glu Thr Asp Asp Asp Thr Thr Gln Lys
 85 90 95
 Thr Leu Trp Lys Leu His Asp Gly Thr Leu Leu Glu Ser Val Leu Met
 100 105 110
 Arg Tyr Ser Asp Arg Ser Thr Leu Cys Ile Ser Ser Gln Ala Gly Cys
 115 120 125
 Gly Met Ala Cys Pro Phe Cys Ala Thr Gly Gln Gly Gly Leu Asp Arg
 130 135 140
 Asn Leu Ser Ile Gly Glu Ile Val Asp Gln Val Arg Asn Ala Ala Ala
 145 150 155 160
 Thr Met Gln Ser Glu Gly Gly Arg Leu Ser Asn Ile Val Phe Met Gly
 165 170 175
 Met Gly Glu Pro Leu Ala Asn Tyr Lys Arg Val Val Ser Ala Val Arg
 180 185 190
 Gln Ile Thr Gln Pro Ser Pro Ala Gly Phe Gly Ile Ser Gln Arg Ser
 195 200 205
 Val Thr Val Ser Thr Val Gly Leu Ala Pro Ala Ile Arg Lys Leu Ala
 210 215 220
 Asp Glu Glu Met Ser Val Thr Leu Ala Val Ser Leu His Thr Pro Asp
 225 230 235 240
 Asp Glu Leu Arg Asp Thr Leu Val Pro Val Asn Asn Arg Trp Pro Val
 245 250 255
 Ala Glu Val Leu Asp Ala Ala Arg Tyr Tyr Ala Asp Lys Ser Gly Arg
 260 265 270
 Arg Val Ser Ile Glu Tyr Ala Leu Ile Arg Asp Val Asn Asp Gln Asp
 275 280 285
 Trp Arg Ala Asp Met Leu Gly Glu Lys Leu His Lys Ala Leu Gly Ser
 290 295 300
 Arg Val His Val Asn Leu Ile Pro Leu Asn Pro Thr Pro Gly Ser Lys
 305 310 315 320
 Trp Asp Ala Ala Pro Lys Ala Arg Gln Asp Glu Phe Val Arg Arg Val
 325 330 335
 Ile Ala Lys Gly Val Pro Cys Thr Val Arg Asp Thr Lys Gly Gln Glu
 340 345 350
 Ile Ala Ala Ala Cys Gly Gln Leu Ala Ala Glu Glu Ser Ala
 355 360 365

<210> 2133

<211> 573

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXA01187

<400> 2133

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gtgattctac gagttcaatg gctgtatgag caacagacct gtg gat cca ttt gag 115
                               Val Asp Pro Phe Glu
                               1           5

acc aac cca aac gac ctt ccc acc ggt tta gac cca gca tac gaa ggt 163
Thr Asn Pro Asn Asp Leu Pro Thr Gly Leu Asp Pro Ala Tyr Glu Gly
                10                15                20

aac agt gag tta aac ccg ctt gga gga aaa aat att ccc gac gag cct 211
Asn Ser Glu Leu Asn Pro Leu Gly Gly Lys Asn Ile Pro Asp Glu Pro
                25                30                35

gag gtg act gca aac aca cct gca gtt caa gaa gaa cct gct tac tcg 259
Glu Val Thr Ala Asn Thr Pro Ala Val Gln Glu Glu Pro Ala Tyr Ser
                40                45                50

gag cca gaa act gcc gtt gag tcg aag cgt cag gcg aag cag aac aca 307
Glu Pro Glu Thr Ala Val Glu Ser Lys Arg Gln Ala Lys Gln Asn Thr
                55                60                65

aag aag tcc gaa cct gtt gtg gct cca aaa caa aca ctt gcc ggt gcc 355
Lys Lys Ser Glu Pro Val Val Ala Pro Lys Gln Thr Leu Ala Gly Gly
                70                75                80                85

acg tgg gta gct ctc atc gta ggc gca ctt ttg cta atc cta ctg ttg 403
Thr Trp Val Ala Leu Ile Val Gly Ala Leu Leu Leu Ile Leu Leu Leu
                90                95                100

gtc ttc atc atg cag aac caa acc acc gta gag ctt aac ctt ttt gcg 451
Val Phe Ile Met Gln Asn Gln Thr Thr Val Glu Leu Asn Leu Phe Ala
                105                110                115

tgg acc ttc caa ttc cca gcc gga atc ggt ttc cta cta gca gcc att 499
Trp Thr Phe Gln Phe Pro Ala Gly Ile Gly Phe Leu Leu Ala Ala Ile
                120                125                130

acc ggt gca ttg att atg gcg ctt ggt ggt gcc gtg cgc atg ttt gag 547
Thr Gly Ala Leu Ile Met Ala Leu Gly Gly Gly Val Arg Met Phe Glu
                135                140                145

tac cgt cgc agt taagaaaaat ccgt 573
Tyr Arg Arg Ser
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<210> 2134

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 2134

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Val Asp Pro Phe Glu Thr Asn Pro Asn Asp Leu Pro Thr Gly Leu Asp
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tca gta act ttg ctt gat cgt aga gat cca gct gct gat gag gcg gtt 355
 Ser Val Thr Leu Leu Asp Arg Arg Asp Pro Ala Ala Asp Glu Ala Val
 70 75 80 85

 ttt atg tct caa ggc tta aaa att ctg cac att aaa tcc aaa aat gat 403
 Phe Met Ser Gln Gly Leu Lys Ile Leu His Ile Lys Ser Lys Asn Asp
 90 95 100

 cag att gaa tta gct ttg gac gcc cac ggg gag atg gcg ttt act gcc 451
 Gln Ile Glu Leu Ala Leu Asp Ala His Gly Glu Met Ala Phe Thr Ala
 105 110 115

 tgg ttg gaa gca gca cca gat gcg cgg gcg gag cat tca ttg aat cca 499
 Trp Leu Glu Ala Ala Pro Asp Ala Arg Ala Glu His Ser Leu Asn Pro
 120 125 130

 cgt gat ttc aac cgc ttt cga gcc agc aaa gac acc cgc aaa aac cgc 547
 Arg Asp Phe Asn Arg Phe Arg Ala Ser Lys Asp Thr Arg Lys Asn Arg
 135 140 145

 taagtagacg tcattgttat ggt 570

<210> 2136

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 2136

Val Ile Val Ala Val Ser Ala Val Leu Leu Ala Ala Trp Arg Phe Phe
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 Thr Leu Arg Ser Arg Gly Thr Thr Val Ile Leu Arg Glu Leu Pro Gln
 20 25 30

 Ser Gly Val His Gly Trp Arg His Gly Ser Phe Arg Tyr Asn Gly Asn
 35 40 45

 Asp Leu Glu Tyr Phe Lys Leu Arg Ser Leu Ser Pro Met Ala Asp Leu
 50 55 60

 Ile Leu Asn Arg Leu Ser Val Thr Leu Leu Asp Arg Arg Asp Pro Ala
 65 70 75 80

 Ala Asp Glu Ala Val Phe Met Ser Gln Gly Leu Lys Ile Leu His Ile
 85 90 95

 Lys Ser Lys Asn Asp Gln Ile Glu Leu Ala Leu Asp Ala His Gly Glu
 100 105 110

 Met Ala Phe Thr Ala Trp Leu Glu Ala Ala Pro Asp Ala Arg Ala Glu
 115 120 125

 His Ser Leu Asn Pro Arg Asp Phe Asn Arg Phe Arg Ala Ser Lys Asp
 130 135 140

 Thr Arg Lys Asn Arg
 145

<210> 2137
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA01196

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gcaaaaaccg ctaagtagac gtcattgtta tgggtgggtgc atg cgt tta gtc atc 115
Met Arg Leu Val Ile
1 5
gcc cgt tgc tca gtt gat tat gtt ggc cgt ttg gaa gct cat ctt ccg 163
Ala Arg Cys Ser Val Asp Tyr Val Gly Arg Leu Glu Ala His Leu Pro
10 15 20
tcc gcc gat cgc ctt ttg atg gtt aag gcg gat ggt tct gta tcc atc 211
Ser Ala Asp Arg Leu Leu Met Val Lys Ala Asp Gly Ser Val Ser Ile
25 30 35
cat gcc gat gac cgt gcc tat aag cca ctg aac tgg atg aca cct cca 259
His Ala Asp Asp Arg Ala Tyr Lys Pro Leu Asn Trp Met Thr Pro Pro
40 45 50
tgt tct tta gtt gaa act ccc atc act gat gaa gat ggt gaa gca aca 307
Cys Ser Leu Val Glu Thr Pro Ile Thr Asp Glu Asp Gly Glu Ala Thr
55 60 65
ggg gaa agc ctg tgg gtg gtg gaa aac aaa aag ggc gag cag ctt cga 355
Gly Glu Ser Leu Trp Val Val Glu Asn Lys Lys Gly Glu Gln Leu Arg
70 75 80 85
att act gtg gaa gaa att cat tcg gaa caa aac ttc gat cta ggc caa 403
Ile Thr Val Glu Glu Ile His Ser Glu Gln Asn Phe Asp Leu Gly Gln
90 95 100
gac cca ggt ttg gtg aaa gac gga gtg gaa gat cat ctc caa gag ctt 451
Asp Pro Gly Leu Val Lys Asp Gly Val Glu Asp His Leu Gln Glu Leu
105 110 115
ctt gca gag cac atc act acg ttg ggt gat ggg tac aca ttg att cgt 499
Leu Ala Glu His Ile Thr Thr Leu Gly Asp Gly Tyr Thr Leu Ile Arg
120 125 130
cgg gag tat cca aca gct att ggg cct gtc gat att ttg tgt cgc aac 547
Arg Glu Tyr Pro Thr Ala Ile Gly Pro Val Asp Ile Leu Cys Arg Asn
135 140 145
tct gac ggc gag act gtc gct gtg gag atc aag cgt cgt ggt ggc atc 595
Ser Asp Gly Glu Thr Val Ala Val Glu Ile Lys Arg Arg Gly Gly Ile
150 155 160 165
gac ggc gtt gag cag ttg acc agg tat ttg gaa ttg ctc aac cgt gat 643
Asp Gly Val Glu Gln Leu Thr Arg Tyr Leu Glu Leu Leu Asn Arg Asp
170 175 180

gaa ttg ctc aag cct gtt cat gga gtg ttt gca gcc cag gag att aag 691
 Glu Leu Leu Lys Pro Val His Gly Val Phe Ala Ala Gln Glu Ile Lys
 185 190 195
 cct cag gca aag act ctc gcg gag gat cgt ggc atc aag tgc gtg acg 739
 Pro Gln Ala Lys Thr Leu Ala Glu Asp Arg Gly Ile Lys Cys Val Thr
 200 205 210
 ttg gat tat caa gcg ctt cgt ggc att gag tcc aat gag ctg aca ttg 787
 Leu Asp Tyr Gln Ala Leu Arg Gly Ile Glu Ser Asn Glu Leu Thr Leu
 215 220 225
 ttc taagaacatg ggccgaaaaa ata 813
 Phe
 230

<210> 2138

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 2138

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 20 25 30
 Gly Ser Val Ser Ile His Ala Asp Asp Arg Ala Tyr Lys Pro Leu Asn
 35 40 45
 Trp Met Thr Pro Pro Cys Ser Leu Val Glu Thr Pro Ile Thr Asp Glu
 50 55 60
 Asp Gly Glu Ala Thr Gly Glu Ser Leu Trp Val Val Glu Asn Lys Lys
 65 70 75 80
 Gly Glu Gln Leu Arg Ile Thr Val Glu Glu Ile His Ser Glu Gln Asn
 85 90 95
 Phe Asp Leu Gly Gln Asp Pro Gly Leu Val Lys Asp Gly Val Glu Asp
 100 105 110
 His Leu Gln Glu Leu Leu Ala Glu His Ile Thr Thr Leu Gly Asp Gly
 115 120 125
 Tyr Thr Leu Ile Arg Arg Glu Tyr Pro Thr Ala Ile Gly Pro Val Asp
 130 135 140
 Ile Leu Cys Arg Asn Ser Asp Gly Glu Thr Val Ala Val Glu Ile Lys
 145 150 155 160
 Arg Arg Gly Gly Ile Asp Gly Val Glu Gln Leu Thr Arg Tyr Leu Glu
 165 170 175
 Leu Leu Asn Arg Asp Glu Leu Leu Lys Pro Val His Gly Val Phe Ala
 180 185 190
 Ala Gln Glu Ile Lys Pro Gln Ala Lys Thr Leu Ala Glu Asp Arg Gly
 195 200 205

Ile Lys Cys Val Thr Leu Asp Tyr Gln Ala Leu Arg Gly Ile Glu Ser
 210 215 220

Asn Glu Leu Thr Leu Phe
 225 230

<210> 2139

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(553)

<223> RXA01197

<400> 2139

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tcctcaatat tccccacct gctatgccta aaattaagcc atg tct acc gaa cag 115
 Met Ser Thr Glu Gln
 1 5

tct ttg aat atc ccc cac gaa tac gtc atc tgc ctc gat cat gtt ggc 163
 Ser Leu Asn Ile Pro His Glu Tyr Val Ile Cys Leu Asp His Val Gly
 10 15 20

atc gcc gtc cct gac ctc gag gaa gcc atc gaa ttt tac cgt tcc gca 211
 Ile Ala Val Pro Asp Leu Glu Glu Ala Ile Glu Phe Tyr Arg Ser Ala
 25 30 35

ttc ggc tgg gta aac cac cac caa gaa atc aat gag gaa caa ggc att 259
 Phe Gly Trp Val Asn His His Gln Glu Ile Asn Glu Glu Gln Gly Ile
 40 45 50

tca gag gcc atg atc ggc ccc aaa gac att aaa agc aca gaa ggc atg 307
 Ser Glu Ala Met Ile Gly Pro Lys Asp Ile Lys Ser Thr Glu Gly Met
 55 60 65

att cag ctc atc gcg ccg ctc aac gag gac tcc aca atc gcc aaa ttc 355
 Ile Gln Leu Ile Ala Pro Leu Asn Glu Asp Ser Thr Ile Ala Lys Phe
 70 75 80 85

ctc gaa aag aaa ggt ccc ggc atc cag caa atg tgc ctg cgc acc aac 403
 Leu Glu Lys Lys Gly Pro Gly Ile Gln Gln Met Cys Leu Arg Thr Asn
 90 95 100

aac atc gat gcg ctc tcc gag cac ctg cgc cgc caa ggc gtg cgc ctg 451
 Asn Ile Asp Ala Leu Ser Glu His Leu Arg Arg Gln Gly Val Arg Leu
 105 110 115

ctc tac ccc gaa ccc aaa aac ggc acc ggc ggt gcc cgc atc aac ttc 499
 Leu Tyr Pro Glu Pro Lys Asn Gly Thr Gly Gly Ala Arg Ile Asn Phe
 120 125 130

ctg cac ccc aaa gac gcg ggc ggc gtg ctg ctc gag atc acg cag cct 547
 Leu His Pro Lys Asp Ala Gly Gly Val Leu Leu Glu Ile Thr Gln Pro
 135 140 145

caa agc taattgctta tcgacgctcc cag
Gln Ser
150

576

<210> 2140
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 2140
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Leu Asp His Val Gly Ile Ala Val Pro Asp Leu Glu Glu Ala Ile Glu
20 25 30
Phe Tyr Arg Ser Ala Phe Gly Trp Val Asn His His Gln Glu Ile Asn
35 40 45
Glu Glu Gln Gly Ile Ser Glu Ala Met Ile Gly Pro Lys Asp Ile Lys
50 55 60
Ser Thr Glu Gly Met Ile Gln Leu Ile Ala Pro Leu Asn Glu Asp Ser
65 70 75 80
Thr Ile Ala Lys Phe Leu Glu Lys Lys Gly Pro Gly Ile Gln Gln Met
85 90 95
Cys Leu Arg Thr Asn Asn Ile Asp Ala Leu Ser Glu His Leu Arg Arg
100 105 110
Gln Gly Val Arg Leu Leu Tyr Pro Glu Pro Lys Asn Gly Thr Gly Gly
115 120 125
Ala Arg Ile Asn Phe Leu His Pro Lys Asp Ala Gly Gly Val Leu Leu
130 135 140
Glu Ile Thr Gln Pro Gln Ser
145 150

<210> 2141
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(403)
<223> RXA01198

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gctagtcatc acatgccaac cccaaggtag ggtggcagat atg att gtt gct ttt 115
Met Ile Val Ala Phe
1 5
tct gta gcc ccg act gtt act gat aat cca gat gct gag atg gcc gat 163
Ser Val Ala Pro Thr Val Thr Asp Asn Pro Asp Ala Glu Met Ala Asp

	10	15	20	
gcg gtc acg gag gcg att cga atc gtc cgc gca tcg ggt ctg cct aat				211
Ala Val Thr Glu Ala Ile Arg Ile Val Arg Ala Ser Gly Leu Pro Asn				
	25	30	35	
gaa act aac gcg atg ttc acg ctc att gag ggg gag tgg gat gag gtg				259
Glu Thr Asn Ala Met Phe Thr Leu Ile Glu Gly Glu Trp Asp Glu Val				
	40	45	50	
atg gcg gtg att aag gag gcc act gag gcg atc tct agg gta tct ccg				307
Met Ala Val Ile Lys Glu Ala Thr Glu Ala Ile Ser Arg Val Ser Pro				
	55	60	65	
cgt aca tcg ttg gta att aag gct gat att cgt ccg gga cac act ggc				355
Arg Thr Ser Leu Val Ile Lys Ala Asp Ile Arg Pro Gly His Thr Gly				
	70	75	80	85
caa ttg acg agg aag gtg gag gcg gtg gag gaa cgc cta gct agg gat				403
Gln Leu Thr Arg Lys Val Glu Ala Val Glu Glu Arg Leu Ala Arg Asp				
	90	95	100	
tagctttgta cttaaacttg ttg				426

<210> 2142

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 2142

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Ala	Glu	Met	Ala	Asp	Ala	Val	Thr	Glu	Ala	Ile	Arg	Ile	Val	Arg	Ala
		20						25					30		

Ser	Gly	Leu	Pro	Asn	Glu	Thr	Asn	Ala	Met	Phe	Thr	Leu	Ile	Glu	Gly
		35					40					45			

Glu	Trp	Asp	Glu	Val	Met	Ala	Val	Ile	Lys	Glu	Ala	Thr	Glu	Ala	Ile
	50					55					60				

Ser	Arg	Val	Ser	Pro	Arg	Thr	Ser	Leu	Val	Ile	Lys	Ala	Asp	Ile	Arg
65					70					75				80	

Pro	Gly	His	Thr	Gly	Gln	Leu	Thr	Arg	Lys	Val	Glu	Ala	Val	Glu	Glu
				85					90					95	

Arg	Leu	Ala	Arg	Asp
				100

<210> 2143

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(748)

<223> RXA01207 .

<400> 2143

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                                   Val Ser Arg Ile Tyr
                                   1 5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
              10              15              20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
              25              30              35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
              40              45              50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
              55              60              65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
              70              75              80              85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
              90              95              100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
              105              110              115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
              120              125              130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
              135              140              145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
              150              155              160              165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
              170              175              180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
              185              190              195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
              200              205              210

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 Ser Leu Arg
 215

771

<210> 2144
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2144
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 Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
 20 25 30
 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80
 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110
 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125
 Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140
 Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
 145 150 155 160
 Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175
 Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190
 Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
 195 200 205
 Gly Val Ser Ala Glu Ser Leu Arg
 210 215

<210> 2145
 <211> 1350
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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<222> (101)..(1327)

<223> RXA01213

<400> 2145

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catatcaacc aaacggtgta gttcttctaa gctttcacccc atg aca aat ccc aca 115

Met Thr Asn Pro Thr

1

5

gag gag cgc aac gca cgc cgc ctc att tgg gcc aac ggc ctg caa aac 163

Glu Glu Arg Asn Ala Arg Arg Leu Ile Trp Ala Asn Gly Leu Gln Asn

10

15

20

atc ggc gat caa atc gtt gcc gcc aaa aca gtc ctg ccc tgg ttg ctg 211

Ile Gly Asp Gln Ile Val Ala Ala Lys Thr Val Leu Pro Trp Leu Leu

25

30

35

caa gcc gct ggc gcg ccg ggc ttt ttg ctg gcg ctt ctg gtt cca atc 259

Gln Ala Ala Gly Ala Pro Gly Phe Leu Leu Ala Leu Leu Val Pro Ile

40

45

50

cgc gaa gcc gga tcg atg ctg ccg caa gct gcc att act ggc tgg gtg 307

Arg Glu Ala Gly Ser Met Leu Pro Gln Ala Ala Ile Thr Gly Trp Val

55

60

65

ctg agg cag acg tcg aga agc aaa gtc tgg gtg att ggc tcg aac ggc 355

Leu Arg Gln Thr Ser Arg Ser Lys Val Trp Val Ile Gly Ser Asn Gly

70

75

80

85

cag ttc gtc tcg gcg ctg ggt atc ggc gtg gct gcg ctg ttt ttg cgt 403

Gln Phe Val Ser Ala Leu Gly Ile Gly Val Ala Ala Leu Phe Leu Arg

90

95

100

ggg tgg gcg ctg ggc atc acg gtg atc gtg ctg ctt gcg gcg ctg tcg 451

Gly Trp Ala Leu Gly Ile Thr Val Ile Val Leu Leu Ala Ala Leu Ser

105

110

115

ctg ttt cga tcg atg tgt tcg att gca tcg aag gat gtt cag ggc aag 499

Leu Phe Arg Ser Met Cys Ser Ile Ala Ser Lys Asp Val Gln Gly Lys

120

125

130

gtg att tcc aag ggc aag cgt ggg ctg gta acg ggc cgc gcg acg gtg 547

Val Ile Ser Lys Gly Lys Arg Gly Leu Val Thr Gly Arg Ala Thr Val

135

140

145

att ggc ggt gtg atg ggc ctg gtt gca ggc ctg gcg atc gct att ttc 595

Ile Gly Gly Val Met Gly Leu Val Ala Gly Leu Ala Ile Ala Ile Phe

150

155

160

165

ttg ggc tcg cat tcc ccg acg agg gtg ctg gcc gca gtg gtg atc gcg 643

Leu Gly Ser His Ser Pro Thr Arg Val Leu Ala Ala Val Val Ile Ala

170

175

180

agc tcg ttt agc tgg ctg ttt gcc tcc att gtt ttc gcg cgc atc gaa 691

Ser Ser Phe Ser Trp Leu Phe Ala Ser Ile Val Phe Ala Arg Ile Glu

185

190

195

tac gcg aag cca gcg act cca aaa aac gcg cct tcc gca aac ccg tgg 739

Tyr Ala Lys Pro Ala Thr Pro Lys Asn Ala Pro Ser Ala Asn Pro Trp

200

205

210

gtg cgt cgc tgc atc gcc gca tta aaa gat gat aaa gct ttt cga cgt 787
 Val Arg Arg Cys Ile Ala Ala Leu Lys Asp Asp Lys Ala Phe Arg Arg
 215 220 225

ttc gtt ctg gtt cgc tca atg atg ctg gtg aca gca ctc tcc acg gct 835
 Phe Val Leu Val Arg Ser Met Met Leu Val Thr Ala Leu Ser Thr Ala
 230 235 240 245

ttc atc gtc gca ctc gcc gct gaa tcc gga aac agc atc gac tcc ttg 883
 Phe Ile Val Ala Leu Ala Ala Glu Ser Gly Asn Ser Ile Asp Ser Leu
 250 255 260

gga ttc ttc ctc atc gcc tcc ggc ttg gcg tcc atg gtt ggt ggc cga 931
 Gly Phe Phe Leu Ile Ala Ser Gly Leu Ala Ser Met Val Gly Gly Arg
 265 270 275

atc tct gga atc tgg tgc gat cat tcc tcc aaa aac gtc atg gcg ggc 979
 Ile Ser Gly Ile Trp Ser Asp His Ser Ser Lys Asn Val Met Ala Gly
 280 285 290

ggt gcc cta ttc ggt tcc atc gtg tta atc ctc gtg gtg ctc agc tcc 1027
 Gly Ala Leu Phe Gly Ser Ile Val Leu Ile Leu Val Val Leu Ser Ser
 295 300 305

gcg ttt gca ccc gcg cag atc aac acg ctg gtg ttc ccg ttg agt ttc 1075
 Ala Phe Ala Pro Ala Gln Ile Asn Thr Leu Val Phe Pro Leu Ser Phe
 310 315 320 325

ttc ctc atc acc ttg gcc cac acc gcc atc cgc gtg gcc cgc aaa act 1123
 Phe Leu Ile Thr Leu Ala His Thr Ala Ile Arg Val Ala Arg Lys Thr
 330 335 340

tat gta atg gac atg gct gaa ggt gat cag cgc acc cgc tat gtt gcc 1171
 Tyr Val Met Asp Met Ala Glu Gly Asp Gln Arg Thr Arg Tyr Val Ala
 345 350 355

gac gcc aac aca cta atg ggt gta gtt ttg ctc att gtt ggc gca tta 1219
 Asp Ala Asn Thr Leu Met Gly Val Val Leu Leu Ile Val Gly Ala Leu
 360 365 370

tct ggc ttc att gca att ttc gga aac gaa gcc gca ctg ctc ttc ttg 1267
 Ser Gly Phe Ile Ala Ile Phe Gly Asn Glu Ala Ala Leu Leu Phe Leu
 375 380 385

gcg gca att ggc ctg ctt gga acc att agc gcc cgt ggc ctc aag gaa 1315
 Ala Ala Ile Gly Leu Leu Gly Thr Ile Ser Ala Arg Gly Leu Lys Glu
 390 395 400 405

gta tcc gcc gga tagttttaca actttttccac cca 1350
 Val Ser Ala Gly

<210> 2146

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 2146

Met Thr Asn Pro Thr Glu Glu Arg Asn Ala Arg Arg Leu Ile Trp Ala

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Asn Gly Leu Gln Asn Ile Gly Asp Gln Ile Val Ala Ala Lys Thr Val	20	25	30
Leu Pro Trp Leu Leu Gln Ala Ala Gly Ala Pro Gly Phe Leu Leu Ala	35	40	45
Leu Leu Val Pro Ile Arg Glu Ala Gly Ser Met Leu Pro Gln Ala Ala	50	55	60
Ile Thr Gly Trp Val Leu Arg Gln Thr Ser Arg Ser Lys Val Trp Val	65	70	75
Ile Gly Ser Asn Gly Gln Phe Val Ser Ala Leu Gly Ile Gly Val Ala	85	90	95
Ala Leu Phe Leu Arg Gly Trp Ala Leu Gly Ile Thr Val Ile Val Leu	100	105	110
Leu Ala Ala Leu Ser Leu Phe Arg Ser Met Cys Ser Ile Ala Ser Lys	115	120	125
Asp Val Gln Gly Lys Val Ile Ser Lys Gly Lys Arg Gly Leu Val Thr	130	135	140
Gly Arg Ala Thr Val Ile Gly Gly Val Met Gly Leu Val Ala Gly Leu	145	150	155
Ala Ile Ala Ile Phe Leu Gly Ser His Ser Pro Thr Arg Val Leu Ala	165	170	175
Ala Val Val Ile Ala Ser Ser Phe Ser Trp Leu Phe Ala Ser Ile Val	180	185	190
Phe Ala Arg Ile Glu Tyr Ala Lys Pro Ala Thr Pro Lys Asn Ala Pro	195	200	205
Ser Ala Asn Pro Trp Val Arg Arg Cys Ile Ala Ala Leu Lys Asp Asp	210	215	220
Lys Ala Phe Arg Arg Phe Val Leu Val Arg Ser Met Met Leu Val Thr	225	230	235
Ala Leu Ser Thr Ala Phe Ile Val Ala Leu Ala Ala Glu Ser Gly Asn	245	250	255
Ser Ile Asp Ser Leu Gly Phe Phe Leu Ile Ala Ser Gly Leu Ala Ser	260	265	270
Met Val Gly Gly Arg Ile Ser Gly Ile Trp Ser Asp His Ser Ser Lys	275	280	285
Asn Val Met Ala Gly Gly Ala Leu Phe Gly Ser Ile Val Leu Ile Leu	290	295	300
Val Val Leu Ser Ser Ala Phe Ala Pro Ala Gln Ile Asn Thr Leu Val	305	310	315
Phe Pro Leu Ser Phe Phe Leu Ile Thr Leu Ala His Thr Ala Ile Arg	325	330	335

Val Ala Arg Lys Thr Tyr Val Met Asp Met Ala Glu Gly Asp Gln Arg
 340 345 350

Thr Arg Tyr Val Ala Asp Ala Asn Thr Leu Met Gly Val Val Leu Leu
 355 360 365

Ile Val Gly Ala Leu Ser Gly Phe Ile Ala Ile Phe Gly Asn Glu Ala
 370 375 380

Ala Leu Leu Phe Leu Ala Ala Ile Gly Leu Leu Gly Thr Ile Ser Ala
 385 390 395 400

Arg Gly Leu Lys Glu Val Ser Ala Gly
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<210> 2147

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXA01218

<400> 2147

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tcacattagc caaaaggcac tttgaggaag tggaactcct atg gca cga ctt cag 115
 Met Ala Arg Leu Gln
 1 5

cac gac atg att ttc atc aac cta cca gta tct gac ctt gca gca tct 163
 His Asp Met Ile Phe Ile Asn Leu Pro Val Ser Asp Leu Ala Ala Ser
 10 15 20

aag cgt ttt tat gca ggt ctt ggc ttc aaa gaa aac acc gtc ttc agt 211
 Lys Arg Phe Tyr Ala Gly Leu Gly Phe Lys Glu Asn Thr Val Phe Ser
 25 30 35

gat gag cac act gca tct ttt gag gtc agt gac gcc atc gtg gtg atg 259
 Asp Glu His Thr Ala Ser Phe Glu Val Ser Asp Ala Ile Val Val Met
 40 45 50

ctt ctg gaa acc gcg cgc ttc agt gat ttc act aag cgc ccc atc gtg 307
 Leu Leu Glu Thr Ala Arg Phe Ser Asp Phe Thr Lys Arg Pro Ile Val
 55 60 65

gag aag aac ggc tcc cgc gaa gtg ctc aac tgc ctg tct gta tgt tcc 355
 Glu Lys Asn Gly Ser Arg Glu Val Leu Asn Cys Leu Ser Val Cys Ser
 70 75 80 85

acc gag gat gcg gat gag ttc gtg cgt cgc gcc cag gaa ttc gga ggc 403
 Thr Glu Asp Ala Asp Glu Phe Val Arg Arg Ala Gln Glu Phe Gly Gly
 90 95 100

acg atc acc cgt gag ctt gca gcg gaa ggc ccc atg tac ggc gga gct 451
 Thr Ile Thr Arg Glu Leu Ala Ala Glu Gly Pro Met Tyr Gly Gly Ala
 105 110 115

ttt gat gat cca gat gga cac ggt tgg gag ctg atg tac ttc gat cca 499
Phe Asp Asp Pro Asp Gly His Gly Trp Glu Leu Met Tyr Phe Asp Pro
120 125 130

gag gca ctc gct cag atg atg cct gag ggc taaatattct tcagggttc 549
Glu Ala Leu Ala Gln Met Met Pro Glu Gly
135 140

tcg 552

<210> 2148

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 2148

Met Ala Arg Leu Gln His Asp Met Ile Phe Ile Asn Leu Pro Val Ser
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Asp Leu Ala Ala Ser Lys Arg Phe Tyr Ala Gly Leu Gly Phe Lys Glu
20 25 30

Asn Thr Val Phe Ser Asp Glu His Thr Ala Ser Phe Glu Val Ser Asp
35 40 45

Ala Ile Val Val Met Leu Leu Glu Thr Ala Arg Phe Ser Asp Phe Thr
50 55 60

Lys Arg Pro Ile Val Glu Lys Asn Gly Ser Arg Glu Val Leu Asn Cys
65 70 75 80

Leu Ser Val Cys Ser Thr Glu Asp Ala Asp Glu Phe Val Arg Arg Ala
85 90 95

Gln Glu Phe Gly Gly Thr Ile Thr Arg Glu Leu Ala Ala Glu Gly Pro
100 105 110

Met Tyr Gly Gly Ala Phe Asp Asp Pro Asp Gly His Gly Trp Glu Leu
115 120 125

Met Tyr Phe Asp Pro Glu Ala Leu Ala Gln Met Met Pro Glu Gly
130 135 140

<210> 2149

<211> 507

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(484)

<223> RXA01234

<400> 2149

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tgcatttatt cgggtcactt caacgttgaa aagcatagga atg tgg aag ttc atg 115
Met Trp Lys Phe Met

5

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<400> 2150
Met Trp Lys Phe Met Lys Thr Gln Tyr Val Cys Thr Thr Tyr Phe Ile
  1          5          10          15

Ala Ala Pro Glu Asp Glu Asp Glu Ala Tyr Gln Thr Tyr Arg Ser Arg
      20          25          30

Met Asn Ser Leu Ala Ala Leu Asn Gly Ala Asp Val Val Ser Val Ala
  35          40          45

Asp Gly Leu Arg Met Glu Val Asp Gln Asp Ile Trp Gly Ser Leu Ala
  50          55          60

Glu Gln Tyr Gln Ile Glu Gln Glu Gly Leu Tyr Pro Thr Gly His Asn
  65          70          75          80

Leu Tyr Phe Val Val Thr Val Val Asn Leu Asp Asp Ser Asp Glu Val
      85          90          95

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Tyr Asp Arg Thr Met Glu His Leu Ile Met Asp Asp Pro Tyr Val Arg
 100 105 110

Val Asp Arg Phe Pro Ser Thr Val His Ala Ser Thr Gln Ile Met Leu
 115 120 125

<210> 2151

<211> 564

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(541)

<223> RXA01237

<400> 2151

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aaaccaaaaa tcacgacgca ttaagtaaca gagacttaaa ttaagaactc cgaacaacaa 60
cttcggattg tttcattttt gaggatgaaa gagctttttca atg aac gta cag ttt 115
                                         Met Asn Val Gln Phe
                                         1 5

gaa tca gac atg gcc gtc caa cca gga aac acc atg gaa gct acc gtc 163
Glu Ser Asp Met Ala Val Gln Pro Gly Asn Thr Met Glu Ala Thr Val
                        10 15 20

acc gac att cgt gat gcc aag cgt aaa aca acc cag ctt gat tca gta 211
Thr Asp Ile Arg Asp Ala Lys Arg Lys Thr Thr Gln Leu Asp Ser Val
                        25 30 35

acg ccg ttt aag aag aat tgc ccg agc cgc acc ttg ctc gac acc atc 259
Thr Pro Phe Lys Lys Asn Cys Pro Ser Arg Thr Leu Leu Asp Thr Ile
                        40 45 50

agt gac aag tgg gcg gtg ctg atc ctg ctc agc atg gaa aat ggt cca 307
Ser Asp Lys Trp Ala Val Leu Ile Leu Leu Ser Met Glu Asn Gly Pro
                        55 60 65

cag cgc aat ggt gaa atc aaa gat cag gtc caa gga att acc cca aag 355
Gln Arg Asn Gly Glu Ile Lys Asp Gln Val Gln Gly Ile Thr Pro Lys
                        70 75 80 85

atg ctc acc cag cgt ctt gga gtg ttg gtg gaa gac gga ctg gtc act 403
Met Leu Thr Gln Arg Leu Gly Val Leu Val Glu Asp Gly Leu Val Thr
                        90 95 100

cgc acc tcc cac gca gtt gtg ccg cct cgt gtg gat tat cag ctc acc 451
Arg Thr Ser His Ala Val Val Pro Pro Arg Val Asp Tyr Gln Leu Thr
                        105 110 115

gat ctg ggt gct tct gtc att gag cct tgc cgt gcg atg tat tcc tgg 499
Asp Leu Gly Ala Ser Val Ile Glu Pro Cys Arg Ala Met Tyr Ser Trp
                        120 125 130

gca gtg gag aac att aag caa gtg gag gcc tac cgc tca gca 541
Ala Val Glu Asn Ile Lys Gln Val Glu Ala Tyr Arg Ser Ala
                        135 140 145

taagaacact tggcaaacct cac 564

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<210> 2152

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 2152

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Met Glu Ala Thr Val Thr Asp Ile Arg Asp Ala Lys Arg Lys Thr Thr
 20 25 30

Gln Leu Asp Ser Val Thr Pro Phe Lys Lys Asn Cys Pro Ser Arg Thr
 35 40 45

Leu Leu Asp Thr Ile Ser Asp Lys Trp Ala Val Leu Ile Leu Leu Ser
 50 55 60

Met Glu Asn Gly Pro Gln Arg Asn Gly Glu Ile Lys Asp Gln Val Gln
 65 70 75 80

Gly Ile Thr Pro Lys Met Leu Thr Gln Arg Leu Gly Val Leu Val Glu
 85 90 95

Asp Gly Leu Val Thr Arg Thr Ser His Ala Val Val Pro Pro Arg Val
 100 105 110

Asp Tyr Gln Leu Thr Asp Leu Gly Ala Ser Val Ile Glu Pro Cys Arg
 115 120 125

Ala Met Tyr Ser Trp Ala Val Glu Asn Ile Lys Gln Val Glu Ala Tyr
 130 135 140

Arg Ser Ala
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<210> 2153

<211> 1437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1414)

<223> RXA01267

<400> 2153

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gatttttcga attgaagatg tttctgaaag gtatttagat atg tat gca gaa att 115
 Met Tyr Ala Glu Ile
 1 5

aat ggc ggt ttt att cca gag ggc acc gtg cgg gta agc ggc gca aaa 163
 Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg Val Ser Gly Ala Lys
 10 15 20

aac tct gct act aga ctt ctc gcg gcg gca ctg cta acc gat gag gtg 211

Asn	Ser	Ala	Thr	Arg	Leu	Leu	Ala	Ala	Ala	Leu	Leu	Thr	Asp	Glu	Val		
			25					30					35				
gtg	cat	ctt	ggt	aat	ttc	cca	acc	aag	ctt	gtg	gat	gtt	gaa	cat	aaa	259	
Val	His	Leu	Gly	Asn	Phe	Pro	Thr	Lys	Leu	Val	Asp	Val	Glu	His	Lys		
		40					45					50					
att	cgc	ttt	att	gaa	gag	ctt	ggc	gga	aaa	gtg	cat	gtc	gac	cat	gat	307	
Ile	Arg	Phe	Ile	Glu	Glu	Leu	Gly	Gly	Lys	Val	His	Val	Asp	His	Asp		
		55				60					65						
gag	caa	att	tta	gta	gtt	gat	gct	aag	gat	ctt	gca	gcg	cga	gaa	atg	355	
Glu	Gln	Ile	Leu	Val	Val	Asp	Ala	Lys	Asp	Leu	Ala	Ala	Arg	Glu	Met		
	70				75					80					85		
act	act	gat	gaa	ctg	aat	att	ccg	att	cga	act	act	tat	ctc	cta	gca	403	
Thr	Thr	Asp	Glu	Leu	Asn	Ile	Pro	Ile	Arg	Thr	Thr	Tyr	Leu	Leu	Ala		
				90					95					100			
gca	gcg	cag	att	ggg	cgt	ggg	gaa	att	gct	cga	gtt	cct	ttt	cct	ggg	451	
Ala	Ala	Gln	Ile	Gly	Arg	Gly	Glu	Ile	Ala	Arg	Val	Pro	Phe	Pro	Gly		
			105					110					115				
ggg	tgt	gct	att	gga	gga	ggt	cct	gct	ggc	gga	cga	gga	tat	gat	ctt	499	
Gly	Cys	Ala	Ile	Gly	Gly	Gly	Pro	Ala	Gly	Gly	Arg	Gly	Tyr	Asp	Leu		
		120					125					130					
cat	ctt	atg	gtc	tgg	gaa	cag	cta	ggt	tgt	aaa	att	ctt	gaa	aaa	gat	547	
His	Leu	Met	Val	Trp	Glu	Gln	Leu	Gly	Cys	Lys	Ile	Leu	Glu	Lys	Asp		
		135				140					145						
gat	cac	att	gaa	gta	act	gca	ccc	cag	ggc	ttt	atc	ggg	gga	gtt	att	595	
Asp	His	Ile	Glu	Val	Thr	Ala	Pro	Gln	Gly	Phe	Ile	Gly	Gly	Val	Ile		
					155					160					165		
gac	ttt	cct	att	tct	act	gtg	gga	ggc	act	gaa	aac	gcg	tta	cta	tgc	643	
Asp	Phe	Pro	Ile	Ser	Thr	Val	Gly	Gly	Thr	Glu	Asn	Ala	Leu	Leu	Cys		
				170					175					180			
gca	agt	att	gct	tca	ggg	gat	act	aaa	att	gcc	aat	gct	tat	att	acc	691	
Ala	Ser	Ile	Ala	Ser	Gly	Asp	Thr	Lys	Ile	Ala	Asn	Ala	Tyr	Ile	Thr		
			185					190					195				
cct	gag	ata	act	gat	ctt	att	gaa	ctt	ctg	cga	cgt	atg	ggt	gcg	gag	739	
Pro	Glu	Ile	Thr	Asp	Leu	Ile	Glu	Leu	Leu	Arg	Arg	Met	Gly	Ala	Glu		
		200					205					210					
atc	act	gtc	tac	ggt	acc	agc	cgt	att	cat	gta	aag	ggt	cga	gca	ggt	787	
Ile	Thr	Val	Tyr	Gly	Thr	Ser	Arg	Ile	His	Val	Lys	Gly	Arg	Ala	Gly		
		215				220					225						
ctt	ttg	cag	ggc	gca	tat	atg	gac	gta	atg	ccg	gat	cgt	att	gag	gca	835	
Leu	Leu	Gln	Gly	Ala	Tyr	Met	Asp	Val	Met	Pro	Asp	Arg	Ile	Glu	Ala		
				235						240					245		
ttg	acg	tgg	atc	gtg	tat	gga	att	att	tca	ggc	gga	agg	att	acc	gtc	883	
Leu	Thr	Trp	Ile	Val	Tyr	Gly	Ile	Ile	Ser	Gly	Gly	Arg	Ile	Thr	Val		
				250					255					260			
gaa	ggt	gtt	cca	ttt	agc	tcg	atg	gaa	gtt	cct	ttt	atc	cac	ctt	gag	931	
Glu	Gly	Val	Pro	Phe	Ser	Ser	Met	Glu	Val	Pro	Phe	Ile	His	Leu	Glu		

265	270	275	
aag gct gga gtg gat ctt ttc cgt aat tca agt tcc gta tat att aca			979
Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser Ser Val Tyr Ile Thr			
280	285	290	
cca gaa tgc ttg cct tca ggc tca gtt cag cca ttt gag cta gcg tgt			1027
Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro Phe Glu Leu Ala Cys			
295	300	305	
gga act cac ccc gga gta att tcg gac atg cag gca ctt ttt gtt ctt			1075
Gly Thr His Pro Gly Val Ile Ser Asp Met Gln Ala Leu Phe Val Leu			
310	315	320	325
tta gga tta aaa ggt gca gga act tca cgc gtc tat gac tat cga tac			1123
Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val Tyr Asp Tyr Arg Tyr			
330	335	340	
cca gaa aga att gca ttt gtt gag gaa ttg aca aat cta gtt tcg ggc			1171
Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr Asn Leu Val Ser Gly			
345	350	355	
gac aaa tta agt gca gag gct ggc aag atc act atc cag gga gat gct			1219
Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr Ile Gln Gly Asp Ala			
360	365	370	
act ttc cgg cca gga tat gcg aac tca act gat cta cgt ggt tct atg			1267
Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp Leu Arg Gly Ser Met			
375	380	385	
gct gtt gtt tta gcg gcg ctt tgc gct gat gga aag tcc acg att aat			1315
Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly Lys Ser Thr Ile Asn			
390	395	400	405
aac gtc cat atg gcg tta cgt ggg tac aac gag ttg gat aaa aaa ctt			1363
Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu Leu Asp Lys Lys Leu			
410	415	420	
cgt tta ctt ggt gcg gat tta act atc aga gaa ggc gaa gtt cct tca			1411
Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu Gly Glu Val Pro Ser			
425	430	435	
cct taagaacgaa agttttacat tga			1437
Pro			

<210> 2154

<211> 438

<212> PRT

<213> Corynebacterium glutamicum

<400> 2154

Met	Tyr	Ala	Glu	Ile	Asn	Gly	Gly	Phe	Ile	Pro	Glu	Gly	Thr	Val	Arg
1				5					10					15	

Val	Ser	Gly	Ala	Lys	Asn	Ser	Ala	Thr	Arg	Leu	Leu	Ala	Ala	Ala	Leu
		20						25					30		

Leu	Thr	Asp	Glu	Val	Val	His	Leu	Gly	Asn	Phe	Pro	Thr	Lys	Leu	Val
		35					40					45			

Asp Val Glu His Lys Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val
 50 55 60
 His Val Asp His Asp Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu
 65 70 75 80
 Ala Ala Arg Glu Met Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr
 85 90 95
 Thr Tyr Leu Leu Ala Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg
 100 105 110
 Val Pro Phe Pro Gly Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly
 115 120 125
 Arg Gly Tyr Asp Leu His Leu Met Val Trp Glu Gln Leu Gly Cys Lys
 130 135 140
 Ile Leu Glu Lys Asp Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe
 145 150 155 160
 Ile Gly Gly Val Ile Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu
 165 170 175
 Asn Ala Leu Leu Cys Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala
 180 185 190
 Asn Ala Tyr Ile Thr Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg
 195 200 205
 Arg Met Gly Ala Glu Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val
 210 215 220
 Lys Gly Arg Ala Gly Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro
 225 230 235 240
 Asp Arg Ile Glu Ala Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly
 245 250 255
 Gly Arg Ile Thr Val Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro
 260 265 270
 Phe Ile His Leu Glu Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser
 275 280 285
 Ser Val Tyr Ile Thr Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro
 290 295 300
 Phe Glu Leu Ala Cys Gly Thr His Pro Gly Val Ile Ser Asp Met Gln
 305 310 315 320
 Ala Leu Phe Val Leu Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val
 325 330 335
 Tyr Asp Tyr Arg Tyr Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr
 340 345 350
 Asn Leu Val Ser Gly Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr
 355 360 365

Ile Gln Gly Asp Ala Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp
 370 375 380

Leu Arg Gly Ser Met Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly
 385 390 395 400

Lys Ser Thr Ile Asn Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu
 405 410 415

Leu Asp Lys Lys Leu Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu
 420 425 430

Gly Glu Val Pro Ser Pro
 435

<210> 2155
 <211> 963
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(940)
 <223> RXA01268

<400> 2155
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gctgatagtt ggaactccga aagcttcatt gctgggagtc gtg gca gca cga att 115
 Val Ala Ala Arg Ile
 1 5

gct cga gtg cca cga att gtc tat gtg gca cat ggg ctg cgc tct gaa 163
 Ala Arg Val Pro Arg Ile Val Tyr Val Ala His Gly Leu Arg Ser Glu
 10 15 20

act gtt tta ggc tta aaa aag aag att cta gtg ttt ttg gaa tat ttg 211
 Thr Val Leu Gly Leu Lys Lys Lys Ile Leu Val Phe Leu Glu Tyr Leu
 25 30 35

acc cag ttg ttt gca cat caa act ttg gct gta agt cat tct ctg aag 259
 Thr Gln Leu Phe Ala His Gln Thr Leu Ala Val Ser His Ser Leu Lys
 40 45 50

aaa gca att gaa gat gcg cac cct cgt ttt aaa gga aga gtg caa gtc 307
 Lys Ala Ile Glu Asp Ala His Pro Arg Phe Lys Gly Arg Val Gln Val
 55 60 65

tta ggt tat ggc agt atg aat gga gtt gag ctt gat cgc ttt aga gtt 355
 Leu Gly Tyr Gly Ser Met Asn Gly Val Glu Leu Asp Arg Phe Arg Val
 70 75 80 85

cca tcc ctt gaa gag aaa tta tct gct cgt aat gct tta aac ctg cct 403
 Pro Ser Leu Glu Glu Lys Leu Ser Ala Arg Asn Ala Leu Asn Leu Pro
 90 95 100

agt aaa tct gtc att gtt ggt ttt gtc ggc aga ata aat aaa gat aag 451
 Ser Lys Ser Val Ile Val Gly Phe Val Gly Arg Ile Asn Lys Asp Lys
 105 110 115

gga gga gat ctt ctc gct gct ctt aca aaa cat gag gct ttt acc cga 499
 Gly Gly Asp Leu Leu Ala Ala Leu Thr Lys His Glu Ala Phe Thr Arg
 120 125 130
 ttg cga ctg cat ctc tta att att ggt gaa ttg gaa gac gat gac ttg 547
 Leu Arg Leu His Leu Leu Ile Ile Gly Glu Leu Glu Asp Asp Asp Leu
 135 140 145
 cga gaa gca ttc att aaa tta gtt aat gaa ggg cag gtt acg att aca 595
 Arg Glu Ala Phe Ile Lys Leu Val Asn Glu Gly Gln Val Thr Ile Thr
 150 155 160 165
 gga tgg att gat ttc cct gaa gaa cca tta gct gca gtt gat gtt ttg 643
 Gly Trp Ile Asp Phe Pro Glu Glu Pro Leu Ala Ala Val Asp Val Leu
 170 175 180
 ctt cac cca act cag cga gaa ggt tta ggt atg tct ttg ctg gaa gct 691
 Leu His Pro Thr Gln Arg Glu Gly Leu Gly Met Ser Leu Leu Glu Ala
 185 190 195
 cag gct atg gga gtg cct gta ttg acg aat gct gtg act gga aca gtt 739
 Gln Ala Met Gly Val Pro Val Leu Thr Asn Ala Val Thr Gly Thr Val
 200 205 210
 gat gca gta aca agt gga gaa ggt ggc ttt ttt gcc gat gac gat tct 787
 Asp Ala Val Thr Ser Gly Glu Gly Gly Phe Phe Ala Asp Asp Asp Ser
 215 220 225
 gtt gag tcc tgg gtt tct aag att gat tta tta gtt tcc gat cct aag 835
 Val Glu Ser Trp Val Ser Lys Ile Asp Leu Leu Val Ser Asp Pro Lys
 230 235 240 245
 tta aga gac cgg atg gga cgt gct ggt cgc cag ttt gtg tca gct cgt 883
 Leu Arg Asp Arg Met Gly Arg Ala Gly Arg Gln Phe Val Ser Ala Arg
 250 255 260
 ttc aat cgt gat gat gtc gca gct cgt ttc agt cat ttc gtg gaa caa 931
 Phe Asn Arg Asp Asp Val Ala Ala Arg Phe Ser His Phe Val Glu Gln
 265 270 275
 ttc aaa aaa tagggctcat tcaatttcaa tat 963
 Phe Lys Lys
 280

<210> 2156

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 2156

Val Ala Ala Arg Ile Ala Arg Val Pro Arg Ile Val Tyr Val Ala His
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Gly Leu Arg Ser Glu Thr Val Leu Gly Leu Lys Lys Lys Ile Leu Val
 20 25 30

Phe Leu Glu Tyr Leu Thr Gln Leu Phe Ala His Gln Thr Leu Ala Val
 35 40 45

Ser His Ser Leu Lys Lys Ala Ile Glu Asp Ala His Pro Arg Phe Lys

50 55 60
 Gly Arg Val Gln Val Leu Gly Tyr Gly Ser Met Asn Gly Val Glu Leu
 65 70 75 80
 Asp Arg Phe Arg Val Pro Ser Leu Glu Glu Lys Leu Ser Ala Arg Asn
 85 90 95
 Ala Leu Asn Leu Pro Ser Lys Ser Val Ile Val Gly Phe Val Gly Arg
 100 105 110
 Ile Asn Lys Asp Lys Gly Gly Asp Leu Leu Ala Ala Leu Thr Lys His
 115 120 125
 Glu Ala Phe Thr Arg Leu Arg Leu His Leu Leu Ile Ile Gly Glu Leu
 130 135 140
 Glu Asp Asp Asp Leu Arg Glu Ala Phe Ile Lys Leu Val Asn Glu Gly
 145 150 155 160
 Gln Val Thr Ile Thr Gly Trp Ile Asp Phe Pro Glu Glu Pro Leu Ala
 165 170 175
 Ala Val Asp Val Leu Leu His Pro Thr Gln Arg Glu Gly Leu Gly Met
 180 185 190
 Ser Leu Leu Glu Ala Gln Ala Met Gly Val Pro Val Leu Thr Asn Ala
 195 200 205
 Val Thr Gly Thr Val Asp Ala Val Thr Ser Gly Glu Gly Gly Phe Phe
 210 215 220
 Ala Asp Asp Asp Ser Val Glu Ser Trp Val Ser Lys Ile Asp Leu Leu
 225 230 235 240
 Val Ser Asp Pro Lys Leu Arg Asp Arg Met Gly Arg Ala Gly Arg Gln
 245 250 255
 Phe Val Ser Ala Arg Phe Asn Arg Asp Asp Val Ala Ala Arg Phe Ser
 260 265 270
 His Phe Val Glu Gln Phe Lys Lys
 275 280

<210> 2157

<211> 1935

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1912)

<223> RXA01271

<400> 2157

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 ttggcgaaac ccaattttatt tcaaaagatg gtggacaaac atg gca ata agc att 115
 Met Ala Ile Ser Ile

1

5

ggt aaa gca gga cag aac tta aaa ggg tca gtg cct atc gga aaa gtc Gly Lys Ala Gly Gln Asn Leu Lys Gly Ser Val Pro Ile Gly Lys Val	163
10 15 20	
ctt ttt ctc att gat gcc ctt gcc tgg att tct gca cta ttt atc ggt Leu Phe Leu Ile Asp Ala Leu Ala Trp Ile Ser Ala Leu Phe Ile Gly	211
25 30 35	
gtg gtt ttg cgg tat gaa ttc aat ctg agt tct atc aac tgg agt gcg Val Val Leu Arg Tyr Glu Phe Asn Leu Ser Ser Ile Asn Trp Ser Ala	259
40 45 50	
ttt gca tgg ttc ggg ctt gct gca gtt att ttg cag ttt gtt ctc gga Phe Ala Trp Phe Gly Leu Ala Ala Val Ile Leu Gln Phe Val Leu Gly	307
55 60 65	
ctt tct ctc cat ctt tac cgc aag gga tta cgt cac ctt ttc ggt agc Leu Ser Leu His Leu Tyr Arg Lys Gly Leu Arg His Leu Phe Gly Ser	355
70 75 80 85	
ttc gaa gat aca cta aac gtt tct atc tgc gtc att gtt gtc ggt gtt Phe Glu Asp Thr Leu Asn Val Ser Ile Ser Val Ile Val Val Gly Val	403
90 95 100	
gtc ctt tgg atc gcc tca cta ttt gtt ggt cag cgt tgg aaa atc tca Val Leu Trp Ile Ala Ser Leu Phe Val Gly Gln Arg Trp Lys Ile Ser	451
105 110 115	
cgc ggt gtc atg ctg cta gtt atc ccg ctt gct ctc gta ttc gta ttg Arg Gly Val Met Leu Leu Val Ile Pro Leu Ala Leu Val Phe Val Leu	499
120 125 130	
gca gtg cgt tat ctc gcg cgt atg cga gtt gag cgt ttt cgt cgt ccg Ala Val Arg Tyr Leu Ala Arg Met Arg Val Glu Arg Phe Arg Arg Pro	547
135 140 145	
gct gcg gat tcc aca cca gca ttg att ctt ggt ggt gga tac atc ggt Ala Ala Asp Ser Thr Pro Ala Leu Ile Leu Gly Gly Gly Tyr Ile Gly	595
150 155 160 165	
acc aac ctg atc cag tgg atg atg tcc gat cct aag tgc cct ttc cgc Thr Asn Leu Ile Gln Trp Met Met Ser Asp Pro Lys Ser Pro Phe Arg	643
170 175 180	
cca gtc ggc gtt att gat gat aac cct gaa tta gca tgc caa cgc gta Pro Val Gly Val Ile Asp Asp Asn Pro Glu Leu Ala Cys Gln Arg Val	691
185 190 195	
cgt ggt gtg ccg gtt ctt ggc aag ttt gat gat atc gcc caa gtt gca Arg Gly Val Pro Val Leu Gly Lys Phe Asp Asp Ile Ala Gln Val Ala	739
200 205 210	
tca gac act ggc gca gaa ctt ctt atc gtt gct att ggt gat gcc gac Ser Asp Thr Gly Ala Glu Leu Leu Ile Val Ala Ile Gly Asp Ala Asp	787
215 220 225	
tct gca ctt tta agg cgt gtc caa gat acc gct aat aaa aat ggt ctt Ser Ala Leu Leu Arg Arg Val Gln Asp Thr Ala Asn Lys Asn Gly Leu	835
230 235 240 245	

tca gta aag gta atg ccg gct att gac cgc gtc gtt tct aag ggc gtt Ser Val Lys Val Met Pro Ala Ile Asp Arg Val Val Ser Lys Gly Val 250 255 260	883
cgt gga aac gat ttg cgt gat ctc tct att gaa gat ttg ctt gga cgt Arg Gly Asn Asp Leu Arg Asp Leu Ser Ile Glu Asp Leu Leu Gly Arg 265 270 275	931
caa cct gtt gaa acc aat gtt tca gaa att act ggc tat cta aca ggt Gln Pro Val Glu Thr Asn Val Ser Glu Ile Thr Gly Tyr Leu Thr Gly 280 285 290	979
aag cgt gtt ctt gtt acc ggt gca ggt ggg tca att ggt tcc cag cta Lys Arg Val Leu Val Thr Gly Ala Gly Gly Ser Ile Gly Ser Gln Leu 295 300 305	1027
tgt acg gaa att gcc aaa tac gga cct gct gag ctt atg atg ctt gat Cys Thr Glu Ile Ala Lys Tyr Gly Pro Ala Glu Leu Met Met Leu Asp 310 315 320 325	1075
cgc gat gag act ggt ttg cag cag gtt ctg att aac gtt gct ggt aac Arg Asp Glu Thr Gly Leu Gln Gln Val Leu Ile Asn Val Ala Gly Asn 330 335 340	1123
ggt ttg ttg gat acg gat gct gtg gtt ctt gcg gat atc cgc gaa gca Gly Leu Leu Asp Thr Asp Ala Val Val Leu Ala Asp Ile Arg Glu Ala 345 350 355	1171
gac gcg atg aaa gag att ttt ctc aag cgt aaa cca gaa gtt gtc ttc Asp Ala Met Lys Glu Ile Phe Leu Lys Arg Lys Pro Glu Val Val Phe 360 365 370	1219
cat gca gca gca tta aag cac ttg cca atg ctg gag cag tat cca gat His Ala Ala Ala Leu Lys His Leu Pro Met Leu Glu Gln Tyr Pro Asp 375 380 385	1267
gag ggc tgg aaa aca aac gtt cta gga act ctt aac gtt ctt gct gcc Glu Gly Trp Lys Thr Asn Val Leu Gly Thr Leu Asn Val Leu Ala Ala 390 395 400 405	1315
gca gaa gct gtt ggt gtt gag act ttc gtc aat att tcc acc gat aag Ala Glu Ala Val Gly Val Glu Thr Phe Val Asn Ile Ser Thr Asp Lys 410 415 420	1363
gca gct aat cca acc agc gtc tta ggg cac tca aag cga gtc gct gaa Ala Ala Asn Pro Thr Ser Val Leu Gly His Ser Lys Arg Val Ala Glu 425 430 435	1411
aag ctg act gcc tgg tat gga cag aat tcc acc agc aag tac cta tcg Lys Leu Thr Ala Trp Tyr Gly Gln Asn Ser Thr Ser Lys Tyr Leu Ser 440 445 450	1459
gtt cga ttt gga aac gtc att ggt agc cgt gga tcg atg ctc ccg act Val Arg Phe Gly Asn Val Ile Gly Ser Arg Gly Ser Met Leu Pro Thr 455 460 465	1507
ttc acc agg cta atc atg gaa gat aaa ccg cta aca gtg acg cac ccg Phe Thr Arg Leu Ile Met Glu Asp Lys Pro Leu Thr Val Thr His Pro 470 475 480 485	1555
gat gtc act agg ttc ttc atg aca att cct gaa gct tgc caa ttg gtc	1603

Asp Val Thr Arg Phe Phe Met Thr Ile Pro Glu Ala Cys Gln Leu Val
 490 495 500
 ctg caa gcc ggt ggt att gga cgt tcc ggc gag gtt ctc atc ctt gac 1651
 Leu Gln Ala Gly Gly Ile Gly Arg Ser Gly Glu Val Leu Ile Leu Asp
 505 510 515
 atg ggt gag cct gta agc atc ctt gaa att gca cag cgc atg atc gca 1699
 Met Gly Glu Pro Val Ser Ile Leu Glu Ile Ala Gln Arg Met Ile Ala
 520 525 530
 atg tcc ggt aaa gat att gac atc gtg ttc acc ggc ctt cgc gag ggc 1747
 Met Ser Gly Lys Asp Ile Asp Ile Val Phe Thr Gly Leu Arg Glu Gly
 535 540 545
 gaa aag atg cac gaa gag ctg gtt ggt gat ggt gaa acc gaa gat cgt 1795
 Glu Lys Met His Glu Glu Leu Val Gly Asp Gly Glu Thr Glu Asp Arg
 550 555 560 565
 cca ttc cac tca aag att tcg cat gca cat gca gaa agc ctc gct cct 1843
 Pro Phe His Ser Lys Ile Ser His Ala His Ala Glu Ser Leu Ala Pro
 570 575 580
 aat aat ctc gat aga gat cga ttt atg caa cgt gct gga aaa cta gct 1891
 Asn Asn Leu Asp Arg Asp Arg Phe Met Gln Arg Ala Gly Lys Leu Ala
 585 590 595
 tca aca gat tcg gag atc atc taaatgacta atgaacgaat ttt 1935
 Ser Thr Asp Ser Glu Ile Ile
 600

<210> 2158

<211> 604

<212> PRT

<213> Corynebacterium glutamicum

<400> 2158

Met Ala Ile Ser Ile Gly Lys Ala Gly Gln Asn Leu Lys Gly Ser Val
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 Pro Ile Gly Lys Val Leu Phe Leu Ile Asp Ala Leu Ala Trp Ile Ser
 20 25 30
 Ala Leu Phe Ile Gly Val Val Leu Arg Tyr Glu Phe Asn Leu Ser Ser
 35 40 45
 Ile Asn Trp Ser Ala Phe Ala Trp Phe Gly Leu Ala Ala Val Ile Leu
 50 55 60
 Gln Phe Val Leu Gly Leu Ser Leu His Leu Tyr Arg Lys Gly Leu Arg
 65 70 75 80
 His Leu Phe Gly Ser Phe Glu Asp Thr Leu Asn Val Ser Ile Ser Val
 85 90 95
 Ile Val Val Gly Val Val Leu Trp Ile Ala Ser Leu Phe Val Gly Gln
 100 105 110
 Arg Trp Lys Ile Ser Arg Gly Val Met Leu Leu Val Ile Pro Leu Ala
 115 120 125

Leu Val Phe Val Leu Ala Val Arg Tyr Leu Ala Arg Met Arg Val Glu
130 135 140

Arg Phe Arg Arg Pro Ala Ala Asp Ser Thr Pro Ala Leu Ile Leu Gly
145 150 155 160

Gly Gly Tyr Ile Gly Thr Asn Leu Ile Gln Trp Met Met Ser Asp Pro
165 170 175

Lys Ser Pro Phe Arg Pro Val Gly Val Ile Asp Asp Asn Pro Glu Leu
180 185 190

Ala Cys Gln Arg Val Arg Gly Val Pro Val Leu Gly Lys Phe Asp Asp
195 200 205

Ile Ala Gln Val Ala Ser Asp Thr Gly Ala Glu Leu Leu Ile Val Ala
210 215 220

Ile Gly Asp Ala Asp Ser Ala Leu Leu Arg Arg Val Gln Asp Thr Ala
225 230 235 240

Asn Lys Asn Gly Leu Ser Val Lys Val Met Pro Ala Ile Asp Arg Val
245 250 255

Val Ser Lys Gly Val Arg Gly Asn Asp Leu Arg Asp Leu Ser Ile Glu
260 265 270

Asp Leu Leu Gly Arg Gln Pro Val Glu Thr Asn Val Ser Glu Ile Thr
275 280 285

Gly Tyr Leu Thr Gly Lys Arg Val Leu Val Thr Gly Ala Gly Gly Ser
290 295 300

Ile Gly Ser Gln Leu Cys Thr Glu Ile Ala Lys Tyr Gly Pro Ala Glu
305 310 315 320

Leu Met Met Leu Asp Arg Asp Glu Thr Gly Leu Gln Gln Val Leu Ile
325 330 335

Asn Val Ala Gly Asn Gly Leu Leu Asp Thr Asp Ala Val Val Leu Ala
340 345 350

Asp Ile Arg Glu Ala Asp Ala Met Lys Glu Ile Phe Leu Lys Arg Lys
355 360 365

Pro Glu Val Val Phe His Ala Ala Ala Leu Lys His Leu Pro Met Leu
370 375 380

Glu Gln Tyr Pro Asp Glu Gly Trp Lys Thr Asn Val Leu Gly Thr Leu
385 390 395 400

Asn Val Leu Ala Ala Ala Glu Ala Val Gly Val Glu Thr Phe Val Asn
405 410 415

Ile Ser Thr Asp Lys Ala Ala Asn Pro Thr Ser Val Leu Gly His Ser
420 425 430

Lys Arg Val Ala Glu Lys Leu Thr Ala Trp Tyr Gly Gln Asn Ser Thr
435 440 445

Ser Lys Tyr Leu Ser Val Arg Phe Gly Asn Val Ile Gly Ser Arg Gly
 450 455 460
 Ser Met Leu Pro Thr Phe Thr Arg Leu Ile Met Glu Asp Lys Pro Leu
 465 470 475 480
 Thr Val Thr His Pro Asp Val Thr Arg Phe Phe Met Thr Ile Pro Glu
 485 490 495
 Ala Cys Gln Leu Val Leu Gln Ala Gly Gly Ile Gly Arg Ser Gly Glu
 500 505 510
 Val Leu Ile Leu Asp Met Gly Glu Pro Val Ser Ile Leu Glu Ile Ala
 515 520 525
 Gln Arg Met Ile Ala Met Ser Gly Lys Asp Ile Asp Ile Val Phe Thr
 530 535 540
 Gly Leu Arg Glu Gly Glu Lys Met His Glu Glu Leu Val Gly Asp Gly
 545 550 555 560
 Glu Thr Glu Asp Arg Pro Phe His Ser Lys Ile Ser His Ala His Ala
 565 570 575
 Glu Ser Leu Ala Pro Asn Asn Leu Asp Arg Asp Arg Phe Met Gln Arg
 580 585 590
 Ala Gly Lys Leu Ala Ser Thr Asp Ser Glu Ile Ile
 595 600

<210> 2159

<211> 1557

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1534)

<223> RXA01273

<400> 2159

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 tctattgggt aaaaattgat ctgcaagagg actgcaaaat atg gaa tta agg gaa 115
 Met Glu Leu Arg Glu
 1 5
 tac gcg aca atc ctg atg aag aat tgg gtg ttg atc gtt atc gca tcc 163
 Tyr Ala Thr Ile Leu Met Lys Asn Trp Val Leu Ile Val Ile Ala Ser
 10 15 20
 att ctt gga att gca gcg ggc gct ggt ttt tcc ctt cta gct aca ccg 211
 Ile Leu Gly Ile Ala Ala Gly Ala Gly Phe Ser Leu Leu Ala Thr Pro
 25 30 35
 gag tat cag tca cgt act cag ttg tat gta tcg gtg cgg tcg ggg gct 259
 Glu Tyr Gln Ser Arg Thr Gln Leu Tyr Val Ser Val Arg Ser Gly Ala
 40 45 50
 ggg aca acc tct gac atg gtt cag ggt gct aac ttt tcg cgt cag att 307

Gly	Thr	Thr	Ser	Asp	Met	Val	Gln	Gly	Ala	Asn	Phe	Ser	Arg	Gln	Ile		
	55					60					65						
gtg	aat	agt	tat	gtt	gat	gtc	att	aag	acg	ggt	gtt	gtt	cta	gag	ccg	355	
Val	Asn	Ser	Tyr	Val	Asp	Val	Ile	Lys	Thr	Gly	Val	Val	Leu	Glu	Pro	85	
70					75				80								
gtt	gtt	gat	gag	ctt	ggt	ctg	gag	ttg	acg	gct	aac	cag	ttg	agt	tct	403	
Val	Val	Asp	Glu	Leu	Gly	Leu	Glu	Leu	Thr	Ala	Asn	Gln	Leu	Ser	Ser	100	
				90					95								
cat	atc	agt	gcg	gct	tct	cct	gct	gat	act	gcg	ttg	atc	aac	atc	act	451	
His	Ile	Ser	Ala	Ala	Ser	Pro	Ala	Asp	Thr	Ala	Leu	Ile	Asn	Ile	Thr	115	
			105					110									
gct	tct	agt	cct	tct	cct	cag	cag	gcg	gct	gag	atc	gcc	aat	gca	gtg	499	
Ala	Ser	Ser	Pro	Ser	Pro	Gln	Gln	Ala	Ala	Glu	Ile	Ala	Asn	Ala	Val		
			120				125					130					
ggg	gag	agt	ttc	aag	aat	gtg	att	cag	act	gaa	ttg	gaa	cca	gac	tcc	547	
Gly	Glu	Ser	Phe	Lys	Asn	Val	Ile	Gln	Thr	Glu	Leu	Glu	Pro	Asp	Ser		
135						140					145						
ggc	gat	ggc	atg	agc	ccg	att	aac	ctg	act	act	act	cag	gtg	gct	ctg	595	
Gly	Asp	Gly	Met	Ser	Pro	Ile	Asn	Leu	Thr	Thr	Thr	Gln	Val	Ala	Leu	165	
150					155					160							
gaa	cca	tct	tct	ccg	gtc	agt	cct	aat	gtg	atg	atg	aat	atc	ctc	ctc	643	
Glu	Pro	Ser	Ser	Pro	Val	Ser	Pro	Asn	Val	Met	Met	Asn	Ile	Leu	Leu		
				170					175					180			
ggc	cta	ctt	gta	ggt	ctt	gca	ata	ggt	gtt	ggt	att	gca	gtg	ctt	cgc	691	
Gly	Leu	Leu	Val	Gly	Leu	Ala	Ile	Gly	Val	Gly	Ile	Ala	Val	Leu	Arg		
			185					190					195				
gcg	gct	ttg	gat	act	cgt	att	cat	tcc	ttg	cgc	gat	att	gaa	gag	gtt	739	
Ala	Ala	Leu	Asp	Thr	Arg	Ile	His	Ser	Leu	Arg	Asp	Ile	Glu	Glu	Val		
		200					205					210					
act	gat	aag	cca	ctt	ttg	ggc	gga	atc	att	gcg	gat	tct	gaa	gtt	gag	787	
Thr	Asp	Lys	Pro	Leu	Leu	Gly	Gly	Ile	Ile	Ala	Asp	Ser	Glu	Val	Glu		
	215					220					225						
aag	cac	ccg	ttg	atc	att	aag	cac	aag	ccg	cat	agt	cct	att	gcg	gag	835	
Lys	His	Pro	Leu	Ile	Ile	Lys	His	Lys	Pro	His	Ser	Pro	Ile	Ala	Glu	245	
230					235					240							
tcc	ttt	cgt	gcg	tta	cgt	act	aac	ctg	cag	ttc	ctt	aac	gtc	ggc	ggc	883	
Ser	Phe	Arg	Ala	Leu	Arg	Thr	Asn	Leu	Gln	Phe	Leu	Asn	Val	Gly	Gly		
				250					255					260			
tca	tct	tca	gta	ttt	gtt	atc	tcc	tct	gct	aat	cct	ggt	gag	ggt	aag	931	
Ser	Ser	Ser	Val	Phe	Val	Ile	Ser	Ser	Ala	Asn	Pro	Gly	Glu	Gly	Lys		
			265					270					275				
tca	acc	act	tct	gta	aac	cta	gct	ttg	gcg	ctt	gca	gag	gcc	ggc	tcc	979	
Ser	Thr	Thr	Ser	Val	Asn	Leu	Ala	Leu	Ala	Leu	Ala	Glu	Ala	Gly	Ser		
			280				285					290					
cgt	gta	gcg	ctg	atc	gaa	gct	gat	ctt	cgc	ttg	cca	cga	gtg	agc	aag	1027	
Arg	Val	Ala	Leu	Ile	Glu	Ala	Asp	Leu	Arg	Leu	Pro	Arg	Val	Ser	Lys		

295	300	305	
tac ctc gga gtt gag ggc aac gca ggt ctg act gac att ctc att ggc Tyr Leu Gly Val Glu Gly Asn Ala Gly Leu Thr Asp Ile Leu Ile Gly 310 315 320 325			1075
aag gcc gag gtt aat gat gtg ttg cag cgt tgg ggt agg act cag ttg Lys Ala Glu Val Asn Asp Val Leu Gln Arg Trp Gly Arg Thr Gln Leu 330 335 340			1123
tac tat ctc ccg gca ggg cgc att ccg ccg aac ccg agt gag ttg ctt Tyr Tyr Leu Pro Ala Gly Arg Ile Pro Pro Asn Pro Ser Glu Leu Leu 345 350 355			1171
ggt tca gct gag atg gac aag gtc att gcg gag ctt gag gaa agc ttt Gly Ser Ala Glu Met Asp Lys Val Ile Ala Glu Leu Glu Glu Ser Phe 360 365 370			1219
gat tat gtg atc atc gat gcc cct ccg gcg ttg gcg gtt acc gat gct Asp Tyr Val Ile Ile Asp Ala Pro Pro Ala Leu Ala Val Thr Asp Ala 375 380 385			1267
gca gtt att ggt cat ggc aag gct ggc atc ctg att gcg gtc tcc gca Ala Val Ile Gly His Gly Lys Ala Gly Ile Leu Ile Ala Val Ser Ala 390 395 400 405			1315
ggt tct aca aag aag cct gag ttg gaa gct acg ctg tcc acg ctt gag Gly Ser Thr Lys Lys Pro Glu Leu Glu Ala Thr Leu Ser Thr Leu Glu 410 415 420			1363
aat gcg gat gcc aat gtt gtt ggc gtt gtc gct acg atg ctc ccg cct Asn Ala Asp Ala Asn Val Val Gly Val Val Ala Thr Met Leu Pro Pro 425 430 435			1411
aag tct gtg gct ggt tat ggc tac gga aat tac ggc tac ggc gac acc Lys Ser Val Ala Gly Tyr Gly Tyr Gly Asn Tyr Gly Tyr Gly Asp Thr 440 445 450			1459
tcc aaa atc aat gcc cct aag ccc gac aac acc gaa cta acc acc acc Ser Lys Ile Asn Ala Pro Lys Pro Asp Asn Thr Glu Leu Thr Thr Thr 455 460 465			1507
gat gct tcc aag gcc aac aat gag caa tagcttcact attctcactg Asp Ala Ser Lys Ala Asn Asn Glu Gln 470 475			1554
tct			1557

<210> 2160

<211> 478

<212> PRT

<213> Corynebacterium glutamicum

<400> 2160

Met	Glu	Leu	Arg	Glu	Tyr	Ala	Thr	Ile	Leu	Met	Lys	Asn	Trp	Val	Leu
1				5				10						15	

Ile	Val	Ile	Ala	Ser	Ile	Leu	Gly	Ile	Ala	Ala	Gly	Ala	Gly	Phe	Ser
			20				25					30			

Leu Leu Ala Thr Pro Glu Tyr Gln Ser Arg Thr Gln Leu Tyr Val Ser
35 40 45

Val Arg Ser Gly Ala Gly Thr Thr Ser Asp Met Val Gln Gly Ala Asn
50 55 60

Phe Ser Arg Gln Ile Val Asn Ser Tyr Val Asp Val Ile Lys Thr Gly
65 70 75 80

Val Val Leu Glu Pro Val Val Asp Glu Leu Gly Leu Glu Leu Thr Ala
85 90 95

Asn Gln Leu Ser Ser His Ile Ser Ala Ala Ser Pro Ala Asp Thr Ala
100 105 110

Leu Ile Asn Ile Thr Ala Ser Ser Pro Ser Pro Gln Gln Ala Ala Glu
115 120 125

Ile Ala Asn Ala Val Gly Glu Ser Phe Lys Asn Val Ile Gln Thr Glu
130 135 140

Leu Glu Pro Asp Ser Gly Asp Gly Met Ser Pro Ile Asn Leu Thr Thr
145 150 155 160

Thr Gln Val Ala Leu Glu Pro Ser Ser Pro Val Ser Pro Asn Val Met
165 170 175

Met Asn Ile Leu Leu Gly Leu Leu Val Gly Leu Ala Ile Gly Val Gly
180 185 190

Ile Ala Val Leu Arg Ala Ala Leu Asp Thr Arg Ile His Ser Leu Arg
195 200 205

Asp Ile Glu Glu Val Thr Asp Lys Pro Leu Leu Gly Gly Ile Ile Ala
210 215 220

Asp Ser Glu Val Glu Lys His Pro Leu Ile Ile Lys His Lys Pro His
225 230 235 240

Ser Pro Ile Ala Glu Ser Phe Arg Ala Leu Arg Thr Asn Leu Gln Phe
245 250 255

Leu Asn Val Gly Gly Ser Ser Ser Val Phe Val Ile Ser Ser Ala Asn
260 265 270

Pro Gly Glu Gly Lys Ser Thr Thr Ser Val Asn Leu Ala Leu Ala Leu
275 280 285

Ala Glu Ala Gly Ser Arg Val Ala Leu Ile Glu Ala Asp Leu Arg Leu
290 295 300

Pro Arg Val Ser Lys Tyr Leu Gly Val Glu Gly Asn Ala Gly Leu Thr
305 310 315 320

Asp Ile Leu Ile Gly Lys Ala Glu Val Asn Asp Val Leu Gln Arg Trp
325 330 335

Gly Arg Thr Gln Leu Tyr Tyr Leu Pro Ala Gly Arg Ile Pro Pro Asn
340 345 350

Pro Ser Glu Leu Leu Gly Ser Ala Glu Met Asp Lys Val Ile Ala Glu

cgc	gaa	cac	ctt	cac	aat	ttg	gct	tat	cgc	gcc	gac	cat	ccg	cgc	aac	403
Arg	Glu	His	Leu	His	Asn	Leu	Ala	Tyr	Arg	Ala	Asp	His	Pro	Arg	Asn	
				90					95					100		
cta	cct	agt	gca	gag	acc	cca	acg	gca	ccc	ctc	cag	gac	atc	gtt	gat	451
Leu	Pro	Ser	Ala	Glu	Thr	Pro	Thr	Ala	Pro	Leu	Gln	Asp	Ile	Val	Asp	
				105					110					115		
gcg	gtc	aca	gat	aaa	ccg	gcg	tgg	atc	cgc	aac	gag	cag	atg	gat	att	499
Ala	Val	Thr	Asp	Lys	Pro	Ala	Trp	Ile	Arg	Asn	Glu	Gln	Met	Asp	Ile	
				120					125					130		
ttg	gct	aca	aat	cgg	ctc	tgc	gcg	gaa	ctt	tac	gcc	ccg	att	ttc	aag	547
Leu	Ala	Thr	Asn	Arg	Leu	Cys	Ala	Glu	Leu	Tyr	Ala	Pro	Ile	Phe	Lys	
				135					140					145		
gat	ctg	ccc	gat	cgg	ccc	aac	act	gcg	cgg	cat	tgc	ttt	atc	ggc	gca	595
Asp	Leu	Pro	Asp	Arg	Pro	Asn	Thr	Ala	Arg	His	Cys	Phe	Ile	Gly	Ala	
				150					155					160		
aca	gcc	tcc	gag	ttc	tgg	gtg	gac	cgg	gat	cag	ttc	agt	gcg	gag	ttc	643
Thr	Ala	Ser	Glu	Phe	Trp	Val	Asp	Arg	Asp	Gln	Phe	Ser	Ala	Glu	Phe	
				170					175					180		
gct	gcc	aaa	cta	cgc	ctc	gag	tac	gcc	cgg	cgc	ccc	agc	gtg	cca	ggt	691
Ala	Ala	Lys	Leu	Arg	Leu	Glu	Tyr	Ala	Arg	Arg	Pro	Ser	Val	Pro	Gly	
				185					190					195		
tta	aag	gag	ctt	atc	gac	gag	ctc	cat	cag	aaa	agt	tct	gtt	ttc	cgc	739
Leu	Lys	Glu	Leu	Ile	Asp	Glu	Leu	His	Gln	Lys	Ser	Ser	Val	Phe	Arg	
				200					205					210		
gat	aat	tgg	gcg	tct	gct	gat	gtt	ttg	tca	ttc	ggc	tct	ggc	atc	aaa	787
Asp	Asn	Trp	Ala	Ser	Ala	Asp	Val	Leu	Ser	Phe	Gly	Ser	Gly	Ile	Lys	
				215					220					225		
cgt	ttc	agg	cac	cca	aca	ctg	ggg	gag	cgg	gtc	tat	gaa	tac	gag	acg	835
Arg	Phe	Arg	His	Pro	Thr	Leu	Gly	Glu	Arg	Val	Tyr	Glu	Tyr	Glu	Thr	
				230					235					240		
ttt	aat	ctc	aat	agt	gca	ccg	ggg	tat	gtg	ttg	agc	att	tac	ttt		880
Phe	Asn	Leu	Asn	Ser	Ala	Pro	Gly	Tyr	Val	Leu	Ser	Ile	Tyr	Phe		
				250					255					260		
taggtggtgg aggggcgcgt cga																903

<210> 2162

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 2162

Met Asp Glu Leu Leu Lys Gln Glu Val Lys Asp Phe Leu Thr Thr Arg
1 5 10 15

Arg Ala Arg Ile Thr Pro Ala Ala Ala Gly Leu Glu Thr Gln Pro Trp
20 25 30

Ser Asp Arg Arg Val Pro Gly Leu Arg Arg Glu Glu Val Ala Asp Leu
35 40 45

Ala Gly Ile Ser Leu Glu Tyr Tyr Ile Arg Phe Glu Arg Gly Asn Leu
50 55 60

Lys Gly Ala Ser Pro Glu Ile Leu Gln Ser Leu Ala Lys Ala Leu Gln
65 70 75 80

Leu Ser Pro Ile Glu Arg Glu His Leu His Asn Leu Ala Tyr Arg Ala
85 90 95

Asp His Pro Arg Asn Leu Pro Ser Ala Glu Thr Pro Thr Ala Pro Leu
100 105 110

Gln Asp Ile Val Asp Ala Val Thr Asp Lys Pro Ala Trp Ile Arg Asn
115 120 125

Glu Gln Met Asp Ile Leu Ala Thr Asn Arg Leu Cys Ala Glu Leu Tyr
130 135 140

Ala Pro Ile Phe Lys Asp Leu Pro Asp Arg Pro Asn Thr Ala Arg His
145 150 155 160

Cys Phe Ile Gly Ala Thr Ala Ser Glu Phe Trp Val Asp Arg Asp Gln
165 170 175

Phe Ser Ala Glu Phe Ala Ala Lys Leu Arg Leu Glu Tyr Ala Arg Arg
180 185 190

Pro Ser Val Pro Gly Leu Lys Glu Leu Ile Asp Glu Leu His Gln Lys
195 200 205

Ser Ser Val Phe Arg Asp Asn Trp Ala Ser Ala Asp Val Leu Ser Phe
210 215 220

Gly Ser Gly Ile Lys Arg Phe Arg His Pro Thr Leu Gly Glu Arg Val
225 230 235 240

Tyr Glu Tyr Glu Thr Phe Asn Leu Asn Ser Ala Pro Gly Tyr Val Leu
245 250 255

Ser Ile Tyr Phe
260

<210> 2163

<211> 789

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(766)

<223> RXA01294

<400> 2163

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ttagagttca ccacaacgac tcaaaaaaga aagtggcagc atg tct acg att cct 115
Met Ser Thr Ile Pro

1

5

gat gtt ttc acc agt gaa gtg ttc cct gaa atc agt ggc acc aaa gaa 163
Asp Val Phe Thr Ser Glu Val Phe Pro Glu Ile Ser Gly Thr Lys Glu
10 15 20

ttc cgt ggc ctg act tat atg ttc ttt gat caa ttc act ttg ccc acc 211
Phe Arg Gly Leu Thr Tyr Met Phe Phe Asp Gln Phe Thr Leu Pro Thr
25 30 35

gca gaa cag ctt gag caa gct aaa gca gct ggc tgg tca ctg atc acc 259
Ala Glu Gln Leu Glu Gln Ala Lys Ala Ala Gly Trp Ser Leu Ile Thr
40 45 50

tgg gga tgg tgg aat agc gac acc gat ctt gag gat gtc gaa ttg gaa 307
Trp Gly Trp Trp Asn Ser Asp Thr Asp Leu Glu Asp Val Glu Leu Glu
55 60 65

gac atc act aat gaa ggc gac agc cta cca aaa ctc acg gat gaa ttc 355
Asp Ile Thr Asn Glu Gly Asp Ser Leu Pro Lys Leu Thr Asp Glu Phe
70 75 80 85

gct gtg tct tca ctg agc acc ttc gat cta aat tcc caa ggt ctg ccc 403
Ala Val Ser Ser Leu Ser Thr Phe Asp Leu Asn Ser Gln Gly Leu Pro
90 95 100

aat gat gat cgt gag ccg caa cca att gaa gaa gcc gac tca cta gat 451
Asn Asp Asp Arg Glu Pro Gln Pro Ile Glu Glu Ala Asp Ser Leu Asp
105 110 115

gac atc ttc tcc gag gaa gag ggc tgg ggt cta atg gca atc aat tgc 499
Asp Ile Phe Ser Glu Glu Glu Gly Trp Gly Leu Met Ala Ile Asn Cys
120 125 130

ccg aat tgg caa gtc cca gca gcg tgt gaa tgg ctc ggc tgc atg aat 547
Pro Asn Trp Gln Val Pro Ala Ala Cys Glu Trp Leu Gly Cys Met Asn
135 140 145

gtt ggt gaa cca ttt gaa atg tca cac gta ctt agg gtg tgg cag aac 595
Val Gly Glu Pro Phe Glu Met Ser His Val Leu Arg Val Trp Gln Asn
150 155 160 165

agt tgg ggc gtc gag gcc ctg gct ttt ggt ggt gaa gaa gac gac gcg 643
Ser Trp Gly Val Glu Ala Leu Ala Phe Gly Gly Glu Glu Asp Asp Ala
170 175 180

gat ctg ctg ctt cga gtc cct gaa gaa agc gaa gag cta ctg aag gct 691
Asp Leu Leu Leu Arg Val Pro Glu Glu Ser Glu Glu Leu Leu Lys Ala
185 190 195

ctc gca gtc gct tct gac caa gtc act acc tac aag cat gaa gat ctg 739
Leu Ala Val Ala Ser Asp Gln Val Thr Thr Tyr Lys His Glu Asp Leu
200 205 210

gga ttc tta gct agt ctt tgg ttt gac taactacaat caatgtcatg 786
Gly Phe Leu Ala Ser Leu Trp Phe Asp
215 220

acc 789

<210> 2164

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 2164

Met Ser Thr Ile Pro Asp Val Phe Thr Ser Glu Val Phe Pro Glu Ile
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Ser Gly Thr Lys Glu Phe Arg Gly Leu Thr Tyr Met Phe Phe Asp Gln
20 25 30

Phe Thr Leu Pro Thr Ala Glu Gln Leu Glu Gln Ala Lys Ala Ala Gly
35 40 45

Trp Ser Leu Ile Thr Trp Gly Trp Trp Asn Ser Asp Thr Asp Leu Glu
50 55 60

Asp Val Glu Leu Glu Asp Ile Thr Asn Glu Gly Asp Ser Leu Pro Lys
65 70 75 80

Leu Thr Asp Glu Phe Ala Val Ser Ser Leu Ser Thr Phe Asp Leu Asn
85 90 95

Ser Gln Gly Leu Pro Asn Asp Asp Arg Glu Pro Gln Pro Ile Glu Glu
100 105 110

Ala Asp Ser Leu Asp Asp Ile Phe Ser Glu Glu Glu Gly Trp Gly Leu
115 120 125

Met Ala Ile Asn Cys Pro Asn Trp Gln Val Pro Ala Ala Cys Glu Trp
130 135 140

Leu Gly Cys Met Asn Val Gly Glu Pro Phe Glu Met Ser His Val Leu
145 150 155 160

Arg Val Trp Gln Asn Ser Trp Gly Val Glu Ala Leu Ala Phe Gly Gly
165 170 175

Glu Glu Asp Asp Ala Asp Leu Leu Leu Arg Val Pro Glu Glu Ser Glu
180 185 190

Glu Leu Leu Lys Ala Leu Ala Val Ala Ser Asp Gln Val Thr Thr Tyr
195 200 205

Lys His Glu Asp Leu Gly Phe Leu Ala Ser Leu Trp Phe Asp
210 215 220

<210> 2165

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01295

<400> 2165

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tggcatgctc agactccttg tgaagaaagt gacagtttcg atg acc gaa aat ctt 115

															Met	Thr	Glu	Asn	Leu	
															1				5	
gat	aat	gcg	ttg	cta	tcc	atg	cgg	atg	aaa	cct	gta	caa	atg	gcg	ctt	163				
Asp	Asn	Ala	Leu	Leu	Ser	Met	Arg	Met	Lys	Pro	Val	Gln	Met	Ala	Leu					
				10					15					20						
atg	aca	ctg	ggc	tac	aac	cat	gac	atg	gcg	gtg	acc	gat	tcc	ggg	atg	211				
Met	Thr	Leu	Gly	Tyr	Asn	His	Asp	Met	Ala	Val	Thr	Asp	Ser	Gly	Met					
			25					30					35							
gaa	ctt	ata	gtg	cgc	cgc	cca	ggg	ctg	acc	gtg	aac	ttc	aac	ttg	gat	259				
Glu	Leu	Ile	Val	Arg	Arg	Pro	Gly	Leu	Thr	Val	Asn	Phe	Asn	Leu	Asp					
			40					45					50							
tcg	gtc	acc	ttg	tgc	atc	gtc	gct	gat	ttc	atg	tgg	cat	ggc	tgt	gtc	307				
Ser	Val	Thr	Leu	Cys	Ile	Val	Ala	Asp	Phe	Met	Trp	His	Gly	Cys	Val					
			55					60					65							
cct	gca	aag	aaa	cag	gca	gag	tac	ctg	cgg	gcc	gct	aat	gaa	ttc	aac	355				
Pro	Ala	Lys	Lys	Gln	Ala	Glu	Tyr	Leu	Arg	Ala	Ala	Asn	Glu	Phe	Asn					
70					75					80					85					
agg	cca	acc	cgt	gat	ctg	cag	gtg	gtt	tta	gat	gaa	gct	gat	tca	aag	403				
Arg	Pro	Thr	Arg	Asp	Leu	Gln	Val	Val	Leu	Asp	Glu	Ala	Asp	Ser	Lys					
				90					95					100						
aac	atg	act	gtg	cga	ggg	cgt	gaa	ttc	ttc	ttc	tca	agc	gtc	ggc	gca	451				
Asn	Met	Thr	Val	Arg	Gly	Arg	Glu	Phe	Phe	Phe	Ser	Ser	Val	Gly	Ala					
			105					110					115							
acg	tgg	gaa	cag	tcg	gca	gag	ttc	gtg	cac	tac	tgc	atg	aat	gat	gtg	499				
Thr	Trp	Glu	Gln	Ser	Ala	Glu	Phe	Val	His	Tyr	Cys	Met	Asn	Asp	Val					
			120					125					130							
gca	acg	act	ttc	gtg	tct	tgg	tgc	gaa	caa	atc	tgg	ccg	aag	ttt	tcc	547				
Ala	Thr	Thr	Phe	Val	Ser	Trp	Cys	Glu	Gln	Ile	Trp	Pro	Lys	Phe	Ser					
			135					140					145							
cct	gaa	cgc	gta	gag	ttc	aac	gca	act	cct	cca	gat	gtg	gat	ttc	gag	595				
Pro	Glu	Arg	Val	Glu	Phe	Asn	Ala	Thr	Pro	Pro	Asp	Val	Asp	Phe	Glu					
150					155					160					165					
ttc	tct	gaa	gat	caa	ctc	aaa	gaa	ggc	aat	ccc	ttc	ggg	ctg	att	gac	643				
Phe	Ser	Glu	Asp	Gln	Leu	Lys	Glu	Gly	Asn	Pro	Phe	Gly	Leu	Ile	Asp					
				170					175					180						
gaa	ccc	acc	cgg	ctg	gtt	tct	ttg	gat	cgt	atc	tac	caa	caa	tac	gaa	691				
Glu	Pro	Thr	Pro	Leu	Val	Ser	Leu	Asp	Arg	Ile	Tyr	Gln	Gln	Tyr	Glu					
			185					190					195							
tta	atg	ggg	gcg	gat	caa	ctc	aag	atg	ggg	gag	gac	ttc	gtt	gag	tat	739				
Leu	Met	Gly	Ala	Asp	Gln	Leu	Lys	Met	Gly	Glu	Asp	Phe	Val	Glu	Tyr					
			200					205					210							
ctg	cat	atg	ggg	caa	cgt	gtc	agt	gca	tgg	ttg	acc	gat	ggc	aac	aac	787				
Leu	His	Met	Gly	Gln	Arg	Val	Ser	Ala	Trp	Leu	Thr	Asp	Gly	Asn	Asn					
			215					220					225							
ggc	agc	gat	cga	aaa	acc	cta	gcg	gtg	tct	tcc	ggg	aca	ggg	gtg	aaa	835				
Gly	Ser	Asp	Arg	Lys	Thr	Leu	Ala	Val	Ser	Ser	Gly	Thr	Gly	Val	Lys					

230	235	240	245	
atc aaa aac aag aag caa ctt cag gaa ctt ctt gga ctg tgc aac ctg				883
Ile Lys Asn Lys Lys Gln Leu Gln Glu Leu Leu Gly Leu Cys Asn Leu				
	250	255	260	
tac tcg aaa gaa cat gta ctg gtc aca gta ttt gcg gaa gag atc gaa				931
Tyr Ser Lys Glu His Val Leu Val Thr Val Phe Ala Glu Glu Ile Glu				
	265	270	275	
aac ggc gca agg tgg ggt att ttc gcc gaa gca cgc atc gat cta ccg				979
Asn Gly Ala Arg Trp Gly Ile Phe Ala Glu Ala Arg Ile Asp Leu Pro				
	280	285	290	
gca ggg tta aac gat cat cag ttg tgg gta ttc ctc gcc aac tcc agc				1027
Ala Gly Leu Asn Asp His Gln Leu Trp Val Phe Leu Ala Asn Ser Ser				
	295	300	305	
aaa tgg act gca gag gtg tgc ctg acc gtg gca cac cga ctg cag aac				1075
Lys Trp Thr Ala Glu Val Cys Leu Thr Val Ala His Arg Leu Gln Asn				
	310	315	320	325
taaaggcaga acttaagcgt tca				1098
<210> 2166				
<211> 325				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 2166				
Met Thr Glu Asn Leu Asp Asn Ala Leu Leu Ser Met Arg Met Lys Pro				
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Val Gln Met Ala Leu Met Thr Leu Gly Tyr Asn His Asp Met Ala Val				
	20	25	30	
Thr Asp Ser Gly Met Glu Leu Ile Val Arg Arg Pro Gly Leu Thr Val				
	35	40	45	
Asn Phe Asn Leu Asp Ser Val Thr Leu Cys Ile Val Ala Asp Phe Met				
	50	55	60	
Trp His Gly Cys Val Pro Ala Lys Lys Gln Ala Glu Tyr Leu Arg Ala				
	65	70	75	80
Ala Asn Glu Phe Asn Arg Pro Thr Arg Asp Leu Gln Val Val Leu Asp				
	85	90	95	
Glu Ala Asp Ser Lys Asn Met Thr Val Arg Gly Arg Glu Phe Phe Phe				
	100	105	110	
Ser Ser Val Gly Ala Thr Trp Glu Gln Ser Ala Glu Phe Val His Tyr				
	115	120	125	
Cys Met Asn Asp Val Ala Thr Thr Phe Val Ser Trp Cys Glu Gln Ile				
	130	135	140	
Trp Pro Lys Phe Ser Pro Glu Arg Val Glu Phe Asn Ala Thr Pro Pro				
	145	150	155	160

Asp Val Asp Phe Glu Phe Ser Glu Asp Gln Leu Lys Glu Gly Asn Pro
 165 170 175
 Phe Gly Leu Ile Asp Glu Pro Thr Pro Leu Val Ser Leu Asp Arg Ile
 180 185 190
 Tyr Gln Gln Tyr Glu Leu Met Gly Ala Asp Gln Leu Lys Met Gly Glu
 195 200 205
 Asp Phe Val Glu Tyr Leu His Met Gly Gln Arg Val Ser Ala Trp Leu
 210 215 220
 Thr Asp Gly Asn Asn Gly Ser Asp Arg Lys Thr Leu Ala Val Ser Ser
 225 230 235 240
 Gly Thr Gly Val Lys Ile Lys Asn Lys Lys Gln Leu Gln Glu Leu Leu
 245 250 255
 Gly Leu Cys Asn Leu Tyr Ser Lys Glu His Val Leu Val Thr Val Phe
 260 265 270
 Ala Glu Glu Ile Glu Asn Gly Ala Arg Trp Gly Ile Phe Ala Glu Ala
 275 280 285
 Arg Ile Asp Leu Pro Ala Gly Leu Asn Asp His Gln Leu Trp Val Phe
 290 295 300
 Leu Ala Asn Ser Ser Lys Trp Thr Ala Glu Val Cys Leu Thr Val Ala
 305 310 315 320
 His Arg Leu Gln Asn
 325

<210> 2167
 <211> 609
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(586)
 <223> RXA01304

<400> 2167
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 Met Pro Ala Gln Asn
 1 5
 aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg . 163
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser
 10 15 20
 gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag 211
 Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln
 25 30 35
 gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt 259
 Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe

40	45	50	
gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc			307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg			
55	60	65	
gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg			355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr			
70	75	80	85
ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg			403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met			
90	95	100	
acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta			451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu			
105	110	115	
tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc			499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu			
120	125	130	
atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg			547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly			
135	140	145	
gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt			596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu			
150	155	160	
ttgcttatcg acg			609
<210> 2168			
<211> 162			
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<213> Corynebacterium glutamicum			
<400> 2168			
Met Pro Ala Gln Asn Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser			
1	5	10	15
Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala			
20	25	30	
Val Asp Leu Leu Gln Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val			
35	40	45	
Val Glu Glu Gly Phe Glu Pro Val His Gln Glu Leu Val Lys Ala Leu			
50	55	60	
Ala Arg Arg Asp Arg Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly			
65	70	75	80
Pro Arg Asn Arg Thr Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu			
85	90	95	
Leu Pro Gly Leu Met Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr			
100	105	110	
Ala Gln Ala Gly Leu Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp			

		115					120					125						
Ser	Thr	Ala	Ala	Leu	Ile	Val	Asn	Ala	Pro	Ser	Ser	Ser	Gly	Gly	Val			
	130					135					140							
Arg	Asp	Ala	Leu	Gly	Val	Val	Cys	Pro	Leu	Phe	Gly	Ser	Ile	Phe	Glu			
145					150					155					160			

Arg Leu

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<210> 2169
<211> 450
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(427)  
<223> RXA01310
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<400> 2169																	
aaggaacgtg	cgcgtgcagc	tttccgaggc	aaagacgact	agtctttaat	ccaagtaagt	60											
accggttcag acagttaaac cagaaagacg agtgaacacc						atg	tcc	tcc	gcg	aaa	115						
						Met	Ser	Ser	Ala	Lys							
						1					5						
aag	aaa	ccc	gca	ccg	gag	cgt	atg	cac	tac	atc	aag	ggc	tat	gta	cct	163	
Lys	Lys	Pro	Ala	Pro	Glu	Arg	Met	His	Tyr	Ile	Lys	Gly	Tyr	Val	Pro		
				10					15					20			
gtg	gcg	tat	agc	tct	cca	cac	tca	tcc	ctc	gag	cgc	agc	gca	acc	tgg	211	
Val	Ala	Tyr	Ser	Ser	Pro	His	Ser	Ser	Leu	Glu	Arg	Ser	Ala	Thr	Trp		
				25					30					35			
ttg	ggc	atg	gga	ttc	ctc	ctc	act	gct	ctg	gca	ggc	gtt	ggc	gca	gtc	259	
Leu	Gly	Met	Gly	Phe	Leu	Leu	Thr	Ala	Leu	Ala	Gly	Val	Gly	Ala	Val		
				40					45					50			
ctc	ttc	gca	gtc	ggc	gca	aac	agc	ggt	ggc	cag	cag	cag	gaa	cac	tgg	307	
Leu	Phe	Ala	Val	Gly	Ala	Asn	Ser	Val	Gly	Gln	Gln	Gln	Glu	His	Trp		
				55					60					65			
gtc	ctc	tac	agc	atc	atc	ggg	gtt	gta	ttc	gcc	gtt	gtc	tgc	aca	gtt	355	
Val	Leu	Tyr	Ser	Ile	Ile	Gly	Val	Val	Phe	Ala	Val	Val	Cys	Thr	Val		
				70					75					80			
																85	
ttg	ggc	acc	gtc	ctg	atc	atc	aag	ggc	cga	gca	cct	tac	aac	cgt	tac	403	
Leu	Gly	Thr	Val	Leu	Ile	Ile	Lys	Gly	Arg	Ala	Pro	Tyr	Asn	Arg	Tyr		
				90					95					100			
gtc	aag	gaa	acc	ggc	cgt	acg	cag	tagtttctgt	atgcaggttc	ttt	450						
Val	Lys	Glu	Thr	Gly	Arg	Thr	Gln										
				105													

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<210> 2170
<211> 109
<212> PRT
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<213> Corynebacterium glutamicum

<400> 2170

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Met Ser Ser Ala Lys Lys Lys Pro Ala Pro Glu Arg Met His Tyr Ile
 1             5             10             15

Lys Gly Tyr Val Pro Val Ala Tyr Ser Ser Pro His Ser Ser Leu Glu
          20             25             30

Arg Ser Ala Thr Trp Leu Gly Met Gly Phe Leu Leu Thr Ala Leu Ala
      35             40             45

Gly Val Gly Ala Val Leu Phe Ala Val Gly Ala Asn Ser Val Gly Gln
 50             55             60

Gln Gln Glu His Trp Val Leu Tyr Ser Ile Ile Gly Val Val Phe Ala
 65             70             75             80

Val Val Cys Thr Val Leu Gly Thr Val Leu Ile Ile Lys Gly Arg Ala
          85             90             95

Pro Tyr Asn Arg Tyr Val Lys Glu Thr Gly Arg Thr Gln
      100             105

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<210> 2171

<211> 968

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(945)

<223> RXA01313

<400> 2171

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gcc cta cgc ctc att tca cag ctg ctt gca cca tct gcg gcg ttg aat   48
Ala Leu Arg Leu Ile Ser Gln Leu Leu Ala Pro Ser Ala Ala Leu Asn
 1             5             10             15

ttt aag tcc gag cgc aat gcc gtc gac gtg gca aaa cac atg ctc gcc   96
Phe Lys Ser Glu Arg Asn Ala Val Asp Val Ala Lys His Met Leu Ala
          20             25             30

agc cag gcc caa caa cgc ggt tcc gca ctc gtt gcg cta gac acc cgc   144
Ser Gln Ala Gln Gln Arg Gly Ser Ala Leu Val Ala Leu Asp Thr Arg
      35             40             45

tcg gaa aac gcc gac gcc gcc acg gca tta aga aag tca ctg ctc atc   192
Ser Glu Asn Ala Asp Ala Ala Thr Ala Leu Arg Lys Ser Leu Leu Ile
 50             55             60

cgc agc tgg acg cag cgc ggc acc cac caa ata ctt gcc gcc gaa gac   240
Arg Ser Trp Thr Gln Arg Gly Thr His Gln Ile Leu Ala Ala Glu Asp
 65             70             75             80

gtc cgc tgg atg acg cta cta tgc tcc cca cgc atc ctg gct gct tca   288
Val Arg Trp Met Thr Leu Leu Cys Ser Pro Arg Ile Leu Ala Ala Ser
      85             90             95

gcc aag cgc cgc tcc agc ctt tcg ctt gat agc gcc gca gtc cag cgc   336

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Ala Lys Arg Arg Ser Ser Leu Ser Leu Asp Ser Ala Ala Val Gln Arg
 100 105 110
 gcc cgc gac gca cta aca acc gcc gcc gaa aaa tcc ccc gta tcc aga 384
 Ala Arg Asp Ala Leu Thr Thr Ala Ala Glu Lys Ser Pro Val Ser Arg
 115 120 125
 acc cag gcc tac gaa att ttc cga tcc gta gac gtt gac ccc ggc gag 432
 Thr Gln Ala Tyr Glu Ile Phe Arg Ser Val Asp Val Asp Pro Gly Glu
 130 135 140
 cac aga ggc caa cat tta ctc cgg cat ttc ggt ggc gaa ggt gac atc 480
 His Arg Gly Gln His Leu Leu Arg His Phe Gly Gly Glu Gly Asp Ile
 145 150 155 160
 gta caa ggc ccg ccc atc gga acg gaa gat tcc ttt gtg ctt ctc gat 528
 Val Gln Gly Pro Pro Ile Gly Thr Glu Asp Ser Phe Val Leu Leu Asp
 165 170 175
 tcc atc tgc ccc ctt tcc cta gca ctt aac ggc gac gaa gcg ctc aca 576
 Ser Ile Cys Pro Leu Ser Leu Ala Leu Asn Gly Asp Glu Ala Leu Thr
 180 185 190
 gag atg acc cgt cgc tac ttc cac tcc cgt ggt gct gcc act gtg aaa 624
 Glu Met Thr Arg Arg Tyr Phe His Ser Arg Gly Ala Ala Thr Val Lys
 195 200 205
 gat ctg gtg tgg tgg acc gga ctg act gtg cgt gat gta aag aaa ggc 672
 Asp Leu Val Trp Trp Thr Gly Leu Thr Val Arg Asp Val Lys Lys Gly
 210 215 220
 atc gct gcc gtg tct tcg gat gga ctg att cac tct gtt gaa ggc ccg 720
 Ile Ala Ala Val Ser Ser Asp Gly Leu Ile His Ser Val Glu Gly Pro
 225 230 235 240
 aat ggt gaa gaa atg tgg atc cct acc tgg gca gat gat gtc aca gac 768
 Asn Gly Glu Glu Met Trp Ile Pro Thr Trp Ala Asp Asp Val Thr Asp
 245 250 255
 gca gag gtt tct gat gca cta gcg ttg gaa cta acc ctc ccc gcc ttt 816
 Ala Glu Val Ser Asp Ala Leu Ala Leu Glu Leu Thr Leu Pro Ala Phe
 260 265 270
 gat gaa tac cta ctt tcc tac acc gac cgc agc cac gtc atg gat ccc 864
 Asp Glu Tyr Leu Leu Ser Tyr Thr Asp Arg Ser His Val Met Asp Pro
 275 280 285
 gag cac ctt ttc agc atc ggt ccc ggc aaa aac ggt gtg ttc aaa ccc 912
 Glu His Leu Phe Ser Ile Gly Pro Gly Lys Asn Gly Val Phe Lys Pro
 290 295 300
 ttc aaa gta gtt cag ggt gag gca ctg ccg gtt tagccagca aaatcttcac 965
 Phe Lys Val Val Gln Gly Glu Ala Leu Pro Val
 305 310 315
 ttg 968

<210> 2172
 <211> 315
 <212> PRT

<213> Corynebacterium glutamicum

<400> 2172

Ala Leu Arg Leu Ile Ser Gln Leu Leu Ala Pro Ser Ala Ala Leu Asn
1 5 10 15
Phe Lys Ser Glu Arg Asn Ala Val Asp Val Ala Lys His Met Leu Ala
20 25 30
Ser Gln Ala Gln Gln Arg Gly Ser Ala Leu Val Ala Leu Asp Thr Arg
35 40 45
Ser Glu Asn Ala Asp Ala Ala Thr Ala Leu Arg Lys Ser Leu Leu Ile
50 55 60
Arg Ser Trp Thr Gln Arg Gly Thr His Gln Ile Leu Ala Ala Glu Asp
65 70 75 80
Val Arg Trp Met Thr Leu Leu Cys Ser Pro Arg Ile Leu Ala Ala Ser
85 90 95
Ala Lys Arg Arg Ser Ser Leu Ser Leu Asp Ser Ala Ala Val Gln Arg
100 105 110
Ala Arg Asp Ala Leu Thr Thr Ala Ala Glu Lys Ser Pro Val Ser Arg
115 120 125
Thr Gln Ala Tyr Glu Ile Phe Arg Ser Val Asp Val Asp Pro Gly Glu
130 135 140
His Arg Gly Gln His Leu Leu Arg His Phe Gly Gly Glu Gly Asp Ile
145 150 155 160
Val Gln Gly Pro Pro Ile Gly Thr Glu Asp Ser Phe Val Leu Leu Asp
165 170 175
Ser Ile Cys Pro Leu Ser Leu Ala Leu Asn Gly Asp Glu Ala Leu Thr
180 185 190
Glu Met Thr Arg Arg Tyr Phe His Ser Arg Gly Ala Ala Thr Val Lys
195 200 205
Asp Leu Val Trp Trp Thr Gly Leu Thr Val Arg Asp Val Lys Lys Gly
210 215 220
Ile Ala Ala Val Ser Ser Asp Gly Leu Ile His Ser Val Glu Gly Pro
225 230 235 240
Asn Gly Glu Glu Met Trp Ile Pro Thr Trp Ala Asp Asp Val Thr Asp
245 250 255
Ala Glu Val Ser Asp Ala Leu Ala Leu Glu Leu Thr Leu Pro Ala Phe
260 265 270
Asp Glu Tyr Leu Leu Ser Tyr Thr Asp Arg Ser His Val Met Asp Pro
275 280 285
Glu His Leu Phe Ser Ile Gly Pro Gly Lys Asn Gly Val Phe Lys Pro
290 295 300
Phe Lys Val Val Gln Gly Glu Ala Leu Pro Val

305

310

315

<210> 2173

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01315

<400> 2173

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aatattgcac tgagtgcgaag tttaactag gtttacttca gtg gat att gaa gag 115
 Val Asp Ile Glu Glu
 1 5

cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata 163
 Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile
 10 15 20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc 211
 Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val
 25 30 35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc 259
 Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe
 40 45 50

ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc 307
 Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala
 55 60 65

aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat 355
 Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His
 70 75 80 85

gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc 403
 Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly
 90 95 100

aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga 451
 Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg
 105 110 115

cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc 499
 Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe
 120 125 130

gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag 547
 Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu
 135 140 145

tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat 595
 Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp
 150 155 160 165

cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa 643

Phe Leu Leu Arg Gly Gly Phe Ser Glu
210 215

<210> 2175

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(403)

<223> RXA01316

<400> 2175

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aaagcgcaag gctaagaagg attccccaga accaggcgat gacgatatca tcgatggaga 60
agtaattcct ccgcagaatt aaggaagtcg gtttcacccc atg gat att tcc atg 115
                                         Met Asp Ile Ser Met
                                         1 5
ctc aac gta ata acg agc tac acc att tgg gcc att ttt gcc atc atc 163
Leu Asn Val Ile Thr Ser Tyr Thr Ile Trp Ala Ile Phe Ala Ile Ile
          10          15          20
ggc atc tgc gga ttc gtt ggt gcc ttc ttg gca gcc acc acc aga gaa 211
Gly Ile Cys Gly Phe Val Gly Ala Phe Leu Ala Ala Thr Thr Arg Glu
          25          30          35
gat gcc ttt gag gtt gct gat cgc caa aag aaa atg gtg tgg gta gca 259
Asp Ala Phe Glu Val Ala Asp Arg Gln Lys Lys Met Val Trp Val Ala
          40          45          50
atc ctt atc gca tcc gga ttt gtc ctc acc gcg cta ggt cca tcg att 307
Ile Leu Ile Ala Ser Gly Phe Val Leu Thr Ala Leu Gly Pro Ser Ile
          55          60          65
ccg atc ctg cca tgg gtc gcc atc atc atg atc gcc ctg tac tgg ttt 355
Pro Ile Leu Pro Trp Val Ala Ile Ile Met Ile Gly Leu Tyr Trp Phe
          70          75          80          85
gat gtt cgc ccg caa atc aag agc atc ctt gaa ggt gcc gcc gcc tgg 403
Asp Val Arg Pro Gln Ile Lys Ser Ile Leu Glu Gly Ala Gly Gly Trp
          90          95          100
taaaagctcc ctgaactgcg aaa 426

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<210> 2176

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 2176

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Met Asp Ile Ser Met Leu Asn Val Ile Thr Ser Tyr Thr Ile Trp Ala
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Ile Phe Ala Ile Ile Gly Ile Cys Gly Phe Val Gly Ala Phe Leu Ala
 20 25 30
Ala Thr Thr Arg Glu Asp Ala Phe Glu Val Ala Asp Arg Gln Lys Lys

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35 40 45
 Met Val Trp Val Ala Ile Leu Ile Ala Ser Gly Phe Val Leu Thr Ala
 50 55 60
 Leu Gly Pro Ser Ile Pro Ile Leu Pro Trp Val Ala Ile Ile Met Ile
 65 70 75 80
 Gly Leu Tyr Trp Phe Asp Val Arg Pro Gln Ile Lys Ser Ile Leu Glu
 85 90 95
 Gly Ala Gly Gly Trp
 100

 <210> 2177
 <211> 543
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(520)
 <223> RXA01317

 <400> 2177
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 ttcccatatc ctcttcggag cttaactagg agtaaccatc atg tcc gat gca aaa 115
 Met Ser Asp Ala Lys
 1 5

 gac gat tcc atc ttg tcc aag tgg agc aat gca gct tcc gag ctc agc 163
 Asp Asp Ser Ile Leu Ser Lys Trp Ser Asn Ala Ala Ser Glu Leu Ser
 10 15 20

 ggt gcc gtc agt gga gta gcg aag aag ctc cgt gaa gaa ctc tct gag 211
 Gly Ala Val Ser Gly Val Ala Lys Lys Leu Arg Glu Glu Leu Ser Glu
 25 30 35

 aag gaa acc ttc agc aag ctt aaa acc gaa gcc agc gaa gcc gtc gat 259
 Lys Glu Thr Phe Ser Lys Leu Lys Thr Glu Ala Ser Glu Ala Val Asp
 40 45 50

 caa gca aag tcc ggc tcc tac cta gat gcc ggt aag gaa ttc gcc cgc 307
 Gln Ala Lys Ser Gly Ser Tyr Leu Asp Ala Gly Lys Glu Phe Ala Arg
 55 60 65

 gac gcc gga tcc atc atc aaa gat gca gcc aaa acc gtc aaa ggt gcc 355
 Asp Ala Gly Ser Ile Ile Lys Asp Ala Ala Lys Thr Val Lys Gly Ala
 70 75 80 85

 gtc agt gat tcc gat aaa aac gac gtg aaa tcc gcc ttc ggt aac gcc 403
 Val Ser Asp Ser Asp Lys Asn Asp Val Lys Ser Ala Phe Gly Asn Ala
 90 95 100

 gtg gaa gct tcc cgc gac aag ttc gat gac acc ctc gaa aag cgc aag 451
 Val Glu Ala Ser Arg Asp Lys Phe Asp Asp Thr Leu Glu Lys Arg Lys
 105 110 115

 gct aag aag gat tcc cca gaa cca ggc gat gac gat atc atc gat gga 499

Ala Lys Lys Asp Ser Pro Glu Pro Gly Asp Asp Asp Ile Ile Asp Gly
 120 125 130

gaa gta att cct ccg cag aat taaggaagtc ggtttcaccc cat
 Glu Val Ile Pro Pro Gln Asn
 135 140

543

<210> 2178

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 2178

Met Ser Asp Ala Lys Asp Asp Ser Ile Leu Ser Lys Trp Ser Asn Ala
 1 5 10 15

Ala Ser Glu Leu Ser Gly Ala Val Ser Gly Val Ala Lys Lys Leu Arg
 20 25 30

Glu Glu Leu Ser Glu Lys Glu Thr Phe Ser Lys Leu Lys Thr Glu Ala
 35 40 45

Ser Glu Ala Val Asp Gln Ala Lys Ser Gly Ser Tyr Leu Asp Ala Gly
 50 55 60

Lys Glu Phe Ala Arg Asp Ala Gly Ser Ile Ile Lys Asp Ala Ala Lys
 65 70 75 80

Thr Val Lys Gly Ala Val Ser Asp Ser Asp Lys Asn Asp Val Lys Ser
 85 90 95

Ala Phe Gly Asn Ala Val Glu Ala Ser Arg Asp Lys Phe Asp Asp Thr
 100 105 110

Leu Glu Lys Arg Lys Ala Lys Lys Asp Ser Pro Glu Pro Gly Asp Asp
 115 120 125

Asp Ile Ile Asp Gly Glu Val Ile Pro Pro Gln Asn
 130 135 140

<210> 2179

<211> 1425

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1402)

<223> RXA01318

<400> 2179

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tcctgcccc gtgtccaccc ctgcgtacat aataggacgc atg gga aaa cat gag 115
 Met Gly Lys His Glu
 1 5

gtt gct cag cag acg gtt ccg ggt cct tcg ccg gaa atg gaa gcg cag 163
 Val Ala Gln Gln Thr Val Pro Gly Pro Ser Pro Glu Met Glu Ala Gln

10	15	20	
cgg cgt aaa gag ttg cgc aag cac aag gcc att gcc act ggc ctg ttg Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile Ala Thr Gly Leu Leu 25 30 35			211
att ttt gct gcc gct gta tat ttt ctt tgc cgt ttc gtg gag acc cgt Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg 40 45 50			259
ccg ggt gaa act gca gcg tgg gta ggt ttt gtg cgc gct gcg gca gag Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val Arg Ala Ala Ala Glu 55 60 65			307
gcc gga atg att ggc ggg ttg gcc gac tgg ttc gcg gtc acc gcg ctg Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe Ala Val Thr Ala Leu 70 75 80 85			355
ttc cgt cat cca ttg tgg ctg cct att ccg cac act gcg att atc ccg Phe Arg His Pro Leu Trp Leu Pro Ile Pro His Thr Ala Ile Ile Pro 90 95 100			403
cgc aag aaa gac cag tta ggt gag gcc tta agc ggg ttt gtg ggg gat Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser Gly Phe Val Gly Asp 105 110 115			451
aac ttc cta aat gcc cag ctc att acg gaa aaa gtc tct cag gcg ccg Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys Val Ser Gln Ala Arg 120 125 130			499
atc cca gag cgc gcc ggg gag tgg ctc gcc cag ccg gaa aac ggg gag Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu 135 140 145			547
aaa gtt tcg cgc gaa gtc ggc aaa ttg acc gct aat att gtg cgc gca Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala Asn Ile Val Arg Ala 150 155 160 165			595
atc gat ccg tca gat gct gaa gcg gtg att aaa tct gcg gtg atc gac Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys Ser Ala Val Ile Asp 170 175 180			643
aag ctt gcg gaa ccc acc tgg ggc cca cca gct ggg ccg ttg ctg gaa Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala Gly Arg Leu Leu Glu 185 190 195			691
caa ctc ctc gcc gaa ggc aaa gcc gaa cca gtt gtc cag gaa ctc gcg Gln Leu Leu Ala Glu Gly Lys Ala Glu Pro Val Val Gln Glu Leu Ala 200 205 210			739
cag tgg ctg cac aaa aag gcg ttg ggc tcc gag ccg ctg att gat cgc Gln Trp Leu His Lys Lys Ala Leu Gly Ser Glu Pro Leu Ile Asp Arg 215 220 225			787
ctg ctc aac gag cgc cgc ccg att tgg gcg ccg aaa ttc act gcg cag Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro Lys Phe Thr Ala Gln 230 235 240 245			835
ctg gtc agc ggc aaa gtc tat gac gag gtc ata aaa ttc act gaa gcc Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile Lys Phe Thr Glu Ala 250 255 260			883

gtc gct gcc gat cct aac cac gag gcc cgc aaa tcg ctg cgc cga ttc 931
 Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys Ser Leu Arg Arg Phe
 265 270 275

ctt aat aaa ttg gcg caa gac ctg cag cat gac cca ggc atg att att 979
 Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp Pro Gly Met Ile Ile
 280 285 290

.aaa gtt gaa gaa atc aaa cgc gac atc atg ggc tcc ggc gcc atc gcg 1027
 Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly Ser Gly Ala Ile Ala
 295 300 305

caa gcc gcg cca acc atc tgg gcg tca gcc tcc gag tcg ctc att gaa 1075
 Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser Glu Ser Leu Ile Glu
 310 315 320 325

tcc gca gaa gat gag tca tca att ctg cgt cgc aaa att gcc gaa gca 1123
 Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg Lys Ile Ala Glu Ala
 330 335 340

gct acc agc tgg ggt caa aga ttg ctt gtc gac gac tcc ctc cgg cat 1171
 Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp Asp Ser Leu Arg His
 345 350 355

tca ctc gac acc cgg att acc ggc gcc gct gct ttc ctc gcc gac aat 1219
 Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn
 360 365 370

tac gcc ccc gaa gtc acc ggc att atc tcc gaa acc att gaa cga tgg 1267
 Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu Thr Ile Glu Arg Trp
 375 380 385

gac gct gaa gaa gct tca gag aaa atc gaa ctc atg gtg ggc aaa gac 1315
 Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu Met Val Gly Lys Asp
 390 395 400 405

ctc caa tac atc cgc ctt aat ggc aca att gta ggt gca tta gca gga 1363
 Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val Gly Ala Leu Ala Gly
 410 415 420

ctg gcc att tac gct att tcc cat atc ctc ttc gga gct taactaggag 1412
 Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe Gly Ala
 425 430

taaccatcat gtc 1425

<210> 2180
 <211> 434
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2180
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 Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg Lys His Lys Ala Ile
 20 25 30
 Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg

35 40 45

Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val
50 55 60

Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe
65 70 75 80

Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp Leu Pro Ile Pro His
85 90 95

Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser
100 105 110

Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys
115 120 125

Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln
130 135 140

Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala
145 150 155 160

Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys
165 170 175

Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala
180 185 190

Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Gly Lys Ala Glu Pro Val
195 200 205

Val Gln Glu Leu Ala Gln Trp Leu His Lys Lys Ala Leu Gly Ser Glu
210 215 220

Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro
225 230 235 240

Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile
245 250 255

Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys
260 265 270

Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp
275 280 285

Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly
290 295 300

Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser
305 310 315 320

Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg
325 330 335

Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp
340 345 350

Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala
355 360 365

Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu
 370 375 380
 Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu
 385 390 395 400
 Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val
 405 410 415
 Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile Ser His Ile Leu Phe
 420 425 430
 Gly Ala

<210> 2181

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA01330

<400> 2181

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cggtgaggcc caatgaaatg cctccgaaac agaaacagggc atg tgg aaa gac tta 115
 Met Trp Lys Asp Leu
 1 5

acc gaa ccg ctg ccc gaa gct tgc gct gag ggc tta gag atc cgg gtg 163
 Thr Glu Pro Leu Glu Ala Cys Ala Glu Gly Leu Glu Ile Arg Val
 10 15 20

gtt aaa tct ccc gaa gag ctg gca gat tac gct gca gtt ctt tct gcg 211
 Val Lys Ser Pro Glu Glu Leu Ala Asp Tyr Ala Ala Val Leu Ser Ala
 25 30 35

aat tgg aat cca ccc gcc gaa act gtg cag cgt ttc tat acc gaa gca 259
 Asn Trp Asn Pro Pro Ala Glu Thr Val Gln Arg Phe Tyr Thr Glu Ala
 40 45 50

gct gaa tac gca ctg aga aag aac tcg ccc gca ctt tat ctg gtg ggt 307
 Ala Glu Tyr Ala Leu Arg Lys Asn Ser Pro Ala Leu Tyr Leu Val Gly
 55 60 65

tat gcg ggc aac cgc gca gtg tgt tct gcg gaa gca ttc ata cac gcg 355
 Tyr Ala Gly Asn Arg Ala Val Cys Ser Ala Glu Ala Phe Ile His Ala
 70 75 80 85

agc gta gtt gga atc tac aat atc tcc acc ctt gag cac aaa cgc cgg 403
 Ser Val Val Gly Ile Tyr Asn Ile Ser Thr Leu Glu His Lys Arg Arg
 90 95 100

cgt ggc tac ggc gga gcc atc acc tta gcc acg ttg cat acc gca cgt 451
 Arg Gly Tyr Gly Gly Ala Ile Thr Leu Ala Thr Leu His Thr Ala Arg
 105 110 115

aac gca ggg.tgt gac acc gcc gtg ttg caa gct tcc gaa gat ggt gag 499
 Asn Ala Gly Cys Asp Thr Ala Val Leu Gln Ala Ser Glu Asp Gly Glu
 120 125 130

ccc gtt tat cgc aaa cta gga ttc acc gac tgc ggt cga ttt act gaa 547
 Pro Val Tyr Arg Lys Leu Gly Phe Thr Asp Cys Gly Arg Phe Thr Glu
 135 140 145

tac tct ttg tgattagtta gggaccgtat gcg 579
 Tyr Ser Leu
 150

<210> 2182

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 2182

Met Trp Lys Asp Leu Thr Glu Pro Leu Pro Glu Ala Cys Ala Glu Gly
 1 5 10 15

Leu Glu Ile Arg Val Val Lys Ser Pro Glu Glu Leu Ala Asp Tyr Ala
 20 25 30

Ala Val Leu Ser Ala Asn Trp Asn Pro Pro Ala Glu Thr Val Gln Arg
 35 40 45

Phe Tyr Thr Glu Ala Ala Glu Tyr Ala Leu Arg Lys Asn Ser Pro Ala
 50 55 60

Leu Tyr Leu Val Gly Tyr Ala Gly Asn Arg Ala Val Cys Ser Ala Glu
 65 70 75 80

Ala Phe Ile His Ala Ser Val Val Gly Ile Tyr Asn Ile Ser Thr Leu
 85 90 95

Glu His Lys Arg Arg Arg Gly Tyr Gly Gly Ala Ile Thr Leu Ala Thr
 100 105 110

Leu His Thr Ala Arg Asn Ala Gly Cys Asp Thr Ala Val Leu Gln Ala
 115 120 125

Ser Glu Asp Gly Glu Pro Val Tyr Arg Lys Leu Gly Phe Thr Asp Cys
 130 135 140

Gly Arg Phe Thr Glu Tyr Ser Leu
 145 150

<210> 2183

<211> 1128

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1105)

<223> RXA01333

<400> 2183

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gaggtacttt cttgcaagtt gtagcgcacc gccgatacca atg cct ggc ggg tgc 115
Met Pro Gly Gly Cys
1 5

tcc ggt aac atc gtc cgc atg ctg cct aaa tcc cgg att ttc tcc gca 163
Ser Gly Asn Ile Val Arg Met Leu Pro Lys Ser Arg Ile Phe Ser Ala
10 15 20

atc ttg ctc gga att ggt gtg gca ctt gtg gtc tgg ggt ctg gtg gct 211
Ile Leu Leu Gly Ile Gly Val Ala Leu Val Val Trp Gly Leu Val Ala
25 30 35

ccg cgc ttt gtg cac gct gat ggc cgt ttg cct ctt gat ttg gag gcg 259
Pro Arg Phe Val His Ala Asp Gly Arg Leu Pro Leu Asp Leu Glu Ala
40 45 50

acg acg tac gtt ctc cat gac tct gac gct cag acc act att aat tct 307
Thr Thr Tyr Val Leu His Asp Ser Asp Ala Gln Thr Thr Ile Asn Ser
55 60 65

gat ccg ttg gcc ggt gtg gtg act acg ccg gtg act cgt cag ttg cat 355
Asp Pro Leu Ala Gly Val Val Thr Thr Pro Val Thr Arg Gln Leu His
70 75 80 85

ttt gag gtg atg gat cct gcg agt gct gat gat gcc act att cgt att 403
Phe Glu Val Met Asp Pro Ala Ser Ala Asp Asp Ala Thr Ile Arg Ile
90 95 100

ggg gat tcg atg ttg cgt ggt aat cct gat act cag ggt ttt gag cag 451
Gly Asp Ser Met Leu Arg Gly Asn Pro Asp Thr Gln Gly Phe Glu Gln
105 110 115

gaa cgg ctc ctg tca gcg act gtg tcg agt ttc cgc att gat cgc acc 499
Glu Arg Leu Leu Ser Ala Thr Val Ser Ser Phe Arg Ile Asp Arg Thr
120 125 130

tct ggt gag gtt ttg tcc gat att gcg ctg act aat cag ttg gcg agc 547
Ser Gly Glu Val Leu Ser Asp Ile Ala Leu Thr Asn Gln Leu Ala Ser
135 140 145

cct acg gtg cag tat tcg gtg gat ggc att tgg ttg aag ttc cca act 595
Pro Thr Val Gln Tyr Ser Val Asp Gly Ile Trp Leu Lys Phe Pro Thr
150 155 160 165

gac gcg cag gag acc act tac aac gtg gtg gat ccg gtg ctg agg tct 643
Asp Ala Gln Glu Thr Thr Tyr Asn Val Val Asp Pro Val Leu Arg Ser
170 175 180

gcg ctg ccg gcg gat ttt gtg gag tcc acg gag atc gat ggc cgt gag 691
Ala Leu Pro Ala Asp Phe Val Glu Ser Thr Glu Ile Asp Gly Arg Glu
185 190 195

gtg ctg cat tac cgt cag gtg att gat aac gtg aat gtg gcg gag tat 739
Val Leu His Tyr Arg Gln Val Ile Asp Asn Val Asn Val Ala Glu Tyr
200 205 210

ttc gcg gat gcc aac aac acc acc acg ttg act aaa gag gat ggc ggt 787
Phe Ala Asp Ala Asn Asn Thr Thr Thr Leu Thr Lys Glu Asp Gly Gly

215	220	225	
acc acg acg ggc tat	ttt tat cac aat gtg act	cgt gat ttt tgg gtg	835
Thr Thr Thr Gly Tyr	Phe Tyr His Asn Val Thr	Arg Asp Phe Trp Val	
230	235	240 245	
gat cag cgt acc ggt ttg gtt gtc gat	cta gct gaa aat att gat gat		883
Asp Gln Arg Thr Gly Leu Val Val Asp	Leu Ala Glu Asn Ile Asp Asp		
	250 255	260	
ttt tac ggc gac cgc agc ggc cag aag	tac gaa cag aaa ttg ctt ttc		931
Phe Tyr Gly Asp Arg Ser Gly Gln Lys	Tyr Glu Gln Lys Leu Leu Phe		
	265 270	275	
gac gcc tcc ctc gac gat gca gct gtc	tct aag ctg gtt gca cag gcc		979
Asp Ala Ser Leu Asp Asp Ala Ala Val	Ser Lys Leu Val Ala Gln Ala		
	280 285	290	
gaa agc atc cct gat gga gat gtg agc	aaa atc gca aat acc gta ggt		1027
Glu Ser Ile Pro Asp Gly Asp Val Ser	Lys Ile Ala Asn Thr Val Gly		
	295 300	305	
att gtg atc ggt gcg gta ttg gct ctc	gtg ggc ctg gcc ggg tgt ttt		1075
Ile Val Ile Gly Ala Val Leu Ala Leu	Val Gly Leu Ala Gly Cys Phe		
310	315	320 325	
ggg gcg ttt ggg aag aaa cgt cga gaa	gct taacctgctg ttcaaataga		1125
Gly Ala Phe Gly Lys Lys Arg Arg Glu	Ala		
	330 335		
ttt			1128
<210> 2184			
<211> 335			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2184			
Met Pro Gly Gly Cys Ser Gly Asn Ile Val Arg Met Leu Pro Lys Ser			
1	5	10	15
Arg Ile Phe Ser Ala Ile Leu Leu Gly Ile Gly Val Ala Leu Val Val			
	20	25	30
Trp Gly Leu Val Ala Pro Arg Phe Val His Ala Asp Gly Arg Leu Pro			
	35	40	45
Leu Asp Leu Glu Ala Thr Thr Tyr Val Leu His Asp Ser Asp Ala Gln			
	50	55	60
Thr Thr Ile Asn Ser Asp Pro Leu Ala Gly Val Val Thr Thr Pro Val			
	65	70	75 80
Thr Arg Gln Leu His Phe Glu Val Met Asp Pro Ala Ser Ala Asp Asp			
	85	90	95
Ala Thr Ile Arg Ile Gly Asp Ser Met Leu Arg Gly Asn Pro Asp Thr			
	100	105	110
Gln Gly Phe Glu Gln Glu Arg Leu Leu Ser Ala Thr Val Ser Ser Phe			

115 120 125

Arg Ile Asp Arg Thr Ser Gly Glu Val Leu Ser Asp Ile Ala Leu Thr
130 135 140

Asn Gln Leu Ala Ser Pro Thr Val Gln Tyr Ser Val Asp Gly Ile Trp
145 150 155 160

Leu Lys Phe Pro Thr Asp Ala Gln Glu Thr Thr Tyr Asn Val Val Asp
165 170 175

Pro Val Leu Arg Ser Ala Leu Pro Ala Asp Phe Val Glu Ser Thr Glu
180 185 190

Ile Asp Gly Arg Glu Val Leu His Tyr Arg Gln Val Ile Asp Asn Val
195 200 205

Asn Val Ala Glu Tyr Phe Ala Asp Ala Asn Asn Thr Thr Thr Leu Thr
210 215 220

Lys Glu Asp Gly Gly Thr Thr Thr Gly Tyr Phe Tyr His Asn Val Thr
225 230 235 240

Arg Asp Phe Trp Val Asp Gln Arg Thr Gly Leu Val Val Asp Leu Ala
245 250 255

Glu Asn Ile Asp Asp Phe Tyr Gly Asp Arg Ser Gly Gln Lys Tyr Glu
260 265 270

Gln Lys Leu Leu Phe Asp Ala Ser Leu Asp Asp Ala Ala Val Ser Lys
275 280 285

Leu Val Ala Gln Ala Glu Ser Ile Pro Asp Gly Asp Val Ser Lys Ile
290 295 300

Ala Asn Thr Val Gly Ile Val Ile Gly Ala Val Leu Ala Leu Val Gly
305 310 315 320

Leu Ala Gly Cys Phe Gly Ala Phe Gly Lys Lys Arg Arg Glu Ala
325 330 335

<210> 2185
<211> 726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> RXA01336

<400> 2185
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agcgcaagcc gtttttagcag atcacaggta gaattgcgac atg gag ccc acc gta 115
Met Glu Pro Thr Val
1 5
aaa gcc agc gcg cgc cac acc atc cac gtc acc gcc gac acc tgg cgc 163
Lys Ala Ser Ala Arg His Thr Ile His Val Thr Ala Asp Thr Trp Arg

10	15	20	
atc cgc ctg agt gcc tca gcc cac tca cac ccc aac gac gcg tac gcg Ile Arg Leu Ser Ala Ser Ala His Ser His Pro Asn Asp Ala Tyr Ala 25 30 35			211
cgc cgg gct acg gca att tcc gcc ata ggc agc gtg ctt atc gac gtc Arg Arg Ala Thr Ala Ile Ser Ala Ile Gly Ser Val Leu Ile Asp Val 40 45 50			259
ccc ctc caa ggc gaa cgc atc tct gaa tcc act gca tac gac ggc caa Pro Leu Gln Gly Glu Arg Ile Ser Glu Ser Thr Ala Tyr Asp Gly Gln 55 60 65			307
atc aac gcc gac tgg aac gca gaa gtc acc ggc acc gat gtg aac atc Ile Asn Ala Asp Trp Asn Ala Glu Val Thr Gly Thr Asp Val Asn Ile 70 75 80 85			355
gca cgc gac atc atc tcc cgg ctc gca gcg gtg cca gac gtt caa gtc Ala Arg Asp Ile Ile Ser Arg Leu Ala Ala Val Pro Asp Val Gln Val 90 95 100			403
gac ggc ccg ttg tgg tcc ttg agt gac agt ttg gct gca gag gct gct Asp Gly Pro Leu Trp Ser Leu Ser Asp Ser Leu Ala Ala Glu Ala Ala 105 110 115			451
gtg gag gca ttg caa ggt gct gcc gac act gcg cgg aac acc gcg acc Val Glu Ala Leu Gln Gly Ala Ala Asp Thr Ala Arg Asn Thr Ala Thr 120 125 130			499
gcc atc gca gaa tcc ctc ggc ggg cag cta ggt gca ctt ctc tac gca Ala Ile Ala Glu Ser Leu Gly Gly Gln Leu Gly Ala Leu Leu Tyr Ala 135 140 145			547
aca acc gac acc cac agc tcc aca ccg ata cca gca cgc gca gaa atg Thr Thr Asp Thr His Ser Ser Thr Pro Ile Pro Ala Arg Ala Glu Met 150 155 160 165			595
atg gca gca aaa gcc tcc ata cca ccg cgc aca ctc gac cta gaa ctc Met Ala Ala Lys Ala Ser Ile Pro Pro Arg Thr Leu Asp Leu Glu Leu 170 175 180			643
gcc ccc tct gac atc gaa gtc acc aaa gaa atc gcc gtg acc ttt gaa Ala Pro Ser Asp Ile Glu Val Thr Lys Glu Ile Ala Val Thr Phe Glu 185 190 195			691
ttc ctt gca ggc taaaccgcga tttggtattt cgg Phe Leu Ala Gly 200			726

<210> 2186

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 2186

Met	Glu	Pro	Thr	Val	Lys	Ala	Ser	Ala	Arg	His	Thr	Ile	His	Val	Thr
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Ala Asp Thr Trp Arg Ile Arg Leu Ser Ala Ser Ala His Ser His Pro

gaa ctc gtt gac ccc acc gac ttc atc agg ccc aac agc gtg gtc tta	259
Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro Asn Ser Val Val Leu	
40 45 50	
tcc gtt ggc atc gcc ttc gca gaa acg ccc gac ggg ctt cgc gat tgg	307
Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp Gly Leu Arg Asp Trp	
55 60 65	
gca cac cga ctc gcc gac gca ggg gtc atc gcg atc ggg ttc ggc tcc	355
Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala Ile Gly Phe Gly Ser	
70 75 80 85	
ggc ctc acc ttc cca cag gtt ccg cag gcg ctt atc gac gcc tcc ctc	403
Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu Ile Asp Ala Ser Leu	
90 95 100	
cac ctt ggc ctc ggc ctc ttt gaa gtc ccc cgt gaa att cca ttt atc	451
His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg Glu Ile Pro Phe Ile	
105 110 115	
tcg atc acc tcc agc gtg cgt gat gag caa acc cgc cgt gcc ggc cgc	499
Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr Arg Arg Ala Gly Arg	
120 125 130	
ctg caa caa gaa ctc ctc ctg gaa cag gaa cgg ctt aac tcc atc gcc	547
Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg Leu Asn Ser Ile Ala	
135 140 145	
atc tcc ggt ggc atc gaa gcc ctg tgc cgt gct gcc gcc gac tat ttg	595
Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala Ala Ala Asp Tyr Leu	
150 155 160 165	
ggg ggt gca gta acc atc gtg gac agc gac ggc cgc gtg gct tgc tct	643
Gly Gly Ala Val Thr Ile Val Asp Ser Asp Gly Arg Val Ala Cys Ser	
170 175 180	
att acc acc gat gac cta gac gca ctc ccc caa gct gtc tcg cgc ctg	691
Ile Thr Thr Asp Asp Leu Asp Ala Leu Pro Gln Ala Val Ser Arg Leu	
185 190 195	
aac gga tcc agt caa gca ctc acg gat gcc acc aac ttt gga ttc atc	739
Asn Gly Ser Ser Gln Ala Leu Thr Asp Ala Thr Asn Phe Gly Phe Ile	
200 205 210	
cac cgc atg acc cgc tac ggc gac cgc cac cac gtg ctc tca gtc ctt	787
His Arg Met Thr Arg Tyr Gly Asp Arg His His Val Leu Ser Val Leu	
215 220 225	
atg ccc acc cgc ccc aca gac caa cac cgc gcg ctg atc aga cac tgc	835
Met Pro Thr Arg Pro Thr Asp Gln His Arg Ala Leu Ile Arg His Cys	
230 235 240 245	
gca ggc ctt gcc gat att ttg ctc caa cgc ccc gaa gcc atg cgc gac	883
Ala Gly Leu Ala Asp Ile Leu Leu Gln Arg Pro Glu Ala Met Arg Asp	
250 255 260	
cga gaa atc gaa gtg cga tca ctt gcc atg tca cta ctt ctg ggt cga	931
Arg Glu Ile Glu Val Arg Ser Leu Ala Met Ser Leu Leu Leu Gly Arg	
265 270 275	
agc gac gac ctg gcc acc att cac cgc gtg ttc gct gac atc act gat	979

Ser	Asp	Asp	Leu	Ala	Thr	Ile	His	Arg	Val	Phe	Ala	Asp	Ile	Thr	Asp		
		280					285					290					
gct	tcc	gga	aat	atc	cgc	ccc	atc	ctc	atc	acc	ggc	aac	aca	ccc	caa	1027	
Ala	Ser	Gly	Asn	Ile	Arg	Pro	Ile	Leu	Ile	Thr	Gly	Asn	Thr	Pro	Gln		
	295					300					305						
tca	gta	cga	aaa	gca	ctc	tcc	agt	gtc	gcc	acc	gca	ctg	tac	aaa	cag	1075	
Ser	Val	Arg	Lys	Ala	Leu	Ser	Ser	Val	Ala	Thr	Ala	Leu	Tyr	Lys	Gln		
310					315					320					325		
gaa	cga	gca	cta	gct	cat	cta	cgc	ctc	gcc	gaa	tcc	acc	gaa	ctc	ctc	1123	
Glu	Arg	Ala	Leu	Ala	His	Leu	Arg	Leu	Ala	Glu	Ser	Thr	Glu	Leu	Leu		
				330					335					340			
ttc	ctt	cgc	gga	agc	cgc	agc	gtg	cac	aac	atc	gtg	caa	ctt	ttt	ggc	1171	
Phe	Leu	Arg	Gly	Ser	Arg	Ser	Val	His	Asn	Ile	Val	Gln	Leu	Phe	Gly		
		345						350					355				
act	gcc	gca	agc	gga	gtt	cgc	ctc	tgc	att	ggc	ctg	ccc	acc	cga	gcg	1219	
Thr	Ala	Ala	Ser	Gly	Val	Arg	Leu	Cys	Ile	Gly	Leu	Pro	Thr	Arg	Ala		
		360					365					370					
gaa	aac	atc	gat	aag	aaa	ctc	atc	cgc	gaa	ctc	act	gcc	acc	gca	aaa	1267	
Glu	Asn	Ile	Asp	Lys	Lys	Leu	Ile	Arg	Glu	Leu	Thr	Ala	Thr	Ala	Lys		
	375					380					385						
acc	cta	caa	ctt	gga	acc	cac	gcc	gaa	ccc	cgt	gac	ggc	acc	ttg	ctg	1315	
Thr	Leu	Gln	Leu	Gly	Thr	His	Ala	Glu	Pro	Arg	Asp	Gly	Thr	Leu	Leu		
390					395					400					405		
tgg	ctc	caa	aac	ccc	gag	ctg	cgc	aaa	atc	ctt	aag	atc	cga	tcc	cgc	1363	
Trp	Leu	Gln	Asn	Pro	Glu	Leu	Arg	Lys	Ile	Leu	Lys	Ile	Arg	Ser	Arg		
			410					415						420			
gac	acc	tac	gac	cgt	ctc	ctc	gac	cac	gac	cgc	acc	aac	aac	acc	gag	1411	
Asp	Thr	Tyr	Asp	Arg	Leu	Leu	Asp	His	Asp	Arg	Thr	Asn	Asn	Thr	Glu		
			425					430					435				
ctc	gcc	ccc	acc	ttg	gtg	tct	ttt	act	cag	cac	agc	gga	cat	ata	ggc	1459	
Leu	Ala	Pro	Thr	Leu	Val	Ser	Phe	Thr	Gln	His	Ser	Gly	His	Ile	Gly		
		440					445					450					
gac	acc	gcc	aaa	gaa	ctg	ggc	atc	cac	cgc	cac	acc	gtg	cgc	acc	cgc	1507	
Asp	Thr	Ala	Lys	Glu	Leu	Gly	Ile	His	Arg	His	Thr	Val	Arg	Thr	Arg		
		455				460					465						
atg	atc	cgc	att	gaa	gag	atc	tgc	gaa	atc	gac	ctc	aat	gat	cca	ctg	1555	
Met	Ile	Arg	Ile	Glu	Glu	Ile	Cys	Glu	Ile	Asp	Leu	Asn	Asp	Pro	Leu		
470					475					480					485		
acc	aga	gcg	gag	ctg	ctc	tta	gtg	atc	gca	acg	aag	gag	gga	gac	gtc	1603	
Thr	Arg	Ala	Glu	Leu	Leu	Val	Ile	Ala	Thr	Lys	Glu	Gly	Asp	Val			
			490					495					500				
gaa	aag	caa	taaaaagacc	ccatgcaaag	cat											1635	
Glu	Lys	Gln															

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 2188

Met Glu Thr Pro Thr Gln Asp Met Asp Val Arg Trp Leu Tyr Thr Gln
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Ser Gln Leu Lys Leu Arg Glu Ile Leu Pro Thr Asn Lys Thr Phe Asp
20 25 30

Val Ile Gln Ile Ser Glu Leu Val Asp Pro Thr Asp Phe Ile Arg Pro
35 40 45

Asn Ser Val Val Leu Ser Val Gly Ile Ala Phe Ala Glu Thr Pro Asp
50 55 60

Gly Leu Arg Asp Trp Ala His Arg Leu Ala Asp Ala Gly Val Ile Ala
65 70 75 80

Ile Gly Phe Gly Ser Gly Leu Thr Phe Pro Gln Val Pro Gln Ala Leu
85 90 95

Ile Asp Ala Ser Leu His Leu Gly Leu Gly Leu Phe Glu Val Pro Arg
100 105 110

Glu Ile Pro Phe Ile Ser Ile Thr Ser Ser Val Arg Asp Glu Gln Thr
115 120 125

Arg Arg Ala Gly Arg Leu Gln Gln Glu Leu Leu Leu Glu Gln Glu Arg
130 135 140

Leu Asn Ser Ile Ala Ile Ser Gly Gly Ile Glu Ala Leu Cys Arg Ala
145 150 155 160

Ala Ala Asp Tyr Leu Gly Gly Ala Val Thr Ile Val Asp Ser Asp Gly
165 170 175

Arg Val Ala Cys Ser Ile Thr Thr Asp Asp Leu Asp Ala Leu Pro Gln
180 185 190

Ala Val Ser Arg Leu Asn Gly Ser Ser Gln Ala Leu Thr Asp Ala Thr
195 200 205

Asn Phe Gly Phe Ile His Arg Met Thr Arg Tyr Gly Asp Arg His His
210 215 220

Val Leu Ser Val Leu Met Pro Thr Arg Pro Thr Asp Gln His Arg Ala
225 230 235 240

Leu Ile Arg His Cys Ala Gly Leu Ala Asp Ile Leu Leu Gln Arg Pro
245 250 255

Glu Ala Met Arg Asp Arg Glu Ile Glu Val Arg Ser Leu Ala Met Ser
260 265 270

Leu Leu Leu Gly Arg Ser Asp Asp Leu Ala Thr Ile His Arg Val Phe
275 280 285

Ala Asp Ile Thr Asp Ala Ser Gly Asn Ile Arg Pro Ile Leu Ile Thr
290 295 300

Gly Asn Thr Pro Gln Ser Val Arg Lys Ala Leu Ser Ser Val Ala Thr
 305 310 315 320
 Ala Leu Tyr Lys Gln Glu Arg Ala Leu Ala His Leu Arg Leu Ala Glu
 325 330 335
 Ser Thr Glu Leu Leu Phe Leu Arg Gly Ser Arg Ser Val His Asn Ile
 340 345 350
 Val Gln Leu Phe Gly Thr Ala Ala Ser Gly Val Arg Leu Cys Ile Gly
 355 360 365
 Leu Pro Thr Arg Ala Glu Asn Ile Asp Lys Lys Leu Ile Arg Glu Leu
 370 375 380
 Thr Ala Thr Ala Lys Thr Leu Gln Leu Gly Thr His Ala Glu Pro Arg
 385 390 395 400
 Asp Gly Thr Leu Leu Trp Leu Gln Asn Pro Glu Leu Arg Lys Ile Leu
 405 410 415
 Lys Ile Arg Ser Arg Asp Thr Tyr Asp Arg Leu Leu Asp His Asp Arg
 420 425 430
 Thr Asn Asn Thr Glu Leu Ala Pro Thr Leu Val Ser Phe Thr Gln His
 435 440 445
 Ser Gly His Ile Gly Asp Thr Ala Lys Glu Leu Gly Ile His Arg His
 450 455 460
 Thr Val Arg Thr Arg Met Ile Arg Ile Glu Glu Ile Cys Glu Ile Asp
 465 470 475 480
 Leu Asn Asp Pro Leu Thr Arg Ala Glu Leu Leu Leu Val Ile Ala Thr
 485 490 495
 Lys Glu Gly Asp Val Glu Lys Gln
 500

<210> 2189

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA01348

<400> 2189

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 attgactggg tatgacgcct cccagcgatt tggggcctcg gtg ggc ttt gtg tgg 115
 Val Gly Phe Val Trp
 1 5

 agt ggt tcc gat tcg cag att tat ccc gaa ctt cga aaa atg gaa gcc 163
 Ser Gly Ser Asp Ser Gln Ile Tyr Pro Glu Leu Arg Lys Met Glu Ala
 10 15 20

gaa gaa ctc ctc gtg gga tcc gat gtt ccc tgg ggc tcc aaa ggc gcc 211
 Glu Glu Leu Leu Val Gly Ser Asp Val Pro Trp Gly Ser Lys Gly Ala
 25 30 35

acc aaa acc gaa tac gcc ttg agt gaa aaa ggc tgg gaa gcg cta aga 259
 Thr Lys Thr Glu Tyr Ala Leu Ser Glu Lys Gly Trp Glu Ala Leu Arg
 40 45 50

aaa gcg tgg tac gag cca gta acc tac ggt ccc acc aga gat cct gcc 307
 Lys Ala Trp Tyr Glu Pro Val Thr Tyr Gly Pro Thr Arg Asp Pro Ala
 55 60 65

agg ctt aaa gcc gcc tat ttt gag gtc ggt aca aat ggc gat gca cgc 355
 Arg Leu Lys Ala Ala Tyr Phe Glu Val Gly Thr Asn Gly Asp Ala Arg
 70 75 80 85

cga cat tta agg gcg cac atc gct cat ttt gaa cag cag aaa att caa 403
 Arg His Leu Arg Ala His Ile Ala His Phe Glu Gln Gln Lys Ile Gln
 90 95 100

tca gaa tca atg att gat gag ctg aaa gca aaa act cat cca acc ttg 451
 Ser Glu Ser Met Ile Asp Glu Leu Lys Ala Lys Thr His Pro Thr Leu
 105 110 115

gca cgg cga ctt gag cgc tcc ccg aaa aag gag cac gag cga ata gtc 499
 Ala Arg Arg Leu Glu Arg Ser Pro Lys Lys Glu His Glu Arg Ile Val
 120 125 130

gcg ttt aaa gtg ctt gcc tat gag ggg cag att gca cgc gct cag gca 547
 Ala Phe Lys Val Leu Ala Tyr Glu Gly Gln Ile Ala Arg Ala Gln Ala
 135 140 145

gag att gaa tgg gcg gaa aag ggc ttg aaa cta ctc gat acc ctt 592
 Glu Ile Glu Trp Ala Glu Lys Gly Leu Lys Leu Leu Asp Thr Leu
 150 155 160

tagttttcga acacgtccgt atc 615

<210> 2190

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 2190

Val Gly Phe Val Trp Ser Gly Ser Asp Ser Gln Ile Tyr Pro Glu Leu
 1 5 10 15

Arg Lys Met Glu Ala Glu Glu Leu Leu Val Gly Ser Asp Val Pro Trp
 20 25 30

Gly Ser Lys Gly Ala Thr Lys Thr Glu Tyr Ala Leu Ser Glu Lys Gly
 35 40 45

Trp Glu Ala Leu Arg Lys Ala Trp Tyr Glu Pro Val Thr Tyr Gly Pro
 50 55 60

Thr Arg Asp Pro Ala Arg Leu Lys Ala Ala Tyr Phe Glu Val Gly Thr
 65 70 75 80

Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr Thr Cys Ile Thr Lys
 105 110 115
 cac cca gaa gca gtg cgc ctg cta ttg atg gaa aac ctg cat agc caa 499
 His Pro Glu Ala Val Arg Leu Leu Leu Met Glu Asn Leu His Ser Gln
 120 125 130
 gac agc gtg gat tcc acc gcg gca tat tcc gat gaa tcc aat gtg ctg 547
 Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp Glu Ser Asn Val Leu
 135 140 145
 ctc aac ctg gat aag ctg ctc atg ctt ggc cag gat gcc gcc gcc ttc 595
 Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln Asp Ala Gly Ala Phe
 150 155 160 165
 cgt cct gga atc tcc gca gaa gac gta ctg gtt ctt att agc tcc ctg 643
 Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val Leu Ile Ser Ser Leu
 170 175 180
 gcc tac ttc cgc gta tcc aac aag gtc acg ttg aag aac ctc tac tcc 691
 Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu Lys Asn Leu Tyr Ser
 185 190 195
 ctt gat ttg gaa tca gag gcc aat att gaa ggc atg aag cgc atc gtc 739
 Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly Met Lys Arg Ile Val
 200 205 210
 gtt gac acg gtg ctg gca ttc ttg acc tca aat att caa aat tct ggc 787
 Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn Ile Gln Asn Ser Gly
 215 220 225
 aac tcc agc tac ctg gtt gtt ggt ggc aag act gca gaa cca gaa act 835
 Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr Ala Glu Pro Glu Thr
 230 235 240 245
 gat gac agc gtc tac agc ttt gat acg gac gtg ttc gaa aac 877
 Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val Phe Glu Asn
 250 255
 taaagggtat cgagtagttt caa 900

<210> 2192

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 2192

Met Ala Thr Ser Arg Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser
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Glu Phe Ile Glu Ser Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val
 20 25 30

Val Ala Thr Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr
 35 40 45

Lys Leu Glu Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile
 50 55 60

His Tyr His Phe Gly Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser

65	70	75	80
Tyr Ala Leu Arg Leu Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp	85	90	95
Ser Ala Val Pro Val Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr	100	105	110
Thr Cys Ile Thr Lys His Pro Glu Ala Val Arg Leu Leu Leu Met Glu	115	120	125
Asn Leu His Ser Gln Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp	130	135	140
Glu Ser Asn Val Leu Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln	145	150	155
Asp Ala Gly Ala Phe Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val	165	170	175
Leu Ile Ser Ser Leu Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu	180	185	190
Lys Asn Leu Tyr Ser Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly	195	200	205
Met Lys Arg Ile Val Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn	210	215	220
Ile Gln Asn Ser Gly Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr	225	230	235
Ala Glu Pro Glu Thr Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val	245	250	255
Phe Glu Asn			

<210> 2193
 <211> 426
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(403)
 <223> RXA01357

<400> 2193
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 ggctacacgc tgcagataat gacacgacgg aaggtggagc atg agc gct gaa gaa 115
 Met Ser Ala Glu Glu
 1 5
 ctc gac aac tac gaa gca gag gtt gaa ctc tct ctt tac cgc gaa tac 163
 Leu Asp Asn Tyr Glu Ala Glu Val Glu Leu Ser Leu Tyr Arg Glu Tyr
 10 15 20
 cgc gac gta gtc agc cag ttt tcc tat gtt gta gaa act gaa cgt cgc 211

Arg Asp Val Val Ser Gln Phe Ser Tyr Val Val Glu Thr Glu Arg Arg
 25 30 35

ttc tac tta gca aat gca gtg cag ctt att cca cac aac agc gga aac 259
 Phe Tyr Leu Ala Asn Ala Val Gln Leu Ile Pro His Asn Ser Gly Asn
 40 45 50

gat gtc tac tac gaa gtc cgc atg tct gac gcc tgg gta tgg gac atg 307
 Asp Val Tyr Tyr Glu Val Arg Met Ser Asp Ala Trp Val Trp Asp Met
 55 60 65

tac cgc tca gca cgc ttc gtt cgc tac gtc cga gtg atc acc tac aag 355
 Tyr Arg Ser Ala Arg Phe Val Arg Tyr Val Arg Val Ile Thr Tyr Lys
 70 75 80 85

gac gtc aac atc gaa gaa tta gat aag cct gac atc atc atg cct gag 403
 Asp Val Asn Ile Glu Glu Leu Asp Lys Pro Asp Ile Ile Met Pro Glu
 90 95 100

tagttcttag gtttaaaatc gct 426

<210> 2194
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2194
 Met Ser Ala Glu Glu Leu Asp Asn Tyr Glu Ala Glu Val Glu Leu Ser
 1 5 10 15

Leu Tyr Arg Glu Tyr Arg Asp Val Val Ser Gln Phe Ser Tyr Val Val
 20 25 30

Glu Thr Glu Arg Arg Phe Tyr Leu Ala Asn Ala Val Gln Leu Ile Pro
 35 40 45

His Asn Ser Gly Asn Asp Val Tyr Tyr Glu Val Arg Met Ser Asp Ala
 50 55 60

Trp Val Trp Asp Met Tyr Arg Ser Ala Arg Phe Val Arg Tyr Val Arg
 65 70 75 80

Val Ile Thr Tyr Lys Asp Val Asn Ile Glu Glu Leu Asp Lys Pro Asp
 85 90 95

Ile Ile Met Pro Glu
 100

<210> 2195
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1282)
 <223> RXA01359

<400> 2195

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ccatggagct	tcggggcact	acatacagtg	aggtagcagc	atg	att	gac	tcc	cgc	115							
				Met	Ile	Asp	Ser	Arg	5							
ttg	ctg	gca	tgg	gcg	tat	ctc	tca	aaa	gtg	gtg	gag	ggt	ccc	aat	gca	163
Leu	Leu	Ala	Trp	Ala	Tyr	Leu	Ser	Lys	Val	Val	Glu	Gly	Pro	Asn	Ala	20
				10					15							
cac	ctg	caa	aag	ctc	ctg	aaa	gaa	ggt	cat	gat	gta	gag	cgg	atc	gca	211
His	Leu	Gln	Lys	Leu	Leu	Lys	Glu	Gly	His	Asp	Val	Glu	Arg	Ile	Ala	35
			25					30								
ttt	ggt	att	aaa	cac	cgc	gaa	gag	tgg	att	ggc	gaa	ggt	ctg	ctg	aaa	259
Phe	Gly	Ile	Lys	His	Arg	Glu	Glu	Trp	Ile	Gly	Glu	Gly	Leu	Leu	Lys	50
		40					45					50				
aac	acc	gat	tcc	cgg	tac	tcg	att	gat	acc	gcg	caa	act	gat	ctg	gaa	307
Asn	Thr	Asp	Ser	Arg	Tyr	Ser	Ile	Asp	Thr	Ala	Gln	Thr	Asp	Leu	Glu	65
	55					60										
act	atc	gcc	aaa	ctc	ggt	ggg	cgg	ctc	atc	aca	cct	gaa	gac	gac	gaa	355
Thr	Ile	Ala	Lys	Leu	Gly	Gly	Arg	Leu	Ile	Thr	Pro	Glu	Asp	Asp	Glu	85
	70				75					80						
tgg	ccg	atg	gaa	gaa	tta	gac	cat	gct	ttt	gga	ttt	gcc	gct	tct	ggc	403
Trp	Pro	Met	Glu	Glu	Leu	Asp	His	Ala	Phe	Gly	Phe	Ala	Ala	Ser	Gly	90
				90					95					100		
atg	agt	gat	cat	gtg	cgt	acc	tat	caa	gat	gat	gcg	ctg	cca	ccg	cat	451
Met	Ser	Asp	His	Val	Arg	Thr	Tyr	Gln	Asp	Asp	Ala	Leu	Pro	Pro	His	105
			105					110					115			
gcg	ttg	tgg	att	agg	gga	gga	aat	ctc	aga	aca	ctc	agt	gca	cag	tcc	499
Ala	Leu	Trp	Ile	Arg	Gly	Gly	Asn	Leu	Arg	Thr	Leu	Ser	Ala	Gln	Ser	120
		120					125					130				
gtc	aca	ctc	gtg	ggc	acc	agg	gca	ata	agc	caa	tat	ggc	acg	gaa	gta	547
Val	Thr	Leu	Val	Gly	Thr	Arg	Ala	Ile	Ser	Gln	Tyr	Gly	Thr	Glu	Val	135
						140					145					
act	cgg	gaa	ttc	acc	caa	aac	ctt	gtg	tct	cat	cag	tgg	aca	atc	atc	595
Thr	Arg	Glu	Phe	Thr	Gln	Asn	Leu	Val	Ser	His	Gln	Trp	Thr	Ile	Ile	150
					155					160					165	
tca	ggt	ggt	gcc	ttg	gga	gtt	gat	agc	gtc	gcc	cat	agt	gaa	gcc	gta	643
Ser	Gly	Gly	Ala	Leu	Gly	Val	Asp	Ser	Val	Ala	His	Ser	Glu	Ala	Val	170
				170					175					180		
cgt	gca	caa	ggc	tcc	acc	atc	gcg	atc	gca	gca	tgc	gga	ttg	gat	cgc	691
Arg	Ala	Gln	Gly	Ser	Thr	Ile	Ala	Ile	Ala	Ala	Cys	Gly	Leu	Asp	Arg	185
			185					190					195			
tcg	tac	ccc	agc	cac	aat	cga	gat	ctg	ttc	aac	cag					

cgc cac cgc ttt ctc act cgc aat cgt ctc gtt gct gct cta tct caa 835
 Arg His Arg Phe Leu Thr Arg Asn Arg Leu Val Ala Ala Leu Ser Gln
 230 235 240 245

gga act gtc gtg gtg gag gca gcc tgg agg tca ggc gcg cta aac act 883
 Gly Thr Val Val Val Glu Ala Ala Trp Arg Ser Gly Ala Leu Asn Thr
 250 255 260

ttg agc tgg tgt gct ggt tta ggc agg att gct atg gcg gtc cct ggg 931
 Leu Ser Trp Cys Ala Gly Leu Gly Arg Ile Ala Met Ala Val Pro Gly
 265 270 275

ccg gta aat act gct gga tca ctt ggg tgc cac gaa agg att cga aac 979
 Pro Val Asn Thr Ala Gly Ser Leu Gly Cys His Glu Arg Ile Arg Asn
 280 285 290

ggc agc gca caa atg gtc acc agt gcg gat gac gtt cgg tca ctt ctg 1027
 Gly Ser Ala Gln Met Val Thr Ser Ala Asp Asp Val Arg Ser Leu Leu
 295 300 305

ggt gca gtg ggt gca atg gat agc caa act cag tat gaa tta aac ttc 1075
 Gly Ala Val Gly Ala Met Asp Ser Gln Thr Gln Tyr Glu Leu Asn Phe
 310 315 320 325

gcg gcc act cca gta cag ggt tta acc aga aat gag ctg cga gtt ttt 1123
 Ala Ala Thr Pro Val Gln Gly Leu Thr Arg Asn Glu Leu Arg Val Phe
 330 335 340

gat gcg tta gac gac cga gga gag ggg agg gaa gcg gcg agt atc gct 1171
 Asp Ala Leu Asp Asp Arg Gly Glu Gly Arg Glu Ala Ala Ser Ile Ala
 345 350 355

acc gaa gcc ggg ttg acc ttg cag tta aca att ttc ctt ctc att gca 1219
 Thr Glu Ala Gly Leu Thr Leu Gln Leu Thr Ile Phe Leu Leu Ile Ala
 360 365 370

ttg aac aag cgc gga atc gtg aaa cgc gac gga act gct tgg tcg aga 1267
 Leu Asn Lys Arg Gly Ile Val Lys Arg Asp Gly Thr Ala Trp Ser Arg
 375 380 385

aat gcg gaa atg cca taaaacctgg gggttatata aaa 1305
 Asn Ala Glu Met Pro
 390

<210> 2196

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 2196

Met Ile Asp Ser Arg Leu Leu Ala Trp Ala Tyr Leu Ser Lys Val Val
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Glu Gly Pro Asn Ala His Leu Gln Lys Leu Leu Lys Glu Gly His Asp
 20 25 30

Val Glu Arg Ile Ala Phe Gly Ile Lys His Arg Glu Glu Trp Ile Gly
 35 40 45

Glu Gly Leu Leu Lys Asn Thr Asp Ser Arg Tyr Ser Ile Asp Thr Ala
50 55 60

Gln Thr Asp Leu Glu Thr Ile Ala Lys Leu Gly Gly Arg Leu Ile Thr
65 70 75 80

Pro Glu Asp Asp Glu Trp Pro Met Glu Glu Leu Asp His Ala Phe Gly
85 90 95

Phe Ala Ala Ser Gly Met Ser Asp His Val Arg Thr Tyr Gln Asp Asp
100 105 110

Ala Leu Pro Pro His Ala Leu Trp Ile Arg Gly Gly Asn Leu Arg Thr
115 120 125

Leu Ser Ala Gln Ser Val Thr Leu Val Gly Thr Arg Ala Ile Ser Gln
130 135 140

Tyr Gly Thr Glu Val Thr Arg Glu Phe Thr Gln Asn Leu Val Ser His
145 150 155 160

Gln Trp Thr Ile Ile Ser Gly Gly Ala Leu Gly Val Asp Ser Val Ala
165 170 175

His Ser Glu Ala Val Arg Ala Gln Gly Ser Thr Ile Ala Ile Ala Ala
180 185 190

Cys Gly Leu Asp Arg Ser Tyr Pro Ser His Asn Arg Asp Leu Phe Asn
195 200 205

Gln Ile Ala Lys Ser Gly Lys Gly Ala Leu Val Ser Glu Tyr Pro Pro
210 215 220

Gly Thr Pro Pro Gln Arg His Arg Phe Leu Thr Arg Asn Arg Leu Val
225 230 235 240

Ala Ala Leu Ser Gln Gly Thr Val Val Val Glu Ala Ala Trp Arg Ser
245 250 255

Gly Ala Leu Asn Thr Leu Ser Trp Cys Ala Gly Leu Gly Arg Ile Ala
260 265 270

Met Ala Val Pro Gly Pro Val Asn Thr Ala Gly Ser Leu Gly Cys His
275 280 285

Glu Arg Ile Arg Asn Gly Ser Ala Gln Met Val Thr Ser Ala Asp Asp
290 295 300

Val Arg Ser Leu Leu Gly Ala Val Gly Ala Met Asp Ser Gln Thr Gln
305 310 315 320

Tyr Glu Leu Asn Phe Ala Ala Thr Pro Val Gln Gly Leu Thr Arg Asn
325 330 335

Glu Leu Arg Val Phe Asp Ala Leu Asp Asp Arg Gly Glu Gly Arg Glu
340 345 350

Ala Ala Ser Ile Ala Thr Glu Ala Gly Leu Thr Leu Gln Leu Thr Ile
355 360 365

Phe Leu Leu Ile Ala Leu Asn Lys Arg Gly Ile Val Lys Arg Asp Gly

370

375

380

Thr Ala Trp Ser Arg Asn Ala Glu Met Pro
385 390

<210> 2197

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01366

<400> 2197

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gactgtccaa acctaaacca aaggtctaaa ctttggtctt  gtg agt cag ttt cgt  115
                                         Val Ser Gln Phe Arg
                                         1 5
cgt tgt tcc cgc cct ggt tgt ggc aag cct gcc gtc gca acc ctc acc  163
Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala Val Ala Thr Leu Thr
              10              15              20
tac gca tat tcg gat tcc act gcg gtg gtt ggt cct ttg gcg cct gca  211
Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly Pro Leu Ala Pro Ala
              25              30              35
gca gag ccc cat agt tgg gat ctg tgt gag cat cat gcc gag cgt att  259
Ala Glu Pro His Ser Trp Asp Leu Cys Glu His His Ala Glu Arg Ile
              40              45              50
act gcg ccc ctt ggt tgg gag atg ctg cgg gtg aac gac atc aaa gtc  307
Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val Asn Asp Ile Lys Val
              55              60              65
gat gac gat gag gat ctg acg gct ctt gct cag gct gtt cgt gag gct  355
Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln Ala Val Arg Glu Ala
              70              75              80              85
gga cgc act gtg agt ggt ctg gtt cct gaa gac gaa gtg ggc ggc aac  403
Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp Glu Val Gly Gly Asn
              90              95              100
cat ccg gtg aac cgg agt gcg cgg atc gcg gaa cag aag gtt cac cgc  451
His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu Gln Lys Val His Arg
              105              110              115
agg ggt cat ctc tat gtt gtg cct gat cag gac gaa tca taaggtttgc  500
Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp Glu Ser
              120              125              130
tattcggatt gga 513

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<210> 2198

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 2198

Val Ser Gln Phe Arg Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala
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Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly
 20 25 30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
 35 40 45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
 50 55 60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
 65 70 75 80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
 85 90 95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
 100 105 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
 115 120 125

Glu Ser
 130

<210> 2199

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA01367

<400> 2199

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tttccgcaat cggcacggac gcggtctccg cggcccactc atg ccc gtc gaa gtt 115
 Met Pro Val Glu Val
 1 5

ccc cgc cac gcc tct aga cgc caa gcc ttc gac cgc gca gtc tta gag 163
 Pro Arg His Ala Ser Arg Arg Gln Ala Phe Asp Arg Ala Val Leu Glu
 10 15 20

gcc tac tcc cct ctt tac ggg att tac caa aaa gag ctc agc aat cta 211
 Ala Tyr Ser Pro Leu Tyr Gly Ile Tyr Gln Lys Glu Leu Ser Asn Leu
 25 30 35

gac atc gct gtc gat acc gtt cct cgc atg cga ctc agc gcc gac ctt 259
 Asp Ile Ala Val Asp Thr Val Pro Arg Met Arg Leu Ser Ala Asp Leu
 40 45 50

gcc att ctc ccc gat gaa atc acc gcc gac ggc ccc gtt cca ctt ggt 307

Ala Ile Leu Pro Asp Glu Ile Thr Ala Asp Gly Pro Val Pro Leu Gly
 55 60 65

cgc gtc atc cca ccg gcg atc gat acc aag gga aac ccc acg aga gcg 355
 Arg Val Ile Pro Pro Ala Ile Asp Thr Lys Gly Asn Pro Thr Arg Ala
 70 75 80 85

cgc atc gtt att ttc aga atg ccg atc gag caa cga gtc acc aac gct 403
 Arg Ile Val Ile Phe Arg Met Pro Ile Glu Gln Arg Val Thr Asn Ala
 90 95 100

gtg gaa cgc cac gag cta ttg act cat gtt ctc acc tct ttg gtg gcg 451
 Val Glu Arg His Glu Leu Leu Thr His Val Leu Thr Ser Leu Val Ala
 105 110 115

aac tat ctg aat att gat cca cga gac atc gat ccg gga ttc cag gat 499
 Asn Tyr Leu Asn Ile Asp Pro Arg Asp Ile Asp Pro Gly Phe Gln Asp
 120 125 130

ctc tagcgtggcc ggtgcacccat ggg 525
 Leu

<210> 2200

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 2200

Met Pro Val Glu Val Pro Arg His Ala Ser Arg Arg Gln Ala Phe Asp
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Arg Ala Val Leu Glu Ala Tyr Ser Pro Leu Tyr Gly Ile Tyr Gln Lys
 20 25 30

Glu Leu Ser Asn Leu Asp Ile Ala Val Asp Thr Val Pro Arg Met Arg
 35 40 45

Leu Ser Ala Asp Leu Ala Ile Leu Pro Asp Glu Ile Thr Ala Asp Gly
 50 55 60

Pro Val Pro Leu Gly Arg Val Ile Pro Pro Ala Ile Asp Thr Lys Gly
 65 70 75 80

Asn Pro Thr Arg Ala Arg Ile Val Ile Phe Arg Met Pro Ile Glu Gln
 85 90 95

Arg Val Thr Asn Ala Val Glu Arg His Glu Leu Leu Thr His Val Leu
 100 105 110

Thr Ser Leu Val Ala Asn Tyr Leu Asn Ile Asp Pro Arg Asp Ile Asp
 115 120 125

Pro Gly Phe Gln Asp Leu
 130

<210> 2201

<211> 474

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(451)

<223> RXA01370

<400> 2201

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atcgtgtctc tattacgcgg actagaaagg ttttagggac atg ggt gca tgg gac 115
Met Gly Ala Trp Asp
1 5
gat gca atc ttg act gag gaa gtc aac gtt gat ttt ctc gac gag atc 163
Asp Ala Ile Leu Thr Glu Glu Val Asn Val Asp Phe Leu Asp Glu Ile
10 15 20
tca gaa tta gat act caa gac att ctt gag gcg ttg gaa gac gca tgt 211
Ser Glu Leu Asp Thr Gln Asp Ile Leu Glu Ala Leu Glu Asp Ala Cys
25 30 35
ttg ctg gtg gtt aac cag gac aac gcc act gaa gac gaa cac ctc aac 259
Leu Leu Val Val Asn Gln Asp Asn Ala Thr Glu Asp Glu His Leu Asn
40 45 50
ggt cag gcg gct gcg acg atc gcg gcc atc atg ttt ggc gct cca tat 307
Gly Gln Ala Ala Ala Thr Ile Ala Ala Ile Met Phe Gly Ala Pro Tyr
55 60 65
tct gcg ggc cag gtg ctg gag aat tac cca ttt atc cgc gaa ctc gtc 355
Ser Ala Gly Gln Val Leu Glu Asn Tyr Pro Phe Ile Arg Glu Leu Val
70 75 80 85
ggt gag ggc tct gaa gct ctt cgc ggt gct gca gcg cag gtt ttg gaa 403
Gly Glu Gly Ser Glu Ala Leu Arg Gly Ala Ala Ala Gln Val Leu Glu
90 95 100
gag gca gat gtg gaa tat gac ctc gaa gct tat tta gag gcc ctc aac 451
Glu Ala Asp Val Glu Tyr Asp Leu Glu Ala Tyr Leu Glu Ala Leu Asn
105 110 115
tagccctcca ctaaacagct tca 474

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<210> 2202

<211> 117

<212> PRT

<213> Corynebacterium glutamicum

<400> 2202

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Met Gly Ala Trp Asp Asp Ala Ile Leu Thr Glu Glu Val Asn Val Asp
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Phe Leu Asp Glu Ile Ser Glu Leu Asp Thr Gln Asp Ile Leu Glu Ala
20 25 30
Leu Glu Asp Ala Cys Leu Leu Val Val Asn Gln Asp Asn Ala Thr Glu
35 40 45
Asp Glu His Leu Asn Gly Gln Ala Ala Ala Thr Ile Ala Ala Ile Met

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50	55	60
Phe Gly Ala Pro Tyr Ser Ala Gly Gln Val Leu Glu Asn Tyr Pro Phe		
65	70	75
Ile Arg Glu Leu Val Gly Glu Gly Ser Glu Ala Leu Arg Gly Ala Ala		
	85	90
Ala Gln Val Leu Glu Glu Ala Asp Val Glu Tyr Asp Leu Glu Ala Tyr		
	100	105
Leu Glu Ala Leu Asn		
115		

<210> 2203

<211> 614

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(591)

<223> RXA01372

<400> 2203

cag gac acc ttc gtc ctt ccc acc ttg ccc acg gcc gca ggc ttg tcg	48
Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser	
1	5
cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa	96
Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu	
	20
gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc	144
Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys	
	35
att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc	192
Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val	
	50
aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg	240
Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val	
	65
cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc	288
His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala	
	85
cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc	336
Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro	
	100
gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc	384
Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr	
	115
gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta	432
Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val	
	130

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat 480
 Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
 145 150 155 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa 528
 Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
 165 170 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att 576
 Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
 180 185 190

gaa gaa aag gac ttg taaatggagc tattggaagg ctc 614
 Glu Glu Lys Asp Leu
 195

<210> 2204

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 2204

Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
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Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
 20 25 30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
 35 40 45

Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
 50 55 60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65 70 75 80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
 85 90 95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
 100 105 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
 115 120 125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
 130 135 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
 145 150 155 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
 165 170 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
 180 185 190

Glu Glu Lys Asp Leu

195

<210> 2205

<211> 1278

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1278)

<223> RXA01378

<400> 2205

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His	Val	Trp	Ile	Ser	Pro	Gly	Ala	Ser	Asn	Pro	Ile	Lys	Asp	Arg	Leu	
1				5					10					15		
ttc	cct	tgg	aca	ttg	gtg	aag	gct	ttt	ctc	tcc	tcc	cct	gca	gcc	ttg	96
Phe	Pro	Trp	Thr	Leu	Val	Lys	Ala	Phe	Leu	Ser	Ser	Pro	Ala	Ala	Leu	
			20					25					30			
ggc	gaa	aca	gtg	tcc	aat	cgc	ctc	aaa	aag	gcc	tct	gca	cca	gaa	gaa	144
Gly	Glu	Thr	Val	Ser	Asn	Arg	Leu	Lys	Lys	Ala	Ser	Ala	Pro	Glu	Glu	
		35					40					45				
aaa	cgc	gcc	cta	gaa	acc	ctt	tca	caa	ctt	aat	tct	gcg	atc	acc	ccg	192
Lys	Arg	Ala	Leu	Glu	Thr	Leu	Ser	Gln	Leu	Asn	Ser	Ala	Ile	Thr	Pro	
	50					55					60					
cag	acc	tca	cag	aag	tac	caa	tct	cta	ctg	agc	tac	ctc	ggg	gac	atc	240
Gln	Thr	Ser	Gln	Lys	Tyr	Gln	Ser	Leu	Leu	Ser	Tyr	Leu	Gly	Asp	Ile	
65					70					75					80	
gga	gtg	aag	aag	aac	tcc	gat	acc	cgc	gtg	gtg	att	ttc	tct	gag	cgt	288
Gly	Val	Lys	Lys	Asn	Ser	Asp	Thr	Arg	Val	Val	Ile	Phe	Ser	Glu	Arg	
				85					90					95		
gtc	gct	act	ttg	cac	tgg	ctg	cag	gaa	aac	ctc	atc	cgt	gat	ctc	aag	336
Val	Ala	Thr	Leu	His	Trp	Leu	Gln	Glu	Asn	Leu	Ile	Arg	Asp	Leu	Lys	
			100					105					110			
atg	cca	ccc	aac	tct	att	gct	gtt	atg	cac	ggc	ggg	ctc	ccc	gac	cag	384
Met	Pro	Pro	Asn	Ser	Ile	Ala	Val	Met	His	Gly	Gly	Leu	Pro	Asp	Gln	
		115					120					125				
gag	caa	atg	cgc	ctg	gtg	gat	gag	ttt	aaa	aag	acg	gat	tct	ccc	atc	432
Glu	Gln	Met	Arg	Leu	Val	Asp	Glu	Phe	Lys	Lys	Thr	Asp	Ser	Pro	Ile	
	130					135						140				
cgc	atc	atg	atc	acc	ggc	gat	gtt	gcc	tca	gaa	ggg	gtg	aac	ctg	cat	480
Arg	Ile	Met	Ile	Thr	Gly	Asp	Val	Ala	Ser	Glu	Gly	Val	Asn	Leu	His	
145					150					155				160		
act	ctc	tgc	cac	aac	ttg	gtg	cac	tat	gac	atc	ccg	tgg	tca	ctg	atc	528
Thr	Leu	Cys	His	Asn	Leu	Val	His	Tyr	Asp	Ile	Pro	Trp	Ser	Leu	Ile	
				165					170					175		
cgc	att	cag	cag	cgc	aat	ggc	cgt	att	gat	cgt	tat	ggg	caa	acc	cac	576
Arg	Ile	Gln	Gln	Arg	Asn	Gly	Arg	Ile	Asp	Arg	Tyr	Gly	Gln	Thr	His	
		180					185						190			

aac cct tcc atc gtt acc ttc ttg ctc gat ccc gcc gag gat tcc aaa	624
Asn Pro Ser Ile Val Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys	
195 200 205	
gta ggt gaa gtc cat gtg ctg gag agg ctc atg gag cgc gaa cat gag	672
Val Gly Glu Val His Val Leu Glu Arg Leu Met Glu Arg Glu His Glu	
210 215 220	
gcg cac tct ttg ctc ggt gat gcc gca tct ctc atg ggc aag cac tct	720
Ala His Ser Leu Leu Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser	
225 230 235 240	
gag cgt ttg gaa gaa gaa acc atc cgc gaa gtc ctg cgc ggt gcc caa	768
Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln	
245 250 255	
aac ttt aat gat gca gtg gct gat cca gcg gaa gtc cta gaa aac cca	816
Asn Phe Asn Asp Ala Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro	
260 265 270	
gca ggc cta gat gat att gat tgg ttg cta gcc caa atc gcc caa gcc	864
Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala	
275 280 285	
gat gcc aag gca gaa aca gaa gca gaa gca gaa aca gaa aac caa aca	912
Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr	
290 295 300	
gca cca gat gca gct tcc aat agc acg cag cat gca caa cgc cgg ttg	960
Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu	
305 310 315 320	
tat gca cag gaa agc tct ttc ctc tat gac tgc ctc ctc gaa ggt ttc	1008
Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe	
325 330 335	
aat aac gta ccg gag gat tcc atc aac cgc ggt ggc gtg ggg ttc aaa	1056
Asn Asn Val Pro Glu Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys	
340 345 350	
aaa cac gat aat gac atc gtg gag ctc acc ccc acc gat gat ctg cgc	1104
Lys His Asp Asn Asp Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg	
355 360 365	
cgt cgt cta gat ttc ctc ccg cag gat tat gtg gct gct cgg aaa gtt	1152
Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val	
370 375 380	
aag gaa gat ctc cta cta gct tcc aca ctg atg cgt ggc caa gaa cgc	1200
Lys Glu Asp Leu Leu Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg	
385 390 395 400	
ctc aac gct gcg cgc act ggt gaa gat ggc agt acc tgg cca agt gcc	1248
Leu Asn Ala Ala Arg Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala	
405 410 415	
cac tat cta ggc ccc ctg cac cca gtc act	1278
His Tyr Leu Gly Pro Leu His Pro Val Thr	
420 425	

<210> 2206

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 2206

His Val Trp Ile Ser Pro Gly Ala Ser Asn Pro Ile Lys Asp Arg Leu
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Phe Pro Trp Thr Leu Val Lys Ala Phe Leu Ser Ser Pro Ala Ala Leu
20 25 30
Gly Glu Thr Val Ser Asn Arg Leu Lys Lys Ala Ser Ala Pro Glu Glu
35 40 45
Lys Arg Ala Leu Glu Thr Leu Ser Gln Leu Asn Ser Ala Ile Thr Pro
50 55 60
Gln Thr Ser Gln Lys Tyr Gln Ser Leu Leu Ser Tyr Leu Gly Asp Ile
65 70 75 80
Gly Val Lys Lys Asn Ser Asp Thr Arg Val Val Ile Phe Ser Glu Arg
85 90 95
Val Ala Thr Leu His Trp Leu Gln Glu Asn Leu Ile Arg Asp Leu Lys
100 105 110
Met Pro Pro Asn Ser Ile Ala Val Met His Gly Gly Leu Pro Asp Gln
115 120 125
Glu Gln Met Arg Leu Val Asp Glu Phe Lys Lys Thr Asp Ser Pro Ile
130 135 140
Arg Ile Met Ile Thr Gly Asp Val Ala Ser Glu Gly Val Asn Leu His
145 150 155 160
Thr Leu Cys His Asn Leu Val His Tyr Asp Ile Pro Trp Ser Leu Ile
165 170 175
Arg Ile Gln Gln Arg Asn Gly Arg Ile Asp Arg Tyr Gly Gln Thr His
180 185 190
Asn Pro Ser Ile Val Thr Phe Leu Leu Asp Pro Ala Glu Asp Ser Lys
195 200 205
Val Gly Glu Val His Val Leu Glu Arg Leu Met Glu Arg Glu His Glu
210 215 220
Ala His Ser Leu Leu Gly Asp Ala Ala Ser Leu Met Gly Lys His Ser
225 230 235 240
Glu Arg Leu Glu Glu Glu Thr Ile Arg Glu Val Leu Arg Gly Ala Gln
245 250 255
Asn Phe Asn Asp Ala Val Ala Asp Pro Ala Glu Val Leu Glu Asn Pro
260 265 270
Ala Gly Leu Asp Asp Ile Asp Trp Leu Leu Ala Gln Ile Ala Gln Ala
275 280 285

Asp Ala Lys Ala Glu Thr Glu Ala Glu Ala Glu Thr Glu Asn Gln Thr
 290 295 300
 Ala Pro Asp Ala Ala Ser Asn Ser Thr Gln His Ala Gln Arg Arg Leu
 305 310 315 320
 Tyr Ala Gln Glu Ser Ser Phe Leu Tyr Asp Cys Leu Leu Glu Gly Phe
 325 330 335
 Asn Asn Val Pro Glu Asp Ser Ile Asn Arg Gly Gly Val Gly Phe Lys
 340 345 350
 Lys His Asp Asn Asp Ile Val Glu Leu Thr Pro Thr Asp Asp Leu Arg
 355 360 365
 Arg Arg Leu Asp Phe Leu Pro Gln Asp Tyr Val Ala Ala Arg Lys Val
 370 375 380
 Lys Glu Asp Leu Leu Leu Ala Ser Thr Leu Met Arg Gly Gln Glu Arg
 385 390 395 400
 Leu Asn Ala Ala Arg Thr Gly Glu Asp Gly Ser Thr Trp Pro Ser Ala
 405 410 415
 His Tyr Leu Gly Pro Leu His Pro Val Thr
 420 425

<210> 2207

<211> 2039

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2016)

<223> RXA01380

<400> 2207

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Ser Leu Ile Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr	
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ctg ccg ttc aaa aaa cgg cgc aag acg aag gcc gat atc gct agg gag	96
Leu Pro Phe Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu	
20 25 30	
gcg ggc ctg gag ggg ctc gtc gat aag ctt atc gac gcc ccg tcc ctc	144
Ala Gly Leu Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu	
35 40 45	
gac gcc gca gcg cag gca gct gca ttt acg act gag ggc ttt gag gat	192
Asp Ala Ala Ala Gln Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp	
50 55 60	
tcc aaa aaa gtt ttg gat ggc gct cgc gcc att ttg att gac cgc ttc	240
Ser Lys Lys Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe	
65 70 75 80	
gcg ctc gat gcc gat ttg gtg ggc gag gtg cgt gag caa atg tat cgc	288
Ala Leu Asp Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg	

85										90					95					
gcg ggt tcc atg gcg gca tcg gtg gtg gcg ggc aag gag cag gaa ggc	336																			
Ala Gly Ser Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly																				
100 105 110																				
gca aag ttc aag gac tac ttt gag ttt tcc gaa cct ttt gac aag ctt	384																			
Ala Lys Phe Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu																				
115 120 125																				
cca tct cac cga att ttg gcg ctg ctg cgc ggt gaa aac gaa ggt gtg	432																			
Pro Ser His Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val																				
130 135 140																				
ctg agc ctc aac ctc gat gcg ggc gac gac ata atc tac gaa ggt ttg	480																			
Leu Ser Leu Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu																				
145 150 155 160																				
atc gcc gac cga ttc tcc ctg gac acc cac act tct agc tgg ctg gct	528																			
Ile Ala Asp Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala																				
165 170 175																				
gag gct gtg cgc tgg ggt tgg cgc acc aaa ctg tat gtg tcc tcc gga	576																			
Glu Ala Val Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly																				
180 185 190																				
ttg gat gtg cgc atg cgt ctg aaa gaa aaa gca gag gaa ggc gca ctc	624																			
Leu Asp Val Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu																				
195 200 205																				
gat gtg ttt gcc acc aac ctc cgc gac gtt ctc ctt gca gct ccc gct	672																			
Asp Val Phe Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala																				
210 215 220																				
ggt cag cgc tcc aca att ggc ctt gac ccg gga ttc cgc aac ggt gtg	720																			
Gly Gln Arg Ser Thr Ile Gly Leu Asp Pro Gly Phe Arg Asn Gly Val																				
225 230 235 240																				
aaa gta gct gtc gtg gat tcc acc ggt aag gat gtt gcc acc acg atc	768																			
Lys Val Ala Val Val Asp Ser Thr Gly Lys Asp Val Ala Thr Thr Ile																				
245 250 255																				
gtc tac cca cac cag ccc caa aac cgc tgg aag gaa gcc gta tcc gaa	816																			
Val Tyr Pro His Gln Pro Gln Asn Arg Trp Lys Glu Ala Val Ser Glu																				
260 265 270																				
ctg gct aac ctg tgc gcg acc cac ggt gtg gaa ctc atg gcg atc ggc	864																			
Leu Ala Asn Leu Cys Ala Thr His Gly Val Glu Leu Met Ala Ile Gly																				
275 280 285																				
aac gga acc gcc tcg agg gaa acg gaa aaa ctc gcc ggc gaa gta gct	912																			
Asn Gly Thr Ala Ser Arg Glu Thr Glu Lys Leu Ala Gly Glu Val Ala																				
290 295 300																				
gac atg atc aaa gcc gca ggt ggc acg cga cca acc ccc gtg gtg gtc	960																			
Asp Met Ile Lys Ala Ala Gly Gly Thr Arg Pro Thr Pro Val Val Val																				
305 310 315 320																				
tcc gaa tcg ggc gca tcc gtg tac tcg gca tca ccg atc gca gcc gaa	1008																			
Ser Glu Ser Gly Ala Ser Val Tyr Ser Ala Ser Pro Ile Ala Ala Glu																				
325 330 335																				

gaa ttc ccc gac atg gac gtc tcc ctc cgc ggt gca gtt tct atc gcg Glu Phe Pro Asp Met Asp Val Ser Leu Arg Gly Ala Val Ser Ile Ala 340 345 350	1056
agg cga ctc cag gat cca ctg gcg gag ctc gtc aag att gag ccc aaa Arg Arg Leu Gln Asp Pro Leu Ala Glu Leu Val Lys Ile Glu Pro Lys 355 360 365	1104
gcc atc gga gtc ggc cag tac caa cac gat gtc aac cag gtt gca ctt Ala Ile Gly Val Gly Gln Tyr Gln His Asp Val Asn Gln Val Ala Leu 370 375 380	1152
gcc aaa acc ctt gat ggt gtc gtc gaa gac gca gta aac gca gtc gga Ala Lys Thr Leu Asp Gly Val Val Glu Asp Ala Val Asn Ala Val Gly 385 390 395 400	1200
gtt aac ctc aac acc gca tcc gca cca ctt ctt acc cga gtt gcc gga Val Asn Leu Asn Thr Ala Ser Ala Pro Leu Leu Thr Arg Val Ala Gly 405 410 415	1248
gtg acc tcc acc ttg gca aac aat atc gtg gcc tac cgc aac gaa aac Val Thr Ser Thr Leu Ala Asn Asn Ile Val Ala Tyr Arg Asn Glu Asn 420 425 430	1296
ggt gga ttc tcc tcc cga aaa gaa ctg aac aaa gtt cct cgc ctg gga Gly Gly Phe Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly 435 440 445	1344
ccc aaa gcc ttt gaa cag tgt gct ggc ttc ctc cgc att tct gga tcc Pro Lys Ala Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser 450 455 460	1392
acc gac cct ctc gac gcc tcc gct gtt cac ccc gag gcg tac cca gtt Thr Asp Pro Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val 465 470 475 480	1440
gtt cgc aac att gcg aaa gcc aca gga ttg gat gtc tcg gga ctg atc Val Arg Asn Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile 485 490 495	1488
gga aac tct gcg gtg ctc acc aaa ttg aag ccc gct gat ttc gct gat Gly Asn Ser Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp 500 505 510	1536
gaa cga ttc ggc atc ccc acc gtc acc gac atc atc gcc gag ctg gat Glu Arg Phe Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp 515 520 525	1584
aaa ccc gga cgt gac ccc cgc cca gaa ttc aaa acc gcc agc ttc aaa Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys 530 535 540	1632
gaa ggc gtg gag aaa atc tcc gac ctc aca ccc gcc atg atc ctg gaa Glu Gly Val Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu 545 550 555 560	1680
gga act gtc acc aac gtt gcg gcg ttc ggc gca ttc gtt gac gtg gga Gly Thr Val Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly 565 570 575	1728

gtg cac cga gat ggc ctc gtt cac gtt tcc gcg atg agc gac aaa ttc 1776
Val His Arg Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe
580 585 590

atc tcc aac ccc cac gaa gtt gtt cgc tct ggt gag gtc gtg aag gta 1824
Ile Ser Asn Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val
595 600 605

aag gtc atg gaa gtt gac gtc gac cgc aaa cgc atc ggc ctt tcc ctc 1872
Lys Val Met Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu
610 615 620

cgc ttg acc gat gaa ccc ggt gcc cca gct ccg caa aag cgc gga aac 1920
Arg Leu Thr Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn
625 630 635 640

cga cca gcc aaa cag cag cga gct ccg caa aaa cag tcc gct aag ccc 1968
Arg Pro Ala Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro
645 650 655

gcc aca ggt tcc atg gca gat gct tta cga cgc gcc ggc ctc ggt gcc 2016
Ala Thr Gly Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
660 665 670

taaggcaact ttcaaacc aa gcg 2039

<210> 2208

<211> 672

<212> PRT

<213> Corynebacterium glutamicum

<400> 2208

Ser Leu Ile Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr
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Leu Pro Phe Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu
20 25 30

Ala Gly Leu Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu
35 40 45

Asp Ala Ala Ala Gln Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp
50 55 60

Ser Lys Lys Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe
65 70 75 80

Ala Leu Asp Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg
85 90 95

Ala Gly Ser Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly
100 105 110

Ala Lys Phe Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu
115 120 125

Pro Ser His Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val
130 135 140

Leu Ser Leu Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu

145	150	155	160
Ile Ala Asp Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala	165	170	175
Glu Ala Val Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly	180	185	190
Leu Asp Val Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu	195	200	205
Asp Val Phe Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala	210	215	220
Gly Gln Arg Ser Thr Ile Gly Leu Asp Pro Gly Phe Arg Asn Gly Val	225	230	235
Lys Val Ala Val Val Asp Ser Thr Gly Lys Asp Val Ala Thr Thr Ile	245	250	255
Val Tyr Pro His Gln Pro Gln Asn Arg Trp Lys Glu Ala Val Ser Glu	260	265	270
Leu Ala Asn Leu Cys Ala Thr His Gly Val Glu Leu Met Ala Ile Gly	275	280	285
Asn Gly Thr Ala Ser Arg Glu Thr Glu Lys Leu Ala Gly Glu Val Ala	290	295	300
Asp Met Ile Lys Ala Ala Gly Gly Thr Arg Pro Thr Pro Val Val Val	305	310	315
Ser Glu Ser Gly Ala Ser Val Tyr Ser Ala Ser Pro Ile Ala Ala Glu	325	330	335
Glu Phe Pro Asp Met Asp Val Ser Leu Arg Gly Ala Val Ser Ile Ala	340	345	350
Arg Arg Leu Gln Asp Pro Leu Ala Glu Leu Val Lys Ile Glu Pro Lys	355	360	365
Ala Ile Gly Val Gly Gln Tyr Gln His Asp Val Asn Gln Val Ala Leu	370	375	380
Ala Lys Thr Leu Asp Gly Val Val Glu Asp Ala Val Asn Ala Val Gly	385	390	395
Val Asn Leu Asn Thr Ala Ser Ala Pro Leu Leu Thr Arg Val Ala Gly	405	410	415
Val Thr Ser Thr Leu Ala Asn Asn Ile Val Ala Tyr Arg Asn Glu Asn	420	425	430
Gly Gly Phe Ser Ser Arg Lys Glu Leu Asn Lys Val Pro Arg Leu Gly	435	440	445
Pro Lys Ala Phe Glu Gln Cys Ala Gly Phe Leu Arg Ile Ser Gly Ser	450	455	460
Thr Asp Pro Leu Asp Ala Ser Ala Val His Pro Glu Ala Tyr Pro Val	465	470	475
			480

Val Arg Asn Ile Ala Lys Ala Thr Gly Leu Asp Val Ser Gly Leu Ile
485 490 495

Gly Asn Ser Ala Val Leu Thr Lys Leu Lys Pro Ala Asp Phe Ala Asp
500 505 510

Glu Arg Phe Gly Ile Pro Thr Val Thr Asp Ile Ile Ala Glu Leu Asp
515 520 525

Lys Pro Gly Arg Asp Pro Arg Pro Glu Phe Lys Thr Ala Ser Phe Lys
530 535 540

Glu Gly Val Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu
545 550 555 560

Gly Thr Val Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly
565 570 575

Val His Arg Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe
580 585 590

Ile Ser Asn Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val
595 600 605

Lys Val Met Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu
610 615 620

Arg Leu Thr Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn
625 630 635 640

Arg Pro Ala Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro
645 650 655

Ala Thr Gly Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
660 665 670

<210> 2209

<211> 1839

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1816)

<223> RXA01384

<400> 2209

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Met Arg Ser Leu Gln
1 5

tcg gtc ctt gac ctg ctg act tct aag tcc aaa gtg gct acc aaa att 163
Ser Val Leu Asp Leu Leu Thr Ser Lys Ser Lys Val Ala Thr Lys Ile
10 15 20

gtg gtg gaa cga att gaa aag cat cct gtt cat gga ttg gga tgg atg 211
Val Val Glu Arg Ile Glu Lys His Pro Val His Gly Leu Gly Trp Met

25	30	35	
atg tat ccg cca ttt cat cca tgg act gat gct tcg acc ttg acg att Met Tyr Pro Pro Phe His Pro Trp Thr Asp Ala Ser Thr Leu Thr Ile 40 45 50			259
gag cga aac gga acc agt cgg cgc gcg agt cag aat ggc gtt gcg gtt Glu Arg Asn Gly Thr Ser Arg Arg Ala Ser Gln Asn Gly Val Ala Val 55 60 65			307
ctt cat cag cat gag caa gtt caa act atc ggt cta gcc agc tat ttt Leu His Gln His Glu Gln Val Gln Thr Ile Gly Leu Ala Ser Tyr Phe 70 75 80 85			355
atc gac tcc aag att tgg gta aac gag ctg gct ggc ctt gat cgt atc Ile Asp Ser Lys Ile Trp Val Asn Glu Leu Ala Gly Leu Asp Arg Ile 90 95 100			403
aac att tct gag agt gaa gtt gct ggt cgt gac gta tta gtt ctg ccg Asn Ile Ser Glu Ser Glu Val Ala Gly Arg Asp Val Leu Val Leu Pro 105 110 115			451
tta tct gat ctg act tta agc atc gat gcg aaa tac ggc gtg gtt ttg Leu Ser Asp Leu Thr Leu Ser Ile Asp Ala Lys Tyr Gly Val Val Leu 120 125 130			499
gct gcg gaa gac agc gat gaa tca gtg cgc gcg gta tcc gtg gag ttc Ala Ala Glu Asp Ser Asp Glu Ser Val Arg Ala Val Ser Val Glu Phe 135 140 145			547
ctg gac cag tgg gta gat gaa gaa gaa ccc cca gcg gaa gaa gtg cct Leu Asp Gln Trp Val Asp Glu Glu Glu Pro Pro Ala Glu Glu Val Pro 150 155 160 165			595
aaa tat acg gaa acc agg gag gaa ctt cct cca ctt gag att cct ccg Lys Tyr Thr Glu Thr Arg Glu Glu Leu Pro Pro Leu Glu Ile Pro Pro 170 175 180			643
gct cct tcc gga aat cgt aat ctc cga gtt ctg tgc acg tgg gga gcg Ala Pro Ser Gly Asn Arg Asn Leu Arg Val Leu Cys Thr Trp Gly Ala 185 190 195			691
atg gaa gga att att cct gag tgg aaa ccc ggc gat caa gtt tca ctg Met Glu Gly Ile Ile Pro Glu Trp Lys Pro Gly Asp Gln Val Ser Leu 200 205 210			739
ttt ttg tct ttc gac ctc gac gat ccg ccg ttc gaa cag ctc aaa acc Phe Leu Ser Phe Asp Leu Asp Asp Pro Pro Phe Glu Gln Leu Lys Thr 215 220 225			787
act cgt cgc ggg tac acc gaa cct ggc gag att tat gga aac cag gcg Thr Arg Arg Gly Tyr Thr Glu Pro Gly Glu Ile Tyr Gly Asn Gln Arg 230 235 240 245			835
agc tat aaa ttt cac gct gat ggt tgg aac gct gtt att tcc gcc aaa Ser Tyr Lys Phe His Ala Asp Gly Trp Asn Ala Val Ile Ser Ala Lys 250 255 260			883
gtg cca ctg cgc acc gaa gaa aac ctc acc ggc tac ttc acc cac agc Val Pro Leu Arg Thr Glu Glu Asn Leu Thr Gly Tyr Phe Thr His Ser 265 270 275			931

tcc tac gcg gac acg agc cgc cgc acg tca gcg gtc atc acc gca gtc	979
Ser Tyr Ala Asp Thr Ser Arg Arg Thr Ser Ala Val Ile Thr Ala Val	
280 285 290	
tac cgc cac ggt aag gac gca att atc gac gtg acc ctc gac ggt gcg	1027
Tyr Arg His Gly Lys Asp Ala Ile Ile Asp Val Thr Leu Asp Gly Ala	
295 300 305	
aaa cct cct aga tat caa gaa tcc ttg gat tgg agc agc acc agt acc	1075
Lys Pro Pro Arg Tyr Gln Glu Ser Leu Asp Trp Ser Ser Thr Ser Thr	
310 315 320 325	
tgt gac ggt gaa aca atc tgg ctg tcc gat aag agc ttg ccc ttc gtc	1123
Cys Asp Gly Glu Thr Ile Trp Leu Ser Asp Lys Ser Leu Pro Phe Val	
330 335 340	
cgc ggt ttc aat gtc tcc aca ggc aag cta gta cac gag atc tcc ata	1171
Arg Gly Phe Asn Val Ser Thr Gly Lys Leu Val His Glu Ile Ser Ile	
345 350 355	
ccc acc ttc aat gag atc gcc ctc gaa tcc ggc aat aga gcc cgc gca	1219
Pro Thr Phe Asn Glu Ile Ala Leu Glu Ser Gly Asn Arg Ala Arg Ala	
360 365 370	
gcg aaa aaa ctt tgg gaa ctt cca gat ctt aaa gag gca acc gac cct	1267
Ala Lys Lys Leu Trp Glu Leu Pro Asp Leu Lys Glu Ala Thr Asp Pro	
375 380 385	
gtc cca gcg atc ccc gcg ggc tgg aaa cta cac aaa aga ttc ggg aaa	1315
Val Pro Ala Ile Pro Ala Gly Trp Lys Leu His Lys Arg Phe Gly Lys	
390 395 400 405	
aac ttc cat atc gta agc gct gac aac gga acc tgg aaa caa acc atc	1363
Asn Phe His Ile Val Ser Ala Asp Asn Gly Thr Trp Lys Gln Thr Ile	
410 415 420	
ctt agg atc aaa ccc ttc aaa gca att gag ctt gat ctt gga tac gcc	1411
Leu Arg Ile Lys Pro Phe Lys Ala Ile Glu Leu Asp Leu Gly Tyr Ala	
425 430 435	
aag att tcg acg att tac caa tac ggt gaa cga att tat ctg cgt tcc	1459
Lys Ile Ser Thr Ile Tyr Gln Tyr Gly Glu Arg Ile Tyr Leu Arg Ser	
440 445 450	
gat ctt cac cag atc acg ttt aat cag gat ctt gaa atc ctc agt gta	1507
Asp Leu His Gln Ile Thr Phe Asn Gln Asp Leu Glu Ile Leu Ser Val	
455 460 465	
gag gtc cac gga aat ccc gat gca ggt tat tgg cca ctt tcc gat ctt	1555
Glu Val His Gly Asn Pro Asp Ala Gly Tyr Trp Pro Leu Ser Asp Leu	
470 475 480 485	
cca cca ggg gat tct cca acg ctg gga ttt cct atc gga tca ctc atg	1603
Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro Ile Gly Ser Leu Met	
490 495 500	
atg ttc cac gaa caa caa gat atc tac gct ttc cac gat cct aaa aca	1651
Met Phe His Glu Gln Gln Asp Ile Tyr Ala Phe His Asp Pro Lys Thr	
505 510 515	

aca aag caa cta aca act gtg aac ttg ccc aaa agg cag ttt gaa gtg 1699
 Thr Lys Gln Leu Thr Thr Val Asn Leu Pro Lys Arg Gln Phe Glu Val
 520 525 530

gaa tat gct tct cag aac aga att gtt att tcg ctg aaa aat cca gaa 1747
 Glu Tyr Ala Ser Gln Asn Arg Ile Val Ile Ser Leu Lys Asn Pro Glu
 535 540 545

agc cgc ctc att gac aaa ctg ttg gtg tgg gaa cca caa acc agg tgg 1795
 Ser Arg Leu Ile Asp Lys Leu Leu Val Trp Glu Pro Gln Thr Arg Trp
 550 555 560 565

cgg gaa caa aac ctg gag agc tgagcacggt ttgattaacg tcg 1839
 Arg Glu Gln Asn Leu Glu Ser
 570

<210> 2210

<211> 572

<212> PRT

<213> Corynebacterium glutamicum

<400> 2210

Met Arg Ser Leu Gln Ser Val Leu Asp Leu Leu Thr Ser Lys Ser Lys
 1 5 10 15

Val Ala Thr Lys Ile Val Val Glu Arg Ile Glu Lys His Pro Val His
 20 25 30

Gly Leu Gly Trp Met Met Tyr Pro Pro Phe His Pro Trp Thr Asp Ala
 35 40 45

Ser Thr Leu Thr Ile Glu Arg Asn Gly Thr Ser Arg Arg Ala Ser Gln
 50 55 60

Asn Gly Val Ala Val Leu His Gln His Glu Gln Val Gln Thr Ile Gly
 65 70 75 80

Leu Ala Ser Tyr Phe Ile Asp Ser Lys Ile Trp Val Asn Glu Leu Ala
 85 90 95

Gly Leu Asp Arg Ile Asn Ile Ser Glu Ser Glu Val Ala Gly Arg Asp
 100 105 110

Val Leu Val Leu Pro Leu Ser Asp Leu Thr Leu Ser Ile Asp Ala Lys
 115 120 125

Tyr Gly Val Val Leu Ala Ala Glu Asp Ser Asp Glu Ser Val Arg Ala
 130 135 140

Val Ser Val Glu Phe Leu Asp Gln Trp Val Asp Glu Glu Glu Pro Pro
 145 150 155 160

Ala Glu Glu Val Pro Lys Tyr Thr Glu Thr Arg Glu Glu Leu Pro Pro
 165 170 175

Leu Glu Ile Pro Pro Ala Pro Ser Gly Asn Arg Asn Leu Arg Val Leu
 180 185 190

Cys Thr Trp Gly Ala Met Glu Gly Ile Ile Pro Glu Trp Lys Pro Gly
 195 200 205

Asp Gln Val Ser Leu Phe Leu Ser Phe Asp Leu Asp Asp Pro Pro Phe
210 215 220

Glu Gln Leu Lys Thr Thr Arg Arg Gly Tyr Thr Glu Pro Gly Glu Ile
225 230 235 240

Tyr Gly Asn Gln Arg Ser Tyr Lys Phe His Ala Asp Gly Trp Asn Ala
245 250 255

Val Ile Ser Ala Lys Val Pro Leu Arg Thr Glu Glu Asn Leu Thr Gly
260 265 270

Tyr Phe Thr His Ser Ser Tyr Ala Asp Thr Ser Arg Arg Thr Ser Ala
275 280 285

Val Ile Thr Ala Val Tyr Arg His Gly Lys Asp Ala Ile Ile Asp Val
290 295 300

Thr Leu Asp Gly Ala Lys Pro Pro Arg Tyr Gln Glu Ser Leu Asp Trp
305 310 315 320

Ser Ser Thr Ser Thr Cys Asp Gly Glu Thr Ile Trp Leu Ser Asp Lys
325 330 335

Ser Leu Pro Phe Val Arg Gly Phe Asn Val Ser Thr Gly Lys Leu Val
340 345 350

His Glu Ile Ser Ile Pro Thr Phe Asn Glu Ile Ala Leu Glu Ser Gly
355 360 365

Asn Arg Ala Arg Ala Ala Lys Lys Leu Trp Glu Leu Pro Asp Leu Lys
370 375 380

Glu Ala Thr Asp Pro Val Pro Ala Ile Pro Ala Gly Trp Lys Leu His
385 390 395 400

Lys Arg Phe Gly Lys Asn Phe His Ile Val Ser Ala Asp Asn Gly Thr
405 410 415

Trp Lys Gln Thr Ile Leu Arg Ile Lys Pro Phe Lys Ala Ile Glu Leu
420 425 430

Asp Leu Gly Tyr Ala Lys Ile Ser Thr Ile Tyr Gln Tyr Gly Glu Arg
435 440 445

Ile Tyr Leu Arg Ser Asp Leu His Gln Ile Thr Phe Asn Gln Asp Leu
450 455 460

Glu Ile Leu Ser Val Glu Val His Gly Asn Pro Asp Ala Gly Tyr Trp
465 470 475 480

Pro Leu Ser Asp Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro
485 490 495

Ile Gly Ser Leu Met Met Phe His Glu Gln Gln Asp Ile Tyr Ala Phe
500 505 510

His Asp Pro Lys Thr Thr Lys Gln Leu Thr Thr Val Asn Leu Pro Lys
515 520 525

Arg Gln Phe Glu Val Glu Tyr Ala Ser Gln Asn Arg Ile Val Ile Ser
 530 535 540

Leu Lys Asn Pro Glu Ser Arg Leu Ile Asp Lys Leu Leu Val Trp Glu
 545 550 555 560

Pro Gln Thr Arg Trp Arg Glu Gln Asn Leu Glu Ser
 565 570

<210> 2211

<211> 381

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(358)

<223> RXA01396

<400> 2211

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 caaccgctga gatccaggct cagcttcaac ctcccgcggt ttg aag gct ttc aac 115
 Leu Lys Ala Phe Asn
 1 5
 acc aac ttc gca gcc act ttg gct acc gga aag gtt ggc gat atc acc 163
 Thr Asn Phe Ala Ala Thr Leu Ala Thr Gly Lys Val Gly Asp Ile Thr
 10 15 20
 acc acc gtt tta gtt gca ggc gat gat gaa gac gca aag aac gct ctt 211
 Thr Thr Val Leu Val Ala Gly Asp Asp Glu Asp Ala Lys Asn Ala Leu
 25 30 35
 atc acc gac gtc aac gct ggc ggc ctc gac gcc ctt gac gct ggt tcc 259
 Ile Thr Asp Val Asn Ala Gly Gly Leu Asp Ala Leu Asp Ala Gly Ser
 40 45 50
 ctc aag cgt gca cac gag ctt gaa gca gtt ggt ttc ctg cag ctc acc 307
 Leu Lys Arg Ala His Glu Leu Glu Ala Val Gly Phe Leu Gln Leu Thr
 55 60 65
 ctt gca ggt tcc gag aag att gga tgg acc ggc gga ttc ggc ctg gtc 355
 Leu Ala Gly Ser Glu Lys Ile Gly Trp Thr Gly Gly Phe Gly Leu Val
 70 75 80 85
 aag taacacccag cctcaaaagc act 381
 Lys

<210> 2212

<211> 86

<212> PRT

<213> Corynebacterium glutamicum

<400> 2212

Leu Lys Ala Phe Asn Thr Asn Phe Ala Ala Thr Leu Ala Thr Gly Lys
 1 5 10 15

Val Gly Asp Ile Thr Thr Thr Val Leu Val Ala Gly Asp Asp Glu Asp
 20 25 30
 Ala Lys Asn Ala Leu Ile Thr Asp Val Asn Ala Gly Gly Leu Asp Ala
 35 40 45
 Leu Asp Ala Gly Ser Leu Lys Arg Ala His Glu Leu Glu Ala Val Gly
 50 55 60
 Phe Leu Gln Leu Thr Leu Ala Gly Ser Glu Lys Ile Gly Trp Thr Gly
 65 70 75 80
 Gly Phe Gly Leu Val Lys
 85

<210> 2213

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXA01397

<400> 2213

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 actaattact tgacacgtca agtaattagg gtctagtgtt gtg ttc atg atc aaa 115
 Val Phe Met Ile Lys
 1 5
 gaa ctg ctc aac aag ctc ttc gga aac aag aag gct tcc ccg gca atg 163
 Glu Leu Leu Asn Lys Leu Phe Gly Asn Lys Lys Ala Ser Pro Ala Met
 10 15 20
 aca caa tct gaa acc att tca cac aag gag aac aac aca atg acc act 211
 Thr Gln Ser Glu Thr Ile Ser His Lys Glu Asn Asn Thr Met Thr Thr
 25 30 35
 tac acc atc ttc ggc cgc ggc aac atg ggc acc gca atc gca ggc gtc 259
 Tyr Thr Ile Phe Gly Arg Gly Asn Met Gly Thr Ala Ile Ala Gly Val
 40 45 50
 ctc acc aag ggt ggt gca act gta gaa cac atc ggt tct gca gat tct 307
 Leu Thr Lys Gly Gly Ala Thr Val Glu His Ile Gly Ser Ala Asp Ser
 55 60 65
 gac atc gca acc atc aac ggt gac gtt gtt atc ctt gct gtt cct tac 355
 Asp Ile Ala Thr Ile Asn Gly Asp Val Val Ile Leu Ala Val Pro Tyr
 70 75 80 85
 cca gca gta gag tcc atc att gca agc cac aag gat gct ctc gca ggc 403
 Pro Ala Val Glu Ser Ile Ile Ala Ser His Lys Asp Ala Leu Ala Gly
 90 95 100
 aag acc gtt atc gat atc acc aac cca ctt aac ttc gag acc ttc gat 451
 Lys Thr Val Ile Asp Ile Thr Asn Pro Leu Asn Phe Glu Thr Phe Asp
 105 110 115

tcc ctc gtc gtt cca gtt ggt tct tct gca acc gct gag atc cag gct 499
 Ser Leu Val Val Pro Val Gly Ser Ser Ala Thr Ala Glu Ile Gln Ala
 120 125 130

cag ctt caa cct ccc gcg ttt tgaaggcttt caacaccaac ttc 543
 Gln Leu Gln Pro Pro Ala Phe
 135 140

<210> 2214

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 2214

Val Phe Met Ile Lys Glu Leu Leu Asn Lys Leu Phe Gly Asn Lys Lys
 1 5 10 15

Ala Ser Pro Ala Met Thr Gln Ser Glu Thr Ile Ser His Lys Glu Asn
 20 25 30

Asn Thr Met Thr Thr Tyr Thr Ile Phe Gly Arg Gly Asn Met Gly Thr
 35 40 45

Ala Ile Ala Gly Val Leu Thr Lys Gly Gly Ala Thr Val Glu His Ile
 50 55 60

Gly Ser Ala Asp Ser Asp Ile Ala Thr Ile Asn Gly Asp Val Val Ile
 65 70 75 80

Leu Ala Val Pro Tyr Pro Ala Val Glu Ser Ile Ile Ala Ser His Lys
 85 90 95

Asp Ala Leu Ala Gly Lys Thr Val Ile Asp Ile Thr Asn Pro Leu Asn
 100 105 110

Phe Glu Thr Phe Asp Ser Leu Val Val Pro Val Gly Ser Ser Ala Thr
 115 120 125

Ala Glu Ile Gln Ala Gln Leu Gln Pro Pro Ala Phe
 130 135 140

<210> 2215

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXA01401

<400> 2215

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agtatctata gattgataga aaataattta ggaagtttcc atg aac tct ccc cta 115
 Met Asn Ser Pro Leu
 1 5

caa cac agc gcc ttc ccc gtc ccc ggc gcg caa ctc tcc acc tca tac 163

Gln His Ser Ala Phe Pro Val Pro Gly Ala Gln Leu Ser Thr Ser Tyr
 10 15 20
 agc gac gaa cac ggc caa gcc gtc atc caa ctt cac ggc ctc acc tcc 211
 Ser Asp Glu His Gly Gln Ala Val Ile Gln Leu His Gly Leu Thr Ser
 25 30 35
 tcc cgc caa cgc gac cgc ctc ctc gac ctc gac ctc ggc cgt ggc ctt 259
 Ser Arg Gln Arg Asp Arg Leu Leu Asp Leu Gly Arg Gly Leu
 40 45 50
 tcc ggc acg cgc ctt ttg cgt tac gac gcc cgc ggc cac ggc acc tcc 307
 Ser Gly Thr Arg Leu Leu Arg Tyr Asp Ala Arg Gly His Gly Thr Ser
 55 60 65
 acc ggc cgc gct gcc tcc acc gat tat cag tgg gac acc cta gcg ggt 355
 Thr Gly Arg Ala Ala Ser Thr Asp Tyr Gln Trp Asp Thr Leu Ala Gly
 70 75 80 85
 gac ctt taatgcttct cgacgccac ttc 384
 Asp Leu

<210> 2216
 <211> 87
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2216
 Met Asn Ser Pro Leu Gln His Ser Ala Phe Pro Val Pro Gly Ala Gln
 1 5 10 15
 Leu Ser Thr Ser Tyr Ser Asp Glu His Gly Gln Ala Val Ile Gln Leu
 20 25 30
 His Gly Leu Thr Ser Ser Arg Gln Arg Asp Arg Leu Leu Asp Leu Asp
 35 40 45
 Leu Gly Arg Gly Leu Ser Gly Thr Arg Leu Leu Arg Tyr Asp Ala Arg
 50 55 60
 Gly His Gly Thr Ser Thr Gly Arg Ala Ala Ser Thr Asp Tyr Gln Trp
 65 70 75 80
 Asp Thr Leu Ala Gly Asp Leu
 85

<210> 2217
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(574)
 <223> RXA01402

<400> 2217
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gcccacttcc ccacgaacaa gtccacggcg tcggcccctc atg ggt tgc gcc acc 115
                                   Met Gly Cys Ala Thr
                                   1 5

ctc ctc aaa gcc gcg gtg tta aac ccc gac cgc ttc agt gga ttc aca 163
Leu Leu Lys Ala Ala Val Leu Asn Pro Asp Arg Phe Ser Gly Phe Thr
                                   10 15 20

ctc atg ctc cca ccc acc gcc tgg gaa tcc cga aaa gcc caa gcc tcc 211
Leu Met Leu Pro Pro Thr Ala Trp Glu Ser Arg Lys Ala Gln Ala Ser
                                   25 30 35

gaa tac cta tcc cga gca gaa ttc cta gaa acc cac ggc atg gac gcc 259
Glu Tyr Leu Ser Arg Ala Glu Phe Leu Glu Thr His Gly Met Asp Ala
                                   40 45 50

ttc ctc aac gcc gaa aaa ctc cac gcc caa cca cca gca acc gta gga 307
Phe Leu Asn Ala Glu Lys Leu His Ala Gln Pro Pro Ala Thr Val Gly
                                   55 60 65

acc ccc gac aca gtc ccc gac att tcc gcc gaa ctc ctc ccc tgg gct 355
Thr Pro Asp Thr Val Pro Asp Ile Ser Ala Glu Leu Leu Pro Trp Ala
                                   70 75 80 85

tac cga ggc gcc gcc caa agc gac ctc ccc tca aag aaa gaa atc gcc 403
Tyr Arg Gly Ala Ala Gln Ser Asp Leu Pro Ser Lys Lys Glu Ile Ala
                                   90 95 100

aaa ata aca gcc ccc acc act att ctg agc tgg acc gac gat ccc gga 451
Lys Ile Thr Ala Pro Thr Thr Ile Leu Ser Trp Thr Asp Asp Pro Gly
                                   105 110 115

cac ccc gta tcc acg gca atc gag cta acc cgc ctc atg cca aac gcc 499
His Pro Val Ser Thr Ala Ile Glu Leu Thr Arg Leu Met Pro Asn Ala
                                   120 125 130

caa ctg cgc att gcc act acc cca gcg gaa gtc gcg cgg tgg cca caa 547
Gln Leu Arg Ile Ala Thr Thr Pro Ala Glu Val Ala Arg Trp Pro Gln
                                   135 140 145

cac ctt cgc gat gac ctg cag ttg gac taaaaacctt cattatctgg 594
His Leu Arg Asp Asp Leu Gln Leu Asp
150 155

ttt 597

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<210> 2218

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 2218

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Met Gly Cys Ala Thr Leu Leu Lys Ala Ala Val Leu Asn Pro Asp Arg
 1 5 10 15

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Phe Ser Gly Phe Thr Leu Met Leu Pro Pro Thr Ala Trp Glu Ser Arg
 20 25 30

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Lys Ala Gln Ala Ser Glu Tyr Leu Ser Arg Ala Glu Phe Leu Glu Thr

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35	40	45
His Gly Met Asp Ala Phe Leu Asn Ala Glu Lys Leu His Ala Gln Pro		
50	55	60
Pro Ala Thr Val Gly Thr Pro Asp Thr Val Pro Asp Ile Ser Ala Glu		
65	70	75
Leu Leu Pro Trp Ala Tyr Arg Gly Ala Ala Gln Ser Asp Leu Pro Ser		
	85	90
Lys Lys Glu Ile Ala Lys Ile Thr Ala Pro Thr Thr Ile Leu Ser Trp		
	100	105
Thr Asp Asp Pro Gly His Pro Val Ser Thr Ala Ile Glu Leu Thr Arg		
	115	120
Leu Met Pro Asn Ala Gln Leu Arg Ile Ala Thr Thr Pro Ala Glu Val		
	130	135
Ala Arg Trp Pro Gln His Leu Arg Asp Asp Leu Gln Leu Asp		
145	150	155

<210> 2219

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA01405

<400> 2219

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aaacctagaa ttccgaatac gttccgaata ggggtgggggt atg agt aag ata gtt 115
                                   Met Ser Lys Ile Val
                                   1 5

gat ctg cgc tat ggg acc cgg cgt tcc tcg gag ttg agc aaa cgc tct 163
Asp Leu Arg Tyr Gly Thr Arg Arg Ser Ser Glu Leu Ser Lys Arg Ser
                                   10 15 20

gct gaa gtc ttt gcc gaa gct gaa gaa cat ccc att act gtg aca cgt 211
Ala Glu Val Phe Ala Glu Ala Glu Glu His Pro Ile Thr Val Thr Arg
                                   25 30 35

cgt gat ggt gaa gcg ttg gta ttg atg tcg cag cgc gaa gct gac ggg 259
Arg Asp Gly Glu Ala Leu Val Leu Met Ser Gln Arg Glu Ala Asp Gly
                                   40 45 50

cga gcc cgc ctg ctg gag ttg gct gca cag tta att act gtg gcc act 307
Arg Ala Arg Leu Leu Glu Leu Ala Ala Gln Leu Ile Thr Val Ala Thr
                                   55 60 65

gat cat cag ggc acg tta gcc gaa cgt atg gcg aaa gta ttc ccg tgg 355
Asp His Gln Gly Thr Leu Ala Glu Arg Met Ala Lys Val Phe Pro Trp
                                   70 75 80 85

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atg ctg gcc ctg tca gtg gcg gat cgt gag gcg tgt gcc cgt gag att 403
 Met Leu Ala Leu Ser Val Ala Asp Arg Glu Ala Cys Ala Arg Glu Ile
 90 95 100

ctt gac gct gca cga gca tcg ttt gca acc gaa caa cct cac ctc gct 451
 Leu Asp Ala Ala Arg Ala Ser Phe Ala Thr Glu Gln Pro His Leu Ala
 105 110 115

ctt act gaa ctg acc tca tgg aaa gaa aca gca gca gct gtt gct gct 499
 Leu Thr Glu Leu Thr Ser Trp Lys Glu Thr Ala Ala Val Ala Ala
 120 125 130

gga ttg agt aac act gat ctg cag tgg tac gac gat ccg cat ctg gtg 547
 Gly Leu Ser Asn Thr Asp Leu Gln Trp Tyr Asp Asp Pro His Leu Val
 135 140 145

gag cgt ccc taagcgtggc tggaaagaaa agc 579
 Glu Arg Pro
 150

<210> 2220

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 2220

Met Ser Lys Ile Val Asp Leu Arg Tyr Gly Thr Arg Arg Ser Ser Glu
 1 5 10 15

Leu Ser Lys Arg Ser Ala Glu Val Phe Ala Glu Ala Glu Glu His Pro
 20 25 30

Ile Thr Val Thr Arg Arg Asp Gly Glu Ala Leu Val Leu Met Ser Gln
 35 40 45

Arg Glu Ala Asp Gly Arg Ala Arg Leu Leu Glu Leu Ala Ala Gln Leu
 50 55 60

Ile Thr Val Ala Thr Asp His Gln Gly Thr Leu Ala Glu Arg Met Ala
 65 70 75 80

Lys Val Phe Pro Trp Met Leu Ala Leu Ser Val Ala Asp Arg Glu Ala
 85 90 95

Cys Ala Arg Glu Ile Leu Asp Ala Ala Arg Ala Ser Phe Ala Thr Glu
 100 105 110

Gln Pro His Leu Ala Leu Thr Glu Leu Thr Ser Trp Lys Glu Thr Ala
 115 120 125

Ala Ala Val Ala Ala Gly Leu Ser Asn Thr Asp Leu Gln Trp Tyr Asp
 130 135 140

Asp Pro His Leu Val Glu Arg Pro
 145 150

<210> 2221

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXA01413

<400> 2221

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cggggtttcct cagcgttttaa ccattctgaaa ccattctgaga ttg acc cat ctg ttc 115
                                   Leu Thr His Leu Phe
                                   1                               5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163
Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
                                   10                               15                               20

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
                                   25                               30                               35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
                                   40                               45                               50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
                                   55                               60                               65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
                                   70                               75                               80                               85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
                                   90                               95                               100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
                                   105                               110                               115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499
Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
                                   120                               125                               130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
                                   135                               140                               145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
                                   150                               155                               160                               165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
                                   170                               175                               180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
                                   185                               190                               195

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gac aac aag tagagtttta aaataccgat caa
Asp Asn Lys
200

723

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<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 2222
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Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
20 25 30
Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg
35 40 45
Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu
50 55 60
Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr
65 70 75 80
Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala
85 90 95
Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly
100 105 110
Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly
115 120 125
Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val
130 135 140
Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala
145 150 155 160
Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val
165 170 175
Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser
180 185 190
Val Trp Leu Ala Glu Asp Asn Lys
195 200

<210> 2223
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(607)
<223> RXA01414

<400> 2223

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Met Ala Val Phe Asp
1 5

ttc cct aac ccc gtt aac gaa tat gca gct cgc tgc act gcg ggt ttg 163
Phe Pro Asn Pro Val Asn Glu Tyr Ala Ala Arg Cys Thr Ala Gly Leu
10 15 20

gtt gtt ttg ctg agc gcc gcc acg ctt ttt gcc tct ggt gac ctt cgt 211
Val Val Leu Leu Ser Ala Ala Thr Leu Phe Ala Ser Gly Asp Leu Arg
25 30 35

att att ttg gca agc atc ttg acc ttc ggc ttc gca ttg cgc gtg gcc 259
Ile Ile Leu Ala Ser Ile Leu Thr Phe Gly Phe Ala Leu Arg Val Ala
40 45 50

ggc gga ccc cgt tac tcc ccc ttt gga cgt ctt tca gta cac gta ctt 307
Gly Gly Pro Arg Tyr Ser Pro Phe Gly Arg Leu Ser Val His Val Leu
55 60 65

gta cca ctg ctg aag aaa gca ccg atc ctg acc cct ggc cca cca aag 355
Val Pro Leu Leu Lys Lys Ala Pro Ile Leu Thr Pro Gly Pro Pro Lys
70 75 80 85

cgc ttc gcg cag acc atc ggc ctg ggc ttt agc ggt act tcc ctt atc 403
Arg Phe Ala Gln Thr Ile Gly Leu Gly Phe Ser Gly Thr Ser Leu Ile
90 95 100

ctt atg gcc ttt gga ttt aac gtt gca gct tcc gta gtc cta gtc atg 451
Leu Met Ala Phe Gly Phe Asn Val Ala Ala Ser Val Val Leu Val Met
105 110 115

ctc atc gca gca gcc acc tta gaa tcc gtc ttt ggt atc tgc ctc ggt 499
Leu Ile Ala Ala Ala Thr Leu Glu Ser Val Phe Gly Ile Cys Leu Gly
120 125 130

tgc tgg gga ttc ggc aag ctc atg cgc tac ggc gtc atc cca gaa gac 547
Cys Trp Gly Phe Gly Lys Leu Met Arg Tyr Gly Val Ile Pro Glu Asp
135 140 145

gtt tgc gag cag tgc ttc cag aag gaa tcc tcc cgc acc ggc tgg ctc 595
Val Cys Glu Gln Cys Phe Gln Lys Glu Ser Ser Arg Thr Gly Trp Leu
150 155 160 165

gtt agc ctg aag tagcacttcg aatctaagac cac 630
Val Ser Leu Lys

<210> 2224

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 2224

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Cys Thr Ala Gly Leu Val Val Leu Leu Ser Ala Ala Thr Leu Phe Ala
 20 25 30
 Ser Gly Asp Leu Arg Ile Ile Leu Ala Ser Ile Leu Thr Phe Gly Phe
 35 40 45
 Ala Leu Arg Val Ala Gly Gly Pro Arg Tyr Ser Pro Phe Gly Arg Leu
 50 55 60
 Ser Val His Val Leu Val Pro Leu Leu Lys Lys Ala Pro Ile Leu Thr
 65 70 75 80
 Pro Gly Pro Pro Lys Arg Phe Ala Gln Thr Ile Gly Leu Gly Phe Ser
 85 90 95
 Gly Thr Ser Leu Ile Leu Met Ala Phe Gly Phe Asn Val Ala Ala Ser
 100 105 110
 Val Val Leu Val Met Leu Ile Ala Ala Ala Thr Leu Glu Ser Val Phe
 115 120 125
 Gly Ile Cys Leu Gly Cys Trp Gly Phe Gly Lys Leu Met Arg Tyr Gly
 130 135 140
 Val Ile Pro Glu Asp Val Cys Glu Gln Cys Phe Gln Lys Glu Ser Ser
 145 150 155 160
 Arg Thr Gly Trp Leu Val Ser Leu Lys
 165

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<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(697)

<223> RXA01417

<400> 2225

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 Met Thr Asp Lys Phe
 1 5
 gac aga gtc ctt gct gta gag gtg tgc att cag gag tgg atc gac gag 163
 Asp Arg Val Leu Ala Val Glu Val Cys Ile Gln Glu Trp Ile Asp Glu
 10 15 20
 caa aac ctc acg cta gag gtg cca tta atg att gca cgt ttg cag ctt 211
 Gln Asn Leu Thr Leu Glu Val Pro Leu Met Ile Ala Arg Leu Gln Leu
 25 30 35
 aga gac gtc gcg aag gat atc act gct gtt cac gaa gaa aaa ttc tac 259
 Arg Asp Val Ala Lys Asp Ile Thr Ala Val His Glu Glu Lys Phe Tyr
 40 45 50

gac ctc act gat atc gat act gat gcc ttt gtg aaa aac atc aaa ctg 307
 Asp Leu Thr Asp Ile Asp Thr Asp Ala Phe Val Lys Asn Ile Lys Leu
 55 60 65

 gga tgg aat gaa cgc ttg atc aag aaa agc ctc ttt cca caa ccg gac 355
 Gly Trp Asn Glu Arg Leu Ile Lys Lys Ser Leu Phe Pro Gln Pro Asp
 70 75 80 85

 gtg cat aaa caa cat ttc aca gaa act gaa cat ggc att gac gcg act 403
 Val His Lys Gln His Phe Thr Glu Thr Glu His Gly Ile Asp Ala Thr
 90 95 100

 gtg acg gtc tgg tgc aag ggc ttc gat ccg gaa agt ggc ccc gac ttc 451
 Val Thr Val Trp Ser Lys Gly Phe Asp Pro Glu Ser Gly Pro Asp Phe
 105 110 115

 ttg gtt tcc tat gtg gat ggt ctt tgg tca gcc gat att aga aac cgc 499
 Leu Val Ser Tyr Val Asp Gly Leu Trp Ser Ala Asp Ile Arg Asn Arg
 120 125 130

 atc acg aaa ttt cag aat aga gaa atc gtt agc aaa ttc tat ttt act 547
 Ile Thr Lys Phe Gln Asn Arg Glu Ile Val Ser Lys Phe Tyr Phe Thr
 135 140 145

 cca gaa cat att aag gag gat gga gat ttc tcc gca gag att ttt att 595
 Pro Glu His Ile Lys Glu Asp Gly Asp Phe Ser Ala Glu Ile Phe Ile
 150 155 160 165

 aac cga cca gaa aat gac gac gac tca caa gat ttg gtc gag gtg tgg 643
 Asn Arg Pro Glu Asn Asp Asp Asp Ser Gln Asp Leu Val Glu Val Trp
 170 175 180

 act gat caa gac acc aga tac tgc ggt gaa atg atc atc tat ttc aaa 691
 Thr Asp Gln Asp Thr Arg Tyr Cys Gly Glu Met Ile Ile Tyr Phe Lys
 185 190 195

 tgg ctc taaattccac ttttctgcat cag 720
 Trp Leu

<210> 2226

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 2226

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 Glu Trp Ile Asp Glu Gln Asn Leu Thr Leu Glu Val Pro Leu Met Ile
 20 25 30

 Ala Arg Leu Gln Leu Arg Asp Val Ala Lys Asp Ile Thr Ala Val His
 35 40 45

 Glu Glu Lys Phe Tyr Asp Leu Thr Asp Ile Asp Thr Asp Ala Phe Val
 50 55 60

 Lys Asn Ile Lys Leu Gly Trp Asn Glu Arg Leu Ile Lys Lys Ser Leu
 65 70 75 80

70	75	80	85	
aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg				403
Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr Lys Ile Tyr Pro Met				
	90	95	100	
cac ttg att gcg ttg ccg atg ttt att gag gcg tcg gcg aag ttc acg				451
His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala Ser Ala Lys Phe Thr				
	105	110	115	
act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg				497
Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg Glu				
	120	125		
gctgcggaat gcg				510

<210> 2228

<211> 129

<212> PRT

<213> Corynebacterium glutamicum

<400> 2228

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Thr Gly Ala Arg Trp Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala				
	20	25	30	
Leu Val Phe Leu Ser Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala				
	35	40	45	
Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr				
	50	55	60	
Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln				
	65	70	75	80
Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr				
	85	90	95	
Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala				
	100	105	110	
Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg				
	115	120	125	
Glu				

<210> 2229

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> RXA01425

<400> 2229

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ttcggccatt ctgtggttct ggcataaagc gttcagcttt gtg ctg agc cca gat 115
                                   Val Leu Ser Pro Asp
                                   1 5

tcc gga att acc tgg gcc ttg tgg atc atg ttc ttg acc ttc acc gtg 163
Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val
              10              15              20

cgt atg gtt ctg gtc aag ccg atg gtc aac acc atg cgt tca cag cgc 211
Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg
              25              30              35

aag atg caa gac atg gct cca aag atg cag gcc atc cgc gag aag tac 259
Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr
              40              45              50

aaa aat gac cag cag aag atg atg gag gag acc cgc aaa ctt caa aaa 307
Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys
              55              60              65

gaa gtg ggc gtt aac ccc atc gca ggc tgt ttg cca atg ttg gtg cag 355
Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln
              70              75              80              85

atc cca gtg ttc ctg ggt ctg ttc cac gtg ctg cgc tcc ttc aac cgc 403
Ile Pro Val Phe Leu Gly Leu Phe His Val Leu Arg Ser Phe Asn Arg
              90              95              100

acc ggt tct ggc gtt ggc cag ctg gaa atg acc gtt gag caa aac gcg 451
Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr Val Glu Gln Asn Ala
              105              110              115

aac acc ccg aac tac atc ttc ggt gtc gac gag gtt cag tcc ttc ctg 499
Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu Val Gln Ser Phe Leu
              120              125              130

cgt gca gac ctg ttc ggt gcg cca ctg tgg tcc tac atc acc atg cct 547
Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser Tyr Ile Thr Met Pro
              135              140              145

gct gac gcg ttc gac gcg ttc ctt ggc ctg gat gtc tcc cgc ctc aac 595
Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp Val Ser Arg Leu Asn
              150              155              160              165

atc gcg ctg gtt gca gct cca atg att ttg atc att gtc gtg gca act 643
Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile Ile Val Val Ala Thr
              170              175              180

cac atg aac gcg cgt ctg tcc gtc aac cgc cag gaa gct cgc aag gca 691
His Met Asn Ala Arg Leu Ser Val Asn Arg Gln Glu Ala Arg Lys Ala
              185              190              195

gcc ggc aag cag cag gcc gct tcc agc gat cag atg gcc atg cag atg 739
Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln Met Ala Met Gln Met
              200              205              210

caa atg atg aac aag atg atg ctc tgg ttc atg cca gcc acc att ttg 787
Gln Met Met Asn Lys Met Met Leu Trp Phe Met Pro Ala Thr Ile Leu

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215 220 225
 ttc acc ggc ttc atc tgg acc atc ggt ctt ctt gtc tac atg atg tcc 835
 Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu Val Tyr Met Met Ser
 230 235 240 245
 aac aac gtg tgg acc ttc ttc cag cag cgc tac atc ttc gcc aag atg 883
 Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr Ile Phe Ala Lys Met
 250 255 260
 gac gct gag gaa gca gct gag gag gag gaa aag cgc gca gca aag cgc 931
 Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys Arg Ala Ala Lys Arg
 265 270 275
 act acc gct cca aag cct ggc gtg aag cca gaa aac ccc aag aag cgt 979
 Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu Asn Pro Lys Lys Arg
 280 285 290
 aag aag taaaacttca ctaaaaaccg cca 1008
 Lys Lys
 295
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 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2230
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 20 25 30
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 35 40 45
 Ile Arg Glu Lys Tyr Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr
 50 55 60
 Arg Lys Leu Gln Lys Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu
 65 70 75 80
 Pro Met Leu Val Gln Ile Pro Val Phe Leu Gly Leu Phe His Val Leu
 85 90 95
 Arg Ser Phe Asn Arg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr
 100 105 110
 Val Glu Gln Asn Ala Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu
 115 120 125
 Val Gln Ser Phe Leu Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser
 130 135 140
 Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp
 145 150 155 160
 Val Ser Arg Leu Asn Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile
 165 170 175

Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln
180 185 190

Glu Ala Arg Lys Ala Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln
195 200 205

Met Ala Met Gln Met Gln Met Met Asn Lys Met Met Leu Trp Phe Met
210 215 220

Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu
225 230 235 240

Val Tyr Met Met Ser Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr
245 250 255

Ile Phe Ala Lys Met Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys
260 265 270

Arg Ala Ala Lys Arg Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu
275 280 285

Asn Pro Lys Lys Arg Lys Lys
290 295

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<211> 741
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(718)
<223> RXA01429

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Met Leu Gln Ala Ser
1 5

ctt ttc ccg atc gtg cag gaa cac ata gat ttc ctg cac ccc cag gcc 163
Leu Phe Pro Ile Val Gln Glu His Ile Asp Phe Leu His Pro Gln Ala
10 15 20

cgc aag tcg gtg ttt tgg gag ctc gca cct gag gtt gca gct aaa gct 211
Arg Lys Ser Val Phe Trp Glu Leu Ala Pro Glu Val Ala Ala Lys Ala
25 30 35

gat ccg gtg ttt gag aag gaa gcc tgg ctg tcc acc acg ctg ctg gaa 259
Asp Pro Val Phe Glu Lys Glu Ala Trp Leu Ser Thr Thr Leu Leu Glu
40 45 50

tat gaa tcc tgc ggt ttc aac att ggt tac cgc aat gga act ccg gcg 307
Tyr Glu Ser Cys Gly Phe Asn Ile Gly Tyr Arg Asn Gly Thr Pro Ala
55 60 65

ttg gcg tcg gtc att ttc tgc gag cgc gat gcc gcc ccg ggc gcg aag 355
Leu Ala Ser Val Ile Phe Cys Glu Arg Asp Ala Ala Pro Gly Ala Lys

70	75	80	85	
gcg ctg cct acg gca ccg gtg tct agc gac gct gcg atc atc agc agc				403
Ala Leu Pro Thr Ala Pro Val Ser Ser Asp Ala Ala Ile Ile Ser Ser				
	90	95	100	
ctg ttc atc gac gag gtt ttc cgg ggc acg ggc atg gaa tcg gcg ctt				451
Leu Phe Ile Asp Glu Val Phe Arg Gly Thr Gly Met Glu Ser Ala Leu				
	105	110	115	
ctc gac gct tcc ctc atg gaa ctc att cgg cgc gac tac cca gcc gtt				499
Leu Asp Ala Ser Leu Met Glu Leu Ile Arg Arg Asp Tyr Pro Ala Val				
	120	125	130	
gag gcg ttt gga tac cgc tcg gaa aac aca gaa gcg gat gcg atc gca				547
Glu Ala Phe Gly Tyr Arg Ser Glu Asn Thr Glu Ala Asp Ala Ile Ala				
	135	140	145	
gct agg cgt tta gaa atc ggc ctg att gat gtg gag gcg tta gaa tca				595
Ala Arg Arg Leu Glu Ile Gly Leu Ile Asp Val Glu Ala Leu Glu Ser				
	150	155	160	165
gcc ggt ttc gaa gtg gtt gct gac cat ccc gtg tta ccc cgt ctg cgg				643
Ala Gly Phe Glu Val Val Ala Asp His Pro Val Leu Pro Arg Leu Arg				
	170	175	180	
atg gaa tta cca ccc gca acg gtg ctg ctc aca gct aag gat gcc cag				691
Met Glu Leu Pro Pro Ala Thr Val Leu Leu Thr Ala Lys Asp Ala Gln				
	185	190	195	
cga ctc ctt caa gag atg ggc gcg att tagccagcct gctctgattg				738
Arg Leu Leu Gln Glu Met Gly Ala Ile				
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caa				741

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<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 2232

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Leu	His	Pro	Gln	Ala	Arg	Lys	Ser	Val	Phe	Trp	Glu	Leu	Ala	Pro	Glu
		20						25					30		

Val	Ala	Ala	Lys	Ala	Asp	Pro	Val	Phe	Glu	Lys	Glu	Ala	Trp	Leu	Ser
	35						40					45			

Thr	Thr	Leu	Leu	Glu	Tyr	Glu	Ser	Cys	Gly	Phe	Asn	Ile	Gly	Tyr	Arg
	50					55					60				

Asn	Gly	Thr	Pro	Ala	Leu	Ala	Ser	Val	Ile	Phe	Cys	Glu	Arg	Asp	Ala
65					70					75				80	

Ala	Pro	Gly	Ala	Lys	Ala	Leu	Pro	Thr	Ala	Pro	Val	Ser	Ser	Asp	Ala
			85						90					95	

Ala Ile Ile Ser Ser Leu Phe Ile Asp Glu Val Phe Arg Gly Thr Gly
 100 105 110

Met Glu Ser Ala Leu Leu Asp Ala Ser Leu Met Glu Leu Ile Arg Arg
 115 120 125

Asp Tyr Pro Ala Val Glu Ala Phe Gly Tyr Arg Ser Glu Asn Thr Glu
 130 135 140

Ala Asp Ala Ile Ala Ala Arg Arg Leu Glu Ile Gly Leu Ile Asp Val
 145 150 155 160

Glu Ala Leu Glu Ser Ala Gly Phe Glu Val Val Ala Asp His Pro Val
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Leu Pro Arg Leu Arg Met Glu Leu Pro Pro Ala Thr Val Leu Leu Thr
 180 185 190

Ala Lys Asp Ala Gln Arg Leu Leu Gln Glu Met Gly Ala Ile
 195 200 205

<210> 2233
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(646)
 <223> RXA01439

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 Met Thr Arg Tyr Phe
 1 5

gca gtt tcc aat ctt cag gag ctt ggc tcc ctc gaa gta cac aaa ttg 163
 Ala Val Ser Asn Leu Gln Glu Leu Gly Ser Leu Glu Val His Lys Leu
 10 15 20

tac aaa ctt cgt gta gat att ttc gtc cac gag cag cag act ccg tac 211
 Tyr Lys Leu Arg Val Asp Ile Phe Val His Glu Gln Gln Thr Pro Tyr
 25 30 35

gcg gag atc gat gac acc gat gct gcc cca acc acc aat cac atc ctg 259
 Ala Glu Ile Asp Asp Thr Asp Ala Ala Pro Thr Thr Asn His Ile Leu
 40 45 50

gtt tgg gag cgc gcc gac gcc acc cca acc aac ctc atc ggc tgc gca 307
 Val Trp Glu Arg Ala Asp Ala Thr Pro Thr Asn Leu Ile Gly Cys Ala
 55 60 65

cgc ctc gcg ccc atc acc gcc gcc gag ctt aag gcg tac acc ggc aag 355
 Arg Leu Ala Pro Ile Thr Ala Ala Glu Leu Lys Ala Tyr Thr Gly Lys
 70 75 80 85

ggc att tcg ctt gac gac gcc acc ccg ctc tca caa ctc ggc cgc gta 403
 Gly Ile Ser Leu Asp Asp Ala Thr Pro Leu Ser Gln Leu Gly Arg Val

90	95	100	
gcg gtg gca cag gaa ggg cgg ggc tcg ggg ctc tca ggt gag ctc atg Ala Val Ala Gln Glu Gly Arg Gly Ser Gly Leu Ser Gly Glu Leu Met 105 110 115			451
cgc aac gcg ctg cgt ctt gca tat gag cag tac ccc gac cgc gat gtt Arg Asn Ala Leu Arg Leu Ala Tyr Glu Gln Tyr Pro Asp Arg Asp Val 120 125 130			499
gtc ctg acc gcg cag aag cct ttg gta gat ttc tac gca gaa tac ggc Val Leu Thr Ala Gln Lys Pro Leu Val Asp Phe Tyr Ala Glu Tyr Gly 135 140 145			547
ttt gag gtc ttg ggt gag gaa tac ctt gac tcg ggt gtt cct cac ctt Phe Glu Val Leu Gly Glu Glu Tyr Leu Asp Ser Gly Val Pro His Leu 150 155 160 165			595
ccg atg ttg ctc aag gct gat gag ctt gaa agg ttc tca gac cta gac Pro Met Leu Leu Lys Ala Asp Glu Leu Glu Arg Phe Ser Asp Leu Asp 170 175 180			643
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<210> 2234

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 2234

Met Thr Arg Tyr Phe Ala Val Ser Asn Leu Gln Glu Leu Gly Ser Leu 1 5 10 15
Glu Val His Lys Leu Tyr Lys Leu Arg Val Asp Ile Phe Val His Glu 20 25 30
Gln Gln Thr Pro Tyr Ala Glu Ile Asp Asp Thr Asp Ala Ala Pro Thr 35 40 45
Thr Asn His Ile Leu Val Trp Glu Arg Ala Asp Ala Thr Pro Thr Asn 50 55 60
Leu Ile Gly Cys Ala Arg Leu Ala Pro Ile Thr Ala Ala Glu Leu Lys 65 70 75 80
Ala Tyr Thr Gly Lys Gly Ile Ser Leu Asp Asp Ala Thr Pro Leu Ser 85 90 95
Gln Leu Gly Arg Val Ala Val Ala Gln Glu Gly Arg Gly Ser Gly Leu 100 105 110
Ser Gly Glu Leu Met Arg Asn Ala Leu Arg Leu Ala Tyr Glu Gln Tyr 115 120 125
Pro Asp Arg Asp Val Val Leu Thr Ala Gln Lys Pro Leu Val Asp Phe 130 135 140
Tyr Ala Glu Tyr Gly Phe Glu Val Leu Gly Glu Glu Tyr Leu Asp Ser

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<210> 2235
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1108)
<223> RXA01440
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Met Lys Thr Lys Trp 5																
tta gcg atc att cca ttc gtg gcg ctt gcg gtg gtt gca tgc tct gat 163																
Leu Ala Ile Ile Pro Phe Val Ala Leu Ala Val Val Ala Cys Ser Asp 20																
acg cag ccg ccg gtt aca gaa aca gtg aca gaa acc gcc ccg caa cct 211																
Thr Gln Pro Pro Val Thr Glu Thr Val Thr Glu Thr Ala Pro Gln Pro 35																
act tct gaa acg gca gcg cag cca cca caa ccc acg aca cct gcg gaa 259																
Thr Ser Glu Thr Ala Ala Gln Pro Pro Gln Pro Thr Thr Pro Ala Glu 50																
acg acc acg cag cag gca gaa ggt atc aac ttg acg cct cgc tac act 307																
Thr Thr Thr Gln Gln Ala Glu Gly Ile Asn Leu Thr Thr Pro Arg Tyr Thr 65																
cgc caa aat gtg ggg cac ttt tcc agt ggt tat cag cct gga cag gtg 355																
Arg Gln Asn Val Gly His Phe Ser Ser Gly Tyr Gln Pro Gly Gln Val 85																
agt ttt tcc tca gct gat gga acc att aaa tgt gag ttt cgc ccc atg 403																
Ser Phe Ser Ser Ala Asp Gly Thr Ile Lys Cys Glu Phe Arg Pro Met 100																
gaa cag gac gca cct atc aac cgg gag ccc tcc acc gat tgg cgg ttg 451																
Glu Gln Asp Ala Pro Ile Asn Arg Glu Pro Ser Thr Asp Trp Arg Leu 115																
agt ttc gtg cag ggt gcg tgc caa ttc gac gat ggt tac gta gtg gcg 499																
Ser Phe Val Gln Gly Ala Cys Gln Phe Asp Asp Gly Tyr Val Val Ala 130																
gat aca aat gtg gaa aac aga cca ggt ttt gct gag tac acc acg gcg 547																
Asp Thr Asn Val Glu Asn Arg Pro Gly Phe Ala Glu Tyr Thr Thr Ala 145																

att tct cat gtc atg ccg gaa aat tac acc acg ttg ccg ccg gga acc 595
 Ile Ser His Val Met Pro Glu Asn Tyr Thr Thr Leu Pro Pro Gly Thr
 150 155 160 165

tac atc gat tta cac acc atg gct tgt ttc acc gag tct gcc gat gaa 643
 Tyr Ile Asp Leu His Thr Met Ala Cys Phe Thr Glu Ser Ala Asp Glu
 170 175 180

att tcc tgc att aag tac gcg acc aat gaa aca ttc cgc atc agc gcg 691
 Ile Ser Cys Ile Lys Tyr Ala Thr Asn Glu Thr Phe Arg Ile Ser Ala
 185 190 195

cag ggt ttt gag atg ctc tca aat gcc cag cgc gac gcg gaa cta acc 739
 Gln Gly Phe Glu Met Leu Ser Asn Ala Gln Arg Asp Ala Glu Leu Thr
 200 205 210

aca caa ggt ggc ttg tac cag gca ttt tcc aac atc gcg gaa tta cgg 787
 Thr Gln Gly Gly Leu Tyr Gln Ala Phe Ser Asn Ile Ala Glu Leu Arg
 215 220 225

ttc agt gac ggc aac gcc atg tca tgt ttc ttt gac gcg ccg gga tcg 835
 Phe Ser Asp Gly Asn Ala Met Ser Cys Phe Phe Asp Ala Pro Gly Ser
 230 235 240 245

caa gat ttc tgg tgc caa aca ctc agc acc ccc ggc tgg gac gac ggc 883
 Gln Asp Phe Trp Cys Gln Thr Leu Ser Thr Pro Gly Trp Asp Asp Gly
 250 255 260

agc aac ctc att cat ttg acg gtc acc ggc gga aaa ctc agc ctg atg 931
 Ser Asn Leu Ile His Leu Thr Val Thr Gly Gly Lys Leu Ser Leu Met
 265 270 275

ggc acc caa gtg ggc aac ccc ggc ctc gac tat ttc cgc ggc cgc cag 979
 Gly Thr Gln Val Gly Asn Pro Gly Leu Asp Tyr Phe Arg Gly Arg Gln
 280 285 290

ctc att gag gcg cca aat tcg ctt ctc gac gcc tcc ctc tcc gta aca 1027
 Leu Ile Glu Ala Pro Asn Ser Leu Leu Asp Ala Ser Leu Ser Val Thr
 295 300 305

ctc gac ggc gat cgg gtg cgt ttc cgc acc gcg acc ggc gag gag atg 1075
 Leu Asp Gly Asp Arg Val Arg Phe Arg Thr Ala Thr Gly Glu Glu Met
 310 315 320 325

tgg gtg agt tcc agt gac tac gga tta ggc gtc taggtctgag aacctttcaa 1128
 Trp Val Ser Ser Ser Asp Tyr Gly Leu Gly Val
 330 335

gct 1131

<210> 2236

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 2236

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 20 25 30
 Thr Ala Pro Gln Pro Thr Ser Glu Thr Ala Ala Gln Pro Pro Gln Pro
 35 40 45
 Thr Thr Pro Ala Glu Thr Thr Thr Gln Gln Ala Glu Gly Ile Asn Leu
 50 55 60
 Thr Pro Arg Tyr Thr Arg Gln Asn Val Gly His Phe Ser Ser Gly Tyr
 65 70 75 80
 Gln Pro Gly Gln Val Ser Phe Ser Ser Ala Asp Gly Thr Ile Lys Cys
 85 90 95
 Glu Phe Arg Pro Met Glu Gln Asp Ala Pro Ile Asn Arg Glu Pro Ser
 100 105 110
 Thr Asp Trp Arg Leu Ser Phe Val Gln Gly Ala Cys Gln Phe Asp Asp
 115 120 125
 Gly Tyr Val Val Ala Asp Thr Asn Val Glu Asn Arg Pro Gly Phe Ala
 130 135 140
 Glu Tyr Thr Thr Ala Ile Ser His Val Met Pro Glu Asn Tyr Thr Thr
 145 150 155 160
 Leu Pro Pro Gly Thr Tyr Ile Asp Leu His Thr Met Ala Cys Phe Thr
 165 170 175
 Glu Ser Ala Asp Glu Ile Ser Cys Ile Lys Tyr Ala Thr Asn Glu Thr
 180 185 190
 Phe Arg Ile Ser Ala Gln Gly Phe Glu Met Leu Ser Asn Ala Gln Arg
 195 200 205
 Asp Ala Glu Leu Thr Thr Gln Gly Gly Leu Tyr Gln Ala Phe Ser Asn
 210 215 220
 Ile Ala Glu Leu Arg Phe Ser Asp Gly Asn Ala Met Ser Cys Phe Phe
 225 230 235 240
 Asp Ala Pro Gly Ser Gln Asp Phe Trp Cys Gln Thr Leu Ser Thr Pro
 245 250 255
 Gly Trp Asp Asp Gly Ser Asn Leu Ile His Leu Thr Val Thr Gly Gly
 260 265 270
 Lys Leu Ser Leu Met Gly Thr Gln Val Gly Asn Pro Gly Leu Asp Tyr
 275 280 285
 Phe Arg Gly Arg Gln Leu Ile Glu Ala Pro Asn Ser Leu Leu Asp Ala
 290 295 300
 Ser Leu Ser Val Thr Leu Asp Gly Asp Arg Val Arg Phe Arg Thr Ala
 305 310 315 320
 Thr Gly Glu Glu Met Trp Val Ser Ser Ser Asp Tyr Gly Leu Gly Val
 325 330 335

<210> 2237
 <211> 1152
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1129)
 <223> RXA01441

<400> 2237

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aagtggactc cagcacacct cgtgagatgg caggttcac atg gct aga acg aca 115
                                   Met Ala Arg Thr Thr
                                   1 5

aca gcg cac gca gtt ctc atg gcg ctt agt tca gtc ggg ctt ttg atg 163
Thr Ala His Ala Val Leu Met Ala Leu Ser Val Gly Leu Leu Met
              10              15              20

ctc cag gcc tgc tcc gaa cag gaa caa acc cca gaa caa acg cca gcg 211
Leu Gln Ala Cys Ser Glu Gln Glu Gln Thr Pro Glu Gln Thr Pro Ala
              25              30              35

ccc acc ctg act tcg cag gct ccc gag act cct caa gcc tca aca acc 259
Pro Thr Leu Thr Ser Gln Ala Pro Glu Thr Pro Gln Ala Ser Thr Thr
              40              45              50

tcc tca gca agc tcc aca gca act ccc ata gca act ccc ata gca gcc 307
Ser Ser Ala Ser Ser Thr Ala Thr Pro Ile Ala Thr Pro Ile Ala Ala
              55              60              65

acc gag ttg gat tat ctc cac atc gat cca gca acg tat gac atc ggt 355
Thr Glu Leu Asp Tyr Leu His Ile Asp Pro Ala Thr Tyr Asp Ile Gly
              70              75              80              85

gtc caa gac caa gaa act gcc gta ttt acc act ggc gat ggg atc aca 403
Val Gln Asp Gln Glu Thr Ala Val Phe Thr Thr Gly Asp Gly Ile Thr
              90              95              100

gcg cag tgt ttc ttc gag gca aca ccg ggg gag acc agc tat cag atc 451
Ala Gln Cys Phe Phe Glu Ala Thr Pro Gly Glu Thr Ser Tyr Gln Ile
              105              110              115

aag gag ttt gat ttc gac gaa act gcg gga acg tgc gct ttt ggt gat 499
Lys Glu Phe Asp Phe Asp Glu Thr Ala Gly Thr Cys Ala Phe Gly Asp
              120              125              130

caa cac atc agc gtc acc acg gat gaa aat gtc cgg gaa cgc ttt gcc 547
Gln His Ile Ser Val Thr Thr Asp Glu Asn Val Arg Glu Arg Phe Ala
              135              140              145

gaa ttg agt gaa acc gaa gaa gaa tta cca gaa gcg caa gcg act ctc 595
Glu Leu Ser Glu Thr Glu Glu Glu Leu Pro Glu Ala Gln Ala Thr Leu
              150              155              160              165

gat gtt ggt gag atg gtg cat ctt ggt cac atg ggt tgt tgg gcg ccg 643
Asp Val Gly Glu Met Val His Leu Gly His Met Gly Cys Trp Ala Pro
              170              175              180

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agt gta tcg gag ttt agt tgt ctc gat ttc gcc tcc aac cag gcg ttc 691
 Ser Val Ser Glu Phe Ser Cys Leu Asp Phe Ala Ser Asn Gln Ala Phe
 185 190 195

acc atg aat gaa cag ggc ttc cat gag ctt gat cct gca aaa gcc act 739
 Thr Met Asn Glu Gln Gly Phe His Glu Leu Asp Pro Ala Lys Ala Thr
 200 205 210

gag cag cta att aat tcg agt ggc cag gtt caa acg tta tcg aaa atg 787
 Glu Gln Leu Ile Asn Ser Ser Gly Gln Val Gln Thr Leu Ser Lys Met
 215 220 225

acg aat ttc cag ttc acc gat ggc acc agc atc acc tgt gtc agt gag 835
 Thr Asn Phe Gln Phe Thr Asp Gly Thr Ser Ile Thr Cys Val Ser Glu
 230 235 240 245

ttg cag gcg gaa gag ttc ttg tgc cac aac agt ggt cct gga ggc tgg 883
 Leu Gln Ala Glu Glu Phe Leu Cys His Asn Ser Gly Pro Gly Gly Trp
 250 255 260

tca act tca gct ggc cct gcc aac acc ctg tgg tgg aat ctg aac cag 931
 Ser Thr Ser Ala Gly Pro Ala Asn Thr Leu Trp Trp Asn Leu Asn Gln
 265 270 275

gcc gac tcc gag ttt gag ggt gct cgc ccc acg aat cca acg caa agc 979
 Ala Asp Ser Glu Phe Glu Gly Ala Arg Pro Thr Asn Pro Thr Gln Ser
 280 285 290

gtt tat aaa tct caa caa ata ttc ggt ccg gga tcg tat ctc ctc gcg 1027
 Val Tyr Lys Ser Gln Gln Ile Phe Gly Pro Gly Ser Tyr Leu Leu Ala
 295 300 305

aac ggt gtg agt gca gaa ttt gat gga acc acc ctc acg ctg acc acg 1075
 Asn Gly Val Ser Ala Glu Phe Asp Gly Thr Thr Leu Thr Leu Thr Thr
 310 315 320 325

cct cag ggg aat cag tat tgg gca aac aca cac gat ttt gga gcc ggc 1123
 Pro Gln Gly Asn Gln Tyr Trp Ala Asn Thr His Asp Phe Gly Ala Gly
 330 335 340

aca cac taattttagg agcactgatg aaa 1152
 Thr His

<210> 2238

<211> 343

<212> PRT

<213> Corynebacterium glutamicum

<400> 2238

Met Ala Arg Thr Thr Thr Ala His Ala Val Leu Met Ala Leu Ser Ser
 1 5 10 15

Val Gly Leu Leu Met Leu Gln Ala Cys Ser Glu Gln Glu Gln Thr Pro
 20 25 30

Glu Gln Thr Pro Ala Pro Thr Leu Thr Ser Gln Ala Pro Glu Thr Pro
 35 40 45

Gln Ala Ser Thr Thr Ser Ser Ala Ser Ser Thr Ala Thr Pro Ile Ala

50					55					60					
Thr	Pro	Ile	Ala	Ala	Thr	Glu	Leu	Asp	Tyr	Leu	His	Ile	Asp	Pro	Ala
65					70					75					80
Thr	Tyr	Asp	Ile	Gly	Val	Gln	Asp	Gln	Glu	Thr	Ala	Val	Phe	Thr	Thr
				85					90					95	
Gly	Asp	Gly	Ile	Thr	Ala	Gln	Cys	Phe	Phe	Glu	Ala	Thr	Pro	Gly	Glu
				100				105					110		
Thr	Ser	Tyr	Gln	Ile	Lys	Glu	Phe	Asp	Phe	Asp	Glu	Thr	Ala	Gly	Thr
		115					120					125			
Cys	Ala	Phe	Gly	Asp	Gln	His	Ile	Ser	Val	Thr	Thr	Asp	Glu	Asn	Val
	130					135					140				
Arg	Glu	Arg	Phe	Ala	Glu	Leu	Ser	Glu	Thr	Glu	Glu	Glu	Leu	Pro	Glu
145					150					155					160
Ala	Gln	Ala	Thr	Leu	Asp	Val	Gly	Glu	Met	Val	His	Leu	Gly	His	Met
				165					170					175	
Gly	Cys	Trp	Ala	Pro	Ser	Val	Ser	Glu	Phe	Ser	Cys	Leu	Asp	Phe	Ala
			180					185					190		
Ser	Asn	Gln	Ala	Phe	Thr	Met	Asn	Glu	Gln	Gly	Phe	His	Glu	Leu	Asp
		195					200					205			
Pro	Ala	Lys	Ala	Thr	Glu	Gln	Leu	Ile	Asn	Ser	Ser	Gly	Gln	Val	Gln
	210					215					220				
Thr	Leu	Ser	Lys	Met	Thr	Asn	Phe	Gln	Phe	Thr	Asp	Gly	Thr	Ser	Ile
225					230					235					240
Thr	Cys	Val	Ser	Glu	Leu	Gln	Ala	Glu	Glu	Phe	Leu	Cys	His	Asn	Ser
				245					250					255	
Gly	Pro	Gly	Gly	Trp	Ser	Thr	Ser	Ala	Gly	Pro	Ala	Asn	Thr	Leu	Trp
			260					265					270		
Trp	Asn	Leu	Asn	Gln	Ala	Asp	Ser	Glu	Phe	Glu	Gly	Ala	Arg	Pro	Thr
		275					280					285			
Asn	Pro	Thr	Gln	Ser	Val	Tyr	Lys	Ser	Gln	Gln	Ile	Phe	Gly	Pro	Gly
	290					295					300				
Ser	Tyr	Leu	Leu	Ala	Asn	Gly	Val	Ser	Ala	Glu	Phe	Asp	Gly	Thr	Thr
305					310					315					320
Leu	Thr	Leu	Thr	Thr	Pro	Gln	Gly	Asn	Gln	Tyr	Trp	Ala	Asn	Thr	His
				325					330					335	
Asp	Phe	Gly	Ala	Gly	Thr	His									
			340												

<210> 2239

<211> 1116

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1093)

<223> RXA01445

<400> 2239

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                                         Met Ile Pro Leu Ile
                                         1 5

aat gta cgt ttt ccc gtt gcc gcc tta cct ctc gca tta gtg gcg act 163
Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr
                        10 15 20

gta tgg ctt aat gct tgg gca gac cat ctt ctc cta act ggt ttt att 211
Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile
                        25 30 35

gtt tat ctt gct gtg gaa tac gca aca agc cgt ggg cgc ttc gct ctc 259
Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu
                        40 45 50

gca ttg att ttg gga gtt gaa tgg atc tta att gct tat ggg gta gct 307
Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala
                        55 60 65

ttg gaa agg cct ctt gag gct aaa gac tct cca tct ctc att acc gaa 355
Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu
                        70 75 80 85

att ttg ctc ata ctt gta gca gct ggc aca ggg gca ggt cgg tgg aaa 403
Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly Ala Gly Arg Trp Lys
                        90 95 100

att ttg agt gaa cgc aag caa cgt gca att act cag cag gaa atc atc 451
Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile
                        105 110 115

aaa aaa atc cgt act gat ata gcg cac tat ttg cat gac agt atg gca 499
Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala
                        120 125 130

aga tcg ttg gca ata atg ata gtt caa tca aag ctg act gaa cta gag 547
Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu
                        135 140 145

cct gat cca aaa aag att caa gaa aaa cta aac agt att gcc aaa att 595
Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile
                        150 155 160 165

gga caa gag gca gtg gct gat ttg cat caa tta gtt aga cac ctc gtg 643
Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val
                        170 175 180

gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca 691
Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala
                        185 190 195

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gtt tct att cat gac acg gtt aat tct gcc att cag tta tta gta gat 739
 Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp
 200 205 210
 gca gga cat gtc gtt tcc ttt gac agt aga aaa aag aac tat aag ctg 787
 Ala Gly His Val Val Ser Phe Asp Ser Arg Lys Lys Asn Tyr Lys Leu
 215 220 225
 gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc 835
 Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val
 230 235 240 245
 tgt aat gca att aaa cat tct ccg ccc aag gca aac gtt act att cgc 883
 Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg
 250 255 260
 ata aca gaa aaa gca cag tct ctt cag att cta gta atg aat cct att 931
 Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu Val Met Asn Pro Ile
 265 270 275
 gga gat tgg cat gca aat ggg gag tcc gca att cca ggt gtg ggc att 979
 Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile Pro Gly Val Gly Ile
 280 285 290
 ggc gta gaa agc tta acc aga agg ata cgt aat att aaa gga cag gtc 1027
 Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn Ile Lys Gly Gln Val
 295 300 305
 tgt gtg act tca ctg caa gga tac tgg aaa gta gtt att tca cta cct 1075
 Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val Val Ile Ser Leu Pro
 310 315 320 325
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 Leu Lys Cys Glu Asp Ser
 330

<210> 2240

<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 2240

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 Leu Thr Gly Phe Ile Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg
 35 40 45
 Gly Arg Phe Ala Leu Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile
 50 55 60
 Ala Tyr Gly Val Ala Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro
 65 70 75 80
 Ser Leu Ile Thr Glu Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly
 85 90 95

Ala Gly Arg Trp Lys Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr
 100 105 110
 Gln Gln Glu Ile Ile Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu
 115 120 125
 His Asp Ser Met Ala Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys
 130 135 140
 Leu Thr Glu Leu Glu Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn
 145 150 155 160
 Ser Ile Ala Lys Ile Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu
 165 170 175
 Val Arg His Leu Val Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe
 180 185 190
 Gly Ala Trp Ala Ala Val Ser Ile His Asp Thr Val Asn Ser Ala Ile
 195 200 205
 Gln Leu Leu Val Asp Ala Gly His Val Val Ser Phe Asp Ser Arg Lys
 210 215 220
 Lys Asn Tyr Lys Leu Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala
 225 230 235 240
 Phe Asn Glu Ala Val Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala
 245 250 255
 Asn Val Thr Ile Arg Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu
 260 265 270
 Val Met Asn Pro Ile Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile
 275 280 285
 Pro Gly Val Gly Ile Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn
 290 295 300
 Ile Lys Gly Gln Val Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val
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 Val Ile Ser Leu Pro Leu Lys Cys Glu Asp Ser
 325 330

<210> 2241

<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> RXA01447

<400> 2241

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 Met Arg Leu Leu Val

1

5

ttg cgg tgc gat gcc cca cac atc aac gaa ttc cct gcc ctt tcc acc	163
Leu Arg Cys Asp Ala Pro His Ile Asn Glu Phe Pro Ala Leu Ser Thr	
10 15 20	
tct gtg gag atc cac gat ttg cct gcg gtg ccc acc cga aaa gac ctc	211
Ser Val Glu Ile His Asp Leu Pro Ala Val Pro Thr Arg Lys Asp Leu	
25 30 35	
aaa att ctt gat gat gtg gcc ttt gat gtg ctc cct cag gat ccc acg	259
Lys Ile Leu Asp Asp Val Ala Phe Asp Val Leu Pro Gln Asp Pro Thr	
40 45 50	
cct tct ctc gat gag atc gcc aag cag cct gat gtc gag cat ttg agc	307
Pro Ser Leu Asp Glu Ile Ala Lys Gln Pro Asp Val Glu His Leu Ser	
55 60 65	
agc cct aag ttt gcg cca caa cag cct gaa acc cgt ttg cgc atc gtg	355
Ser Pro Lys Phe Ala Pro Gln Gln Pro Glu Thr Arg Leu Arg Ile Val	
70 75 80 85	
gtg atc ggt tcg gat gca gcg ctg tct gcg gtc ctg act cgt ctc atg	403
Val Ile Gly Ser Asp Ala Ala Leu Ser Ala Val Leu Thr Arg Leu Met	
90 95 100	
cgc gcc gat aat ttg tgg gcg gag att gga ttc gtg ccc gtt ggt cct	451
Arg Ala Asp Asn Leu Trp Ala Glu Ile Gly Phe Val Pro Val Gly Pro	
105 110 115	
tca acg gct gcg aag aac tgg ggt ctg ccc gcc gat gag gct gcc gcg	499
Ser Thr Ala Ala Lys Asn Trp Gly Leu Pro Ala Asp Glu Ala Ala Ala	
120 125 130	
ctt gag ctc gca ctg acc gga ttg gtc aat cct gcc ccg ctc atc cgc	547
Leu Glu Leu Ala Leu Thr Gly Leu Val Asn Pro Ala Pro Leu Ile Arg	
135 140 145	
gat gac gtt gcg gtc gcc gtc gcc ggt tca gcc acc atc acc aac tgg	595
Asp Asp Val Ala Val Ala Val Ala Gly Ser Ala Thr Ile Thr Asn Trp	
150 155 160 165	
gag ccg ggt gag atc acc ggc gaa gtc atc gtc gat gat cat gtt ctc	643
Glu Pro Gly Glu Ile Thr Gly Glu Val Ile Val Asp Asp His Val Leu	
170 175 180	
atc cgc cac gag gct gcc tcg aag gcc cca cgc cgt ggc gtc tac ggt	691
Ile Arg His Glu Ala Ala Ser Lys Ala Pro Arg Arg Gly Val Tyr Gly	
185 190 195	
gcc cgc ttg gtg ccg atg ctt gac gcc cca ggc atc gct gcg gtc atc	739
Ala Arg Leu Val Pro Met Leu Asp Ala Pro Gly Ile Ala Ala Val Ile	
200 205 210	
atg gac act ccc ctg ccc ggc gag gtg ccc tcc cgc agc ctg ttc cct	787
Met Asp Thr Pro Leu Pro Gly Glu Val Pro Ser Arg Ser Leu Phe Pro	
215 220 225	
cgc ccc tcg ggc tcg gtt att cca gag agc ttt tcg acg ggc cgt gcc	835
Arg Pro Ser Gly Ser Val Ile Pro Glu Ser Phe Ser Thr Gly Arg Ala	
230 235 240 245	

atg caa gcc ggc ggc ccc tcg cta caa atc cgg gtt gac gga att tcc 883
 Met Gln Ala Gly Gly Pro Ser Leu Gln Ile Arg Val Asp Gly Ile Ser
 250 255 260

cgc aaa cgt aaa gtg gag cgc gtt acc ttc tat cga cat ttg cgc gat 931
 Arg Lys Arg Lys Val Glu Arg Val Thr Phe Tyr Arg His Leu Arg Asp
 265 270 275

ctc caa atc gtg cgg ccg taaaacaagg agccagcatg gca 972
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<210> 2242

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 2242

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Pro Ala Leu Ser Thr Ser Val Glu Ile His Asp Leu Pro Ala Val Pro
 20 25 30

Thr Arg Lys Asp Leu Lys Ile Leu Asp Asp Val Ala Phe Asp Val Leu
 35 40 45

Pro Gln Asp Pro Thr Pro Ser Leu Asp Glu Ile Ala Lys Gln Pro Asp
 50 55 60

Val Glu His Leu Ser Ser Pro Lys Phe Ala Pro Gln Gln Pro Glu Thr
 65 70 75 80

Arg Leu Arg Ile Val Val Ile Gly Ser Asp Ala Ala Leu Ser Ala Val
 85 90 95

Leu Thr Arg Leu Met Arg Ala Asp Asn Leu Trp Ala Glu Ile Gly Phe
 100 105 110

Val Pro Val Gly Pro Ser Thr Ala Ala Lys Asn Trp Gly Leu Pro Ala
 115 120 125

Asp Glu Ala Ala Ala Leu Glu Leu Ala Leu Thr Gly Leu Val Asn Pro
 130 135 140

Ala Pro Leu Ile Arg Asp Asp Val Ala Val Ala Val Ala Gly Ser Ala
 145 150 155 160

Thr Ile Thr Asn Trp Glu Pro Gly Glu Ile Thr Gly Glu Val Ile Val
 165 170 175

Asp Asp His Val Leu Ile Arg His Glu Ala Ala Ser Lys Ala Pro Arg
 180 185 190

Arg Gly Val Tyr Gly Ala Arg Leu Val Pro Met Leu Asp Ala Pro Gly
 195 200 205

Ile Ala Ala Val Ile Met Asp Thr Pro Leu Pro Gly Glu Val Pro Ser
 210 215 220

Arg Ser Leu Phe Pro Arg Pro Ser Gly Ser Val Ile Pro Glu Ser Phe
 225 230 235 240
 Ser Thr Gly Arg Ala Met Gln Ala Gly Gly Pro Ser Leu Gln Ile Arg
 245 250 255
 Val Asp Gly Ile Ser Arg Lys Arg Lys Val Glu Arg Val Thr Phe Tyr
 260 265 270
 Arg His Leu Arg Asp Leu Gln Ile Val Arg Pro
 275 280

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 <222> (101)..(379)
 <223> RXA01452

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 Val Ile Arg Ser Phe
 1 5
 gcc gac cgc gac acc gag ttg gtc tgg ttg cgt gaa ggt gcg aaa cgc 163
 Ala Asp Arg Asp Thr Glu Leu Val Trp Leu Arg Glu Gly Ala Lys Arg
 10 15 20
 gtc gat ccg cga ata cac aaa gtg gcg aat cgg aag ctg cat ctg ctg 211
 Val Asp Pro Arg Ile His Lys Val Ala Asn Arg Lys Leu His Leu Leu
 25 30 35
 gac gcg gcg acg acc ctc gat gct ctg cgt gtg act ccg ggg aat cgc 259
 Asp Ala Ala Thr Thr Leu Asp Ala Leu Arg Val Thr Pro Gly Asn Arg
 40 45 50
 ctg gaa acg ctc gag ggt gat cga gtc ggt cag tac agc att cga gtc 307
 Leu Glu Thr Leu Glu Gly Asp Arg Val Gly Gln Tyr Ser Ile Arg Val
 55 60 65
 aac gac cag tgg cgg atc tgc ttc cgt tgg aac gac tcg ggc ccc gaa 355
 Asn Asp Gln Trp Arg Ile Cys Phe Arg Trp Asn Asp Ser Gly Pro Glu
 70 75 80 85
 aac gtc gag atc gtg gat tat cac tgaggaggag acgatggctc aga 402
 Asn Val Glu Ile Val Asp Tyr His
 90

<210> 2244
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2244

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 Glu Gly Ala Lys Arg Val Asp Pro Arg Ile His Lys Val Ala Asn Arg
 20 25 30
 Lys Leu His Leu Leu Asp Ala Ala Thr Thr Leu Asp Ala Leu Arg Val
 35 40 45
 Thr Pro Gly Asn Arg Leu Glu Thr Leu Glu Gly Asp Arg Val Gly Gln
 50 55 60
 Tyr Ser Ile Arg Val Asn Asp Gln Trp Arg Ile Cys Phe Arg Trp Asn
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 Asp Ser Gly Pro Glu Asn Val Glu Ile Val Asp Tyr His
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<211> 645

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXA01456

<400> 2245

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 Met Asn Asp Ser Ile
 1 5
 ttt agt ccc caa gca ctg aat aaa gcg atg ctc gaa gcc gtc gag ttt 163
 Phe Ser Pro Gln Ala Leu Asn Lys Ala Met Leu Glu Ala Val Glu Phe
 10 15 20
 atc cac gcc gaa ggt tgg gac gcc ggc cct acc ctg ttc gca ttg gtc 211
 Ile His Ala Glu Gly Trp Asp Ala Gly Pro Thr Leu Phe Ala Leu Val
 25 30 35
 ccc act gaa atg ctg gtg gat act ctt gat gag gca gct gac gac tcc 259
 Pro Thr Glu Met Leu Val Asp Thr Leu Asp Glu Ala Ala Asp Asp Ser
 40 45 50
 cca cta acc ctt gtt gta cag gac aac ctc cct gac aac ttg ctg cca 307
 Pro Leu Thr Leu Val Val Gln Asp Asn Leu Pro Asp Asn Leu Leu Pro
 55 60 65
 ggt tcc gaa gcg tta ggt gac tat gtg tcc cgt ttg gcg tgg cca gca 355
 Gly Ser Glu Ala Leu Gly Asp Tyr Val Ser Arg Leu Ala Trp Pro Ala
 70 75 80 85
 gag att gcc ggc gcg gtg ttg gct cag gaa att atg ttc acc gat gct 403
 Glu Ile Ala Gly Ala Val Leu Ala Gln Glu Ile Met Phe Thr Asp Ala
 90 95 100

gcc gtt gca ggc tca gaa cca cga ccc gct cgt ctt ttt tcc ggc gtt 451
 Ala Val Ala Gly Ser Glu Pro Arg Pro Ala Arg Leu Phe Ser Gly Val
 105 110 115

ttg cgc ggc gaa gca gaa ctc acc ctt ctg cag ctt cgc ccc acc gaa 499
 Leu Arg Gly Glu Ala Glu Leu Thr Leu Leu Gln Leu Arg Pro Thr Glu
 120 125 130

gag gaa ttg gca gaa cgc gga ccg ttt gct gaa gat gaa atc gaa ctg 547
 Glu Glu Leu Ala Glu Arg Gly Pro Phe Ala Glu Asp Glu Ile Glu Leu
 135 140 145

cgc ggc ggc cca ggg gtt gca ccg ggt gta atc gca gca ctg cgc tac 595
 Arg Gly Gly Pro Gly Val Ala Pro Gly Val Ile Ala Ala Leu Arg Tyr
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acc ctc gaa gcg gac cca gac gaa atc taaaaactga cttttcgtcc 642
 Thr Leu Glu Ala Asp Pro Asp Glu Ile
 170

agg 645

<210> 2246

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 2246

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 20 25 30

Leu Phe Ala Leu Val Pro Thr Glu Met Leu Val Asp Thr Leu Asp Glu
 35 40 45

Ala Ala Asp Asp Ser Pro Leu Thr Leu Val Val Gln Asp Asn Leu Pro
 50 55 60

Asp Asn Leu Leu Pro Gly Ser Glu Ala Leu Gly Asp Tyr Val Ser Arg
 65 70 75 80

Leu Ala Trp Pro Ala Glu Ile Ala Gly Ala Val Leu Ala Gln Glu Ile
 85 90 95

Met Phe Thr Asp Ala Ala Val Ala Gly Ser Glu Pro Arg Pro Ala Arg
 100 105 110

Leu Phe Ser Gly Val Leu Arg Gly Glu Ala Glu Leu Thr Leu Leu Gln
 115 120 125

Leu Arg Pro Thr Glu Glu Glu Leu Ala Glu Arg Gly Pro Phe Ala Glu
 130 135 140

Asp Glu Ile Glu Leu Arg Gly Gly Pro Gly Val Ala Pro Gly Val Ile
 145 150 155 160

Ala Ala Leu Arg Tyr Thr Leu Glu Ala Asp Pro Asp Glu Ile
 165 170

<210> 2247
 <211> 798
 <212> DNA
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<220>
 <221> CDS
 <222> (101)..(775)
 <223> RXA01457

<400> 2247

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aagttaaccc cgcccacaat ttatttgagg agttcacact gtg gcg tcc acc ccg 115
                               Val Ala Ser Thr Pro
                               1           5

cac aag cat gtc cgc gtt gca ctg gga tta gtg gcg ctc att cct ctt 163
His Lys His Val Arg Val Ala Leu Gly Leu Val Ala Leu Ile Pro Leu
                               10           15           20

tta gct gca tgt acg ggc ggc gga tcc acc gaa act tcc act gaa tcc 211
Leu Ala Ala Cys Thr Gly Gly Gly Ser Thr Glu Thr Ser Thr Glu Ser
                               25           30           35

acg gca gaa aca act cct gcg aca aca acg gaa gca acg aca act cct 259
Thr Ala Glu Thr Thr Pro Ala Thr Thr Thr Glu Ala Thr Thr Thr Pro
                               40           45           50

gct acc act gct tcg tct tca gta att gaa acg aca gag tca agc act 307
Ala Thr Thr Ala Ser Ser Ser Val Ile Glu Thr Thr Glu Ser Ser Thr
                               55           60           65

gcc gaa acg tcg acg aaa gag agt ggg gag acg tcg aca agc aaa cct 355
Ala Glu Thr Ser Thr Lys Glu Ser Gly Glu Thr Ser Thr Ser Lys Pro
                               70           75           80           85

cgt atg acc aag gac gtt gaa gtc gcc tat aaa gct ttc tcc tcg ctc 403
Arg Met Thr Lys Asp Val Glu Val Ala Tyr Lys Ala Phe Ser Ser Leu
                               90           95           100

gcg ccc gtc gag ctt ttt gag caa ttc gaa acc tgc gac ccg tca ggg 451
Ala Pro Val Glu Leu Phe Glu Gln Phe Glu Thr Cys Asp Pro Ser Gly
                               105           110           115

gtc gag gat tcc ttc gcg tgc aac ggg ccg gaa gtt ggc caa ttc caa 499
Val Glu Asp Ser Phe Ala Cys Asn Gly Pro Glu Val Gly Gln Phe Gln
                               120           125           130

ttc ttt gac aat gcg tcg aag gcc acg agc acg acg cag ctg ctc acg 547
Phe Phe Asp Asn Ala Ser Lys Ala Thr Ser Thr Thr Gln Leu Leu Thr
                               135           140           145

gaa ctg cgc agc tca cgc gtg gtt gag gat tcc gga tcc aag gtt gtg 595
Glu Leu Arg Ser Ser Arg Val Val Glu Asp Ser Gly Ser Lys Val Val
                               150           155           160           165

ggc tgg acc acg att ggc acg atg tcg att atc acg gtc gtt gat aat 643
Gly Trp Thr Thr Ile Gly Thr Met Ser Ile Ile Thr Val Val Asp Asn

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170	175	180	
gac caa ggc cta gtg ctg cag caa atg gtg tcc tcc gac aaa atc gat			691
Asp Gln Gly Leu Val Leu Gln Gln Met Val Ser Ser Asp Lys Ile Asp			
185	190	195	
ccg gag gaa cgc atc tac gaa ctt ggg ctg tcg aca ccg aag gac act			739
Pro Glu Glu Arg Ile Tyr Glu Leu Gly Leu Ser Thr Pro Lys Asp Thr			
200	205	210	
gaa gag tcc tcg gaa gaa acc tca gcg tct aaa aac tagccacacg			785
Glu Glu Ser Ser Glu Glu Thr Ser Ala Ser Lys Asn			
215	220	225	
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<210> 2248			
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<400> 2248			
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Ala Leu Ile Pro Leu Leu Ala Ala Cys Thr Gly Gly Gly Ser Thr Glu			
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Thr Ser Thr Glu Ser Thr Ala Glu Thr Thr Pro Ala Thr Thr Thr Glu			
35	40	45	
Ala Thr Thr Thr Pro Ala Thr Thr Ala Ser Ser Ser Val Ile Glu Thr			
50	55	60	
Thr Glu Ser Ser Thr Ala Glu Thr Ser Thr Lys Glu Ser Gly Glu Thr			
65	70	75	80
Ser Thr Ser Lys Pro Arg Met Thr Lys Asp Val Glu Val Ala Tyr Lys			
85	90	95	
Ala Phe Ser Ser Leu Ala Pro Val Glu Leu Phe Glu Gln Phe Glu Thr			
100	105	110	
Cys Asp Pro Ser Gly Val Glu Asp Ser Phe Ala Cys Asn Gly Pro Glu			
115	120	125	
Val Gly Gln Phe Gln Phe Phe Asp Asn Ala Ser Lys Ala Thr Ser Thr			
130	135	140	
Thr Gln Leu Leu Thr Glu Leu Arg Ser Ser Arg Val Val Glu Asp Ser			
145	150	155	160
Gly Ser Lys Val Val Gly Trp Thr Thr Ile Gly Thr Met Ser Ile Ile			
165	170	175	
Thr Val Val Asp Asn Asp Gln Gly Leu Val Leu Gln Gln Met Val Ser			
180	185	190	
Ser Asp Lys Ile Asp Pro Glu Glu Arg Ile Tyr Glu Leu Gly Leu Ser			
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Asn
 225

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 <211> 1287
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1264)
 <223> RXA01463

<400> 2249

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 ctaatgagtt aaaaagggga aatttaaacc attagggggc atg gaa atg tca tac 115
 Met Glu Met Ser Tyr
 1 5
 ttc agc cat cag gac cca aat aat cca gag agt cac atc aac ttc acc 163
 Phe Ser His Gln Asp Pro Asn Asn Pro Glu Ser His Ile Asn Phe Thr
 10 15 20
 atg gcg caa atg gag atc cag cgc tgg act ttg ctg atc tca aac cca 211
 Met Ala Gln Met Glu Ile Gln Arg Trp Thr Leu Leu Ile Ser Asn Pro
 25 30 35
 gag gcg gac gct agc act ctt gtc atg gag ttg aaa acc gtc acg ggg 259
 Glu Ala Asp Ala Ser Thr Leu Val Met Glu Leu Lys Thr Val Thr Gly
 40 45 50
 gaa tcc aag cat ttt atc aac cag gct att aac gcc atg tgg gct tta 307
 Glu Ser Lys His Phe Ile Asn Gln Ala Ile Asn Ala Met Trp Ala Leu
 55 60 65
 atg aag ctg ccc att tta aga gtg gtg gta gaa act cac ttc cac gtt 355
 Met Lys Leu Pro Ile Leu Arg Val Val Val Glu Thr His Phe His Val
 70 75 80 85
 cgg att ccg tac ctg gcc cgc att atg cag gca gtc aag cag gct aaa 403
 Arg Ile Pro Tyr Leu Ala Arg Ile Met Gln Ala Val Lys Gln Ala Lys
 90 95 100
 ccg gag ttg tgg gat gag ttg gac cat cgc att gcc gaa aag ctg aca 451
 Pro Glu Leu Trp Asp Glu Leu Asp His Arg Ile Ala Glu Lys Leu Thr
 105 110 115
 ccg cgc att gct ggc cag gca ctg atg gaa gcc tcc gca ctt gca ggg 499
 Pro Arg Ile Ala Gly Gln Ala Leu Met Glu Ala Ser Ala Leu Ala Gly
 120 125 130
 ctg att act cgc tgg atc aag gaa ctg gat cca acc ttc aca gga aag 547
 Leu Ile Thr Arg Trp Ile Lys Glu Leu Asp Pro Thr Phe Thr Gly Lys
 135 140 145

aag cgt ggg cca aag ggg agt gat ggc acc ttg act ttc cgc cac gtg Lys Arg Gly Pro Lys Gly Ser Asp Gly Thr Leu Thr Phe Arg His Val 150 155 160 165	595
gac ggg cgt acg tac atc agt gga aat att gac ggt gtc acc ggc aag Asp Gly Arg Thr Tyr Ile Ser Gly Asn Ile Asp Gly Val Thr Gly Lys 170 175 180	643
ctg ttc caa aaa gct ctg gaa aaa gtg aaa cag aag ggc gag gac ctc Leu Phe Gln Lys Ala Leu Glu Lys Val Lys Gln Lys Gly Glu Asp Leu 185 190 195	691
gcg cgg gcc ctg gtc acc ttc ctg gcg ggg cgg acc aaa gtg aaa atc Ala Arg Ala Leu Val Thr Phe Leu Ala Gly Arg Thr Lys Val Lys Ile 200 205 210	739
gtc agc gcg gta tac acg ccc ctg gtg ggt ggc gtg tcc tgg att ccg Val Ser Ala Val Tyr Thr Pro Leu Val Gly Gly Val Ser Trp Ile Pro 215 220 225	787
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gcc tcg aag gtc att gac ctg gat acg atc gcc act cgt gtg gaa aat Ala Ser Lys Val Ile Asp Leu Asp Thr Ile Ala Thr Arg Val Glu Asn 250 255 260	883
ggc tac acc cca agt ccc gag cta cgc ctt tat gtg atg ggg cgg gac Gly Tyr Thr Pro Ser Pro Glu Leu Arg Leu Tyr Val Met Gly Arg Asp 265 270 275	931
ggc acc tgt agg cat ccg ggc tgc acg gtg tct gcc gac aac tgc cag Gly Thr Cys Arg His Pro Gly Cys Thr Val Ser Ala Asp Asn Cys Gln 280 285 290	979
atc gat cac gtg atc ccg ttc ggt gag ggt ggg ttg act gtg gcc tgg Ile Asp His Val Ile Pro Phe Gly Glu Gly Gly Leu Thr Val Ala Trp 295 300 305	1027
aac ttg cag tgc ctc tgc gcg cat cat cac aat atg aag act gat ggg Asn Leu Gln Cys Leu Cys Ala His His His Asn Met Lys Thr Asp Gly 310 315 320 325	1075
cgc atc cag gcg gcg att gat tcc atg ggt cgg gtc gcc tgg att ggg Arg Ile Gln Ala Ala Ile Asp Ser Met Gly Arg Val Ala Trp Ile Gly 330 335 340	1123
ccg tgc aat cgc aca gtg gta acc gaa cct gtc gga ccg ttg gcg caa Pro Cys Asn Arg Thr Val Val Thr Glu Pro Val Gly Pro Leu Ala Gln 345 350 355	1171
gag atg ccc acg ggg cag tgg ggg cag act ctg gaa gca cgg atg gag Glu Met Pro Thr Gly Gln Trp Gly Gln Thr Leu Glu Ala Arg Met Glu 360 365 370	1219
aag act ttt gaa aag ctc cgc agt tca ctc gag gta ttg gat gac Lys Thr Phe Glu Lys Leu Arg Ser Ser Leu Glu Val Leu Asp Asp 375 380 385	1264
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<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 2250

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His Ile Asn Phe Thr Met Ala Gln Met Glu Ile Gln Arg Trp Thr Leu
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Leu Ile Ser Asn Pro Glu Ala Asp Ala Ser Thr Leu Val Met Glu Leu
35 40 45
Lys Thr Val Thr Gly Glu Ser Lys His Phe Ile Asn Gln Ala Ile Asn
50 55 60
Ala Met Trp Ala Leu Met Lys Leu Pro Ile Leu Arg Val Val Val Glu
65 70 75 80
Thr His Phe His Val Arg Ile Pro Tyr Leu Ala Arg Ile Met Gln Ala
85 90 95
Val Lys Gln Ala Lys Pro Glu Leu Trp Asp Glu Leu Asp His Arg Ile
100 105 110
Ala Glu Lys Leu Thr Pro Arg Ile Ala Gly Gln Ala Leu Met Glu Ala
115 120 125
Ser Ala Leu Ala Gly Leu Ile Thr Arg Trp Ile Lys Glu Leu Asp Pro
130 135 140
Thr Phe Thr Gly Lys Lys Arg Gly Pro Lys Gly Ser Asp Gly Thr Leu
145 150 155 160
Thr Phe Arg His Val Asp Gly Arg Thr Tyr Ile Ser Gly Asn Ile Asp
165 170 175
Gly Val Thr Gly Lys Leu Phe Gln Lys Ala Leu Glu Lys Val Lys Gln
180 185 190
Lys Gly Glu Asp Leu Ala Arg Ala Leu Val Thr Phe Leu Ala Gly Arg
195 200 205
Thr Lys Val Lys Ile Val Ser Ala Val Tyr Thr Pro Leu Val Gly Gly
210 215 220
Val Ser Trp Ile Pro Gly Val Gly Phe Leu Ser Gln Glu Glu Ser Arg
225 230 235 240
Lys Leu Gly Lys Thr Ala Ser Lys Val Ile Asp Leu Asp Thr Ile Ala
245 250 255
Thr Arg Val Glu Asn Gly Tyr Thr Pro Ser Pro Glu Leu Arg Leu Tyr
260 265 270
Val Met Gly Arg Asp Gly Thr Cys Arg His Pro Gly Cys Thr Val Ser
275 280 285

Ala Asp Asn Cys Gln Ile Asp His Val Ile Pro Phe Gly Glu Gly Gly
 290 295 300

Leu Thr Val Ala Trp Asn Leu Gln Cys Leu Cys Ala His His His Asn
 305 310 315 320

Met Lys Thr Asp Gly Arg Ile Gln Ala Ala Ile Asp Ser Met Gly Arg
 325 330 335

Val Ala Trp Ile Gly Pro Cys Asn Arg Thr Val Val Thr Glu Pro Val
 340 345 350

Gly Pro Leu Ala Gln Glu Met Pro Thr Gly Gln Trp Gly Gln Thr Leu
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Glu Ala Arg Met Glu Lys Thr Phe Glu Lys Leu Arg Ser Ser Leu Glu
 370 375 380

Val Leu Asp Asp
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<210> 2251
 <211> 1155
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1132)
 <223> RXA01469

<400> 2251
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ccagatgagc agcagttcac tgactagtat tctgtaggtc atg gca ttt gca gac 115
 Met Ala Phe Ala Asp
 1 5

att gtg cgc agc gtc gaa aac cgc acc aac gca gcg acc ctc aac tgg 163
 Ile Val Arg Ser Val Glu Asn Arg Thr Asn Ala Ala Thr Leu Asn Trp
 10 15 20

tcc atc aaa aat ggc tgg aag ccc gaa gtc acc gga ttt tcc ggg tac 211
 Ser Ile Lys Asn Gly Trp Lys Pro Glu Val Thr Gly Phe Ser Gly Tyr
 25 30 35

ggc tcc ggg cgt cga gtg cgc gtc ctt gcg cgc gtg ctc atg tcc aac 259
 Gly Ser Gly Arg Arg Val Arg Val Leu Ala Arg Val Leu Met Ser Asn
 40 45 50

ccc gaa aat ttg ctt gtc gac gcc ccc tcc caa tca att acc caa caa 307
 Pro Glu Asn Leu Leu Val Asp Ala Pro Ser Gln Ser Ile Thr Gln Gln
 55 60 65

gca cag cgc ggt tgg cgc cag ttc ttc acc atc caa gtg ccc aac ctg 355
 Ala Gln Arg Gly Trp Arg Gln Phe Phe Thr Ile Gln Val Pro Asn Leu
 70 75 80 85

cca gta act gtc acc gtt ggt ggg aaa aca gtt acc tca tcc acc aac 403

Pro Val Thr Val Thr Val Gly Gly Lys Thr Val Thr Ser Ser Thr Asn	
90 95 100	
gac aac ggc tac gtt gac ctc ctg gtg gaa gac cac aac ctt gac ccc	451
Asp Asn Gly Tyr Val Asp Leu Leu Val Glu Asp His Asn Leu Asp Pro	
105 110 115	
ggc tgg cac acc atc cag atc caa gcc gaa ggt tcc acc ccc gcc gaa	499
Gly Trp His Thr Ile Gln Ile Gln Ala Glu Gly Ser Thr Pro Ala Glu	
120 125 130	
gcc cgc gtc ctc atc gtg gaa aac acc gcc cga atc gga ctc atc tcc	547
Ala Arg Val Leu Ile Val Glu Asn Thr Ala Arg Ile Gly Leu Ile Ser	
135 140 145	
gac atc gac gac acc atc atg gtc acc tgg ctt ccc cga gca ctc ctc	595
Asp Ile Asp Asp Thr Ile Met Val Thr Trp Leu Pro Arg Ala Leu Leu	
150 155 160 165	
gcc gca tgg aac tcg tgg gtt ttg cac acc aac acc cgc aaa cca gtc	643
Ala Ala Trp Asn Ser Trp Val Leu His Thr Asn Thr Arg Lys Pro Val	
170 175 180	
ccc gga atg aac cgc ttc tac gaa gaa ctc ctc aaa gac cac ccc gac	691
Pro Gly Met Asn Arg Phe Tyr Glu Glu Leu Leu Lys Asp His Pro Asp	
185 190 195	
gca ccc gtg ttc tac ctc tcc acc ggc gca tgg aac acc ttt gaa acc	739
Ala Pro Val Phe Tyr Leu Ser Thr Gly Ala Trp Asn Thr Phe Glu Thr	
200 205 210	
ctc caa gag ttc atc aac aaa cac gca ctc ccc gac ggc ccc atg ctg	787
Leu Gln Glu Phe Ile Asn Lys His Ala Leu Pro Asp Gly Pro Met Leu	
215 220 225	
ctc acc gac tgg gga cca acc ccc aca gga cta ttc cgc tca ggt caa	835
Leu Thr Asp Trp Gly Pro Thr Pro Thr Gly Leu Phe Arg Ser Gly Gln	
230 235 240 245	
gag cac aag aaa gtc caa ctg cgc aac ctg ttt atc gaa tac ccc gac	883
Glu His Lys Lys Val Gln Leu Arg Asn Leu Phe Ile Glu Tyr Pro Asp	
250 255 260	
atg aaa tgg atc ctc gtc ggc gac gat ggc caa cac gat ccc ctc atc	931
Met Lys Trp Ile Leu Val Gly Asp Asp Gly Gln His Asp Pro Leu Ile	
265 270 275	
tac ggc gaa gca gtc gaa gaa cac ccc aac cgc atc gca ggc gtt gca	979
Tyr Gly Glu Ala Val Glu Glu His Pro Asn Arg Ile Ala Gly Val Ala	
280 285 290	
atc cgt gag ctc tcc ccc ggc gaa cat gtg ctc tcc cac gga aca act	1027
Ile Arg Glu Leu Ser Pro Gly Glu His Val Leu Ser His Gly Thr Thr	
295 300 305	
gcg tca ctg tcc acc atc acg acc aac ggg ggc caa gga gtc cca gta	1075
Ala Ser Leu Ser Thr Ile Thr Thr Asn Gly Gly Gln Gly Val Pro Val	
310 315 320 325	
gtt cac ggc cgc gat gga tat gag ttg ctg cag cgc tac gag acg aag	1123
Val His Gly Arg Asp Gly Tyr Glu Leu Leu Gln Arg Tyr Glu Thr Lys	

330

335

340

ccg ttc gcc tgagtcctac tgggtgtctc atg
Pro Phe Ala

1155

<210> 2252

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 2252

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20 25 30

Gly Phe Ser Gly Tyr Gly Ser Gly Arg Arg Val Arg Val Leu Ala Arg
35 40 45

Val Leu Met Ser Asn Pro Glu Asn Leu Leu Val Asp Ala Pro Ser Gln
50 55 60

Ser Ile Thr Gln Gln Ala Gln Arg Gly Trp Arg Gln Phe Phe Thr Ile
65 70 75 80

Gln Val Pro Asn Leu Pro Val Thr Val Thr Val Gly Gly Lys Thr Val
85 90 95

Thr Ser Ser Thr Asn Asp Asn Gly Tyr Val Asp Leu Leu Val Glu Asp
100 105 110

His Asn Leu Asp Pro Gly Trp His Thr Ile Gln Ile Gln Ala Glu Gly
115 120 125

Ser Thr Pro Ala Glu Ala Arg Val Leu Ile Val Glu Asn Thr Ala Arg
130 135 140

Ile Gly Leu Ile Ser Asp Ile Asp Asp Thr Ile Met Val Thr Trp Leu
145 150 155 160

Pro Arg Ala Leu Leu Ala Ala Trp Asn Ser Trp Val Leu His Thr Asn
165 170 175

Thr Arg Lys Pro Val Pro Gly Met Asn Arg Phe Tyr Glu Glu Leu Leu
180 185 190

Lys Asp His Pro Asp Ala Pro Val Phe Tyr Leu Ser Thr Gly Ala Trp
195 200 205

Asn Thr Phe Glu Thr Leu Gln Glu Phe Ile Asn Lys His Ala Leu Pro
210 215 220

Asp Gly Pro Met Leu Leu Thr Asp Trp Gly Pro Thr Pro Thr Gly Leu
225 230 235 240

Phe Arg Ser Gly Gln Glu His Lys Lys Val Gln Leu Arg Asn Leu Phe
245 250 255

Ile Glu Tyr Pro Asp Met Lys Trp Ile Leu Val Gly Asp Asp Gly Gln
 260 265 270

His Asp Pro Leu Ile Tyr Gly Glu Ala Val Glu Glu His Pro Asn Arg
 275 280 285

Ile Ala Gly Val Ala Ile Arg Glu Leu Ser Pro Gly Glu His Val Leu
 290 295 300

Ser His Gly Thr Thr Ala Ser Leu Ser Thr Ile Thr Thr Asn Gly Gly
 305 310 315 320

Gln Gly Val Pro Val Val His Gly Arg Asp Gly Tyr Glu Leu Leu Gln
 325 330 335

Arg Tyr Glu Thr Lys Pro Phe Ala
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<210> 2253

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA01470

<400> 2253

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ggaattgaag gcagttaagt gttgccgaag gaaaccgaac atg acg aac aat gca 115
 Met Thr Asn Asn Ala
 1 5

tta acc gtg cca acc cgg acc cgt cat cag gcg gat ttg ctc acg gca 163
 Leu Thr Val Pro Thr Arg Thr Arg His Gln Ala Asp Leu Leu Thr Ala
 10 15 20

gac ttc tgg gaa gac atg ggg ttg ccc caa ctg aaa act acc atc gaa 211
 Asp Phe Trp Glu Asp Met Gly Leu Pro Gln Leu Lys Thr Thr Ile Glu
 25 30 35

gaa tcc atc gac gat gta gcc ctc cca atg cat acc gct gtt cta gaa 259
 Glu Ser Ile Asp Asp Val Ala Leu Pro Met His Thr Ala Val Leu Glu
 40 45 50

atc agc gga atg cca aag gaa ctg cgt cag acc gtg gaa tcc gca atg 307
 Ile Ser Gly Met Pro Lys Glu Leu Arg Gln Thr Val Glu Ser Ala Met
 55 60 65

gtt gtg tgt att ccg agt cct tcg gag ctg tcc ggc tcc aac agg gac 355
 Val Val Cys Ile Pro Ser Pro Ser Glu Leu Ser Gly Ser Asn Arg Asp
 70 75 80 85

ccg ctc acc gca cga tgg ttc act gca tgg cgc cgt gac cca ttc gaa 403
 Pro Leu Thr Ala Arg Trp Phe Thr Ala Trp Arg Arg Asp Pro Phe Glu
 90 95 100

ctt ggc ctc act gag tgt cga gag gtg atc acc gga act cca cgc gaa 451

Leu Gly Leu Thr Glu Cys Arg Glu Val Ile Thr Gly Thr Pro Arg Glu
 105 110 115

ctc gac aaa ctt cga gga gtg ctg gaa tct ctg gct gat gaa tac cgt 499
 Leu Asp Lys Leu Arg Gly Val Leu Glu Ser Leu Ala Asp Glu Tyr Arg
 120 125 130

ttt gaa gtt gag ctg cga atc gtt gac tagaaagcca gtgattcttt 546
 Phe Glu Val Glu Leu Arg Ile Val Asp
 135 140

agc 549

<210> 2254
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2254
 Met Thr Asn Asn Ala Leu Thr Val Pro Thr Arg Thr Arg His Gln Ala
 1 5 10 15

Asp Leu Leu Thr Ala Asp Phe Trp Glu Asp Met Gly Leu Pro Gln Leu
 20 25 30

Lys Thr Thr Ile Glu Glu Ser Ile Asp Asp Val Ala Leu Pro Met His
 35 40 45

Thr Ala Val Leu Glu Ile Ser Gly Met Pro Lys Glu Leu Arg Gln Thr
 50 55 60

Val Glu Ser Ala Met Val Val Cys Ile Pro Ser Pro Ser Glu Leu Ser
 65 70 75 80

Gly Ser Asn Arg Asp Pro Leu Thr Ala Arg Trp Phe Thr Ala Trp Arg
 85 90 95

Arg Asp Pro Phe Glu Leu Gly Leu Thr Glu Cys Arg Glu Val Ile Thr
 100 105 110

Gly Thr Pro Arg Glu Leu Asp Lys Leu Arg Gly Val Leu Glu Ser Leu
 115 120 125

Ala Asp Glu Tyr Arg Phe Glu Val Glu Leu Arg Ile Val Asp
 130 135 140

<210> 2255
 <211> 579
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> RXA01472

<400> 2255
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ctcgggtggaa accgtcgcgg aaaaatggag gatcctcgcc atg aac caa gca aac 115
Met Asn Gln Ala Asn
1 5

ctg cct gcc gaa atc gcg gac ctc tcc gat gaa acc gca ctg tgg gaa 163
Leu Pro Ala Glu Ile Ala Asp Leu Ser Asp Glu Thr Ala Leu Trp Glu
10 15 20

atc atc aac gaa tac aac tgg gac gac ggc ttc gcg gtt ccc ctt gca 211
Ile Ile Asn Glu Tyr Asn Trp Asp Asp Gly Phe Ala Val Pro Leu Ala
25 30 35

gta gtc cga cac ccc aaa tgc gac cga gcg cta gcc ctt cgc ctg ttt 259
Val Val Arg His Pro Lys Cys Asp Arg Ala Leu Ala Leu Arg Leu Phe
40 45 50

tgg gac atc gat gaa acc gcc caa atc cac cac tcc gac gaa gaa tca 307
Trp Asp Ile Asp Glu Thr Ala Gln Ile His His Ser Asp Glu Glu Ser
55 60 65

gcg atc gcc gag ttg tac gcc agc acc gca gaa aac gac cca gca gaa 355
Ala Ile Ala Glu Leu Tyr Ala Ser Thr Ala Glu Asn Asp Pro Ala Glu
70 75 80 85

ttc gac aga atc atg gac tac tgc acc aca ctg gtc gaa ggg ctc cgc 403
Phe Asp Arg Ile Met Asp Tyr Cys Thr Thr Leu Val Glu Gly Leu Arg
90 95 100

aag cag acc tat cct cgg ggc gcc aac cgt ttc gac acg gga ttt ttc 451
Lys Gln Thr Tyr Pro Arg Gly Ala Asn Arg Phe Asp Thr Gly Phe Phe
105 110 115

aac ctc gag gac cct tct ttg acc gac cgt cag cgc aaa atc cgc gcc 499
Asn Leu Glu Asp Pro Ser Leu Thr Asp Arg Gln Arg Lys Ile Arg Ala
120 125 130

ggg aaa acc aaa ttt gcg ctc aag aat ttc gag gaa gct ttc ctc caa 547
Gly Lys Thr Lys Phe Ala Leu Lys Asn Phe Glu Glu Ala Phe Leu Gln
135 140 145

cca gag cta taaaaaaggt tgtagaagaa att 579
Pro Glu Leu
150

<210> 2256

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 2256

Met Asn Gln Ala Asn Leu Pro Ala Glu Ile Ala Asp Leu Ser Asp Glu
1 5 10 15

Thr Ala Leu Trp Glu Ile Ile Asn Glu Tyr Asn Trp Asp Asp Gly Phe
20 25 30

Ala Val Pro Leu Ala Val Val Arg His Pro Lys Cys Asp Arg Ala Leu
35 40 45

Ala Leu Arg Leu Phe Trp Asp Ile Asp Glu Thr Ala Gln Ile His His

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<210> 2257
<211> 888
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(865)  
<223> RXA01473
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<400> 2257
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aaccaacaat atcctggtag ccaagaataa gatcgtgctt atg act gac atc ggt 115
Met Thr Asp Ile Gly
1 5

gat gtc gat caa ata gtc tgg gaa ttc atc cat ttc cac gat gac tcg 163
Asp Val Asp Gln Ile Val Trp Glu Phe Ile His Phe His Asp Asp Ser
10 15 20

ata aat cca ttc ttt gag ttc atc aag agt gat tgc atc aac gat gag 211
Ile Asn Pro Phe Phe Glu Phe Ile Lys Ser Asp Cys Ile Asn Asp Glu
25 30 35

gca atc gaa cgc aaa acc cag atc ctc gga atc atc ttg ggt aac gag 259
Ala Ile Glu Arg Lys Thr Gln Ile Leu Gly Ile Ile Leu Gly Asn Glu
40 45 50

cca tgc ggg agt gtt att cac gcc cgc cag aat aca ata aag ccc atg 307
Pro. Cys Gly Ser Val Ile His Ala Arg Gln Asn Thr Ile Lys Pro Met
55 60 65

agc cat acg gtc tct ttt ggc gac ggc tgg atc caa gtc ctt gag gat 355
 Ser His Thr Val Ser Phe Gly Asp Gly Trp Ile Gln Val Leu Glu Asp
 70 75 80 85

gct gca gaa acc gtg tcg atc acc gac acg ttg gat gcc ctc cga ttt 403
Ala Ala Glu Thr Val Ser Ile Thr Asp Thr Leu Asp Ala Leu Arg Phe
90 95 100

tct ccc gag caa gcg gaa tgg gct gca gaa ttc gga cca cta ctg tgc 451
 Ser Pro Glu Gln Ala Glu Trp Ala Ala Glu Phe Gly Pro Leu Leu Cys
 105 110 115

ggc cca gcg aac caa ccg ccg gcg tat ctc acg gct tta gac ggg cac 499
 Gly Pro Ala Asn Gln Pro Pro Ala Tyr Leu Thr Ala Leu Asp Gly His
 120 125 130

aca aag cta ccg ctt agc ccg cag ctg acg gag ttc tat agc tac gcc 547
 Thr Lys Leu Pro Leu Ser Pro Gln Leu Thr Glu Phe Tyr Ser Tyr Ala
 135 140 145

cga tcc tgg aca aac agt gag gcc ttg gga aac gtc att gat ccc gat 595
 Arg Ser Trp Thr Asn Ser Glu Ala Leu Gly Asn Val Ile Asp Pro Asp
 150 155 160 165

gac tac ctc gat cat ctc acc gac cct cgc ctt cat ttg cag gat ctt 643
 Asp Tyr Leu Asp His Leu Thr Asp Pro Arg Leu His Leu Gln Asp Leu
 170 175 180

ctg gat aat gag ttt gaa ccg gtg ggg gtg ctc gtc gat aag caa aat 691
 Leu Asp Asn Glu Phe Glu Arg Val Gly Val Leu Val Asp Lys Gln Asn
 185 190 195

cgc ccg ctc gac cct gcc ccg tgc gcg ctg ttc tcg ctc gac gca ctt 739
 Arg Pro Leu Asp Pro Ala Arg Cys Ala Leu Phe Ser Leu Asp Ala Leu
 200 205 210

gca cgc gcg ccc tac aac cgc gcc tac ttc gtc ttc gcc gcg ccc gag 787
 Ala Arg Ala Pro Tyr Asn Arg Ala Tyr Phe Val Phe Ala Ala Pro Glu
 215 220 225

cct gag atc tgg gcg ttt gag aac gag cac gtc cac gcg ccg gac ttg 835
 Pro Glu Ile Trp Ala Phe Glu Asn Glu His Val His Ala Pro Asp Leu
 230 235 240 245

cgc gcc tat tta caa gca cgc tta tcg acg taattacact cggtggaaac 885
 Arg Ala Tyr Leu Gln Ala Arg Leu Ser Thr
 250 255

cgt 888

<210> 2258

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 2258

Met Thr Asp Ile Gly Asp Val Asp Gln Ile Val Trp Glu Phe Ile His
 1 5 10 15

Phe His Asp Asp Ser Ile Asn Pro Phe Phe Glu Phe Ile Lys Ser Asp
 20 25 30

Cys Ile Asn Asp Glu Ala Ile Glu Arg Lys Thr Gln Ile Leu Gly Ile
 35 40 45

Ile Leu Gly Asn Glu Pro Cys Gly Ser Val Ile His Ala Arg Gln Asn
 50 55 60

Thr Ile Lys Pro Met Ser His Thr Val Ser Phe Gly Asp Gly Trp Ile
 65 70 75 80
 Gln Val Leu Glu Asp Ala Ala Glu Thr Val Ser Ile Thr Asp Thr Leu
 85 90 95
 Asp Ala Leu Arg Phe Ser Pro Glu Gln Ala Glu Trp Ala Ala Glu Phe
 100 105 110
 Gly Pro Leu Leu Cys Gly Pro Ala Asn Gln Pro Pro Ala Tyr Leu Thr
 115 120 125
 Ala Leu Asp Gly His Thr Lys Leu Pro Leu Ser Pro Gln Leu Thr Glu
 130 135 140
 Phe Tyr Ser Tyr Ala Arg Ser Trp Thr Asn Ser Glu Ala Leu Gly Asn
 145 150 155 160
 Val Ile Asp Pro Asp Asp Tyr Leu Asp His Leu Thr Asp Pro Arg Leu
 165 170 175
 His Leu Gln Asp Leu Leu Asp Asn Glu Phe Glu Arg Val Gly Val Leu
 180 185 190
 Val Asp Lys Gln Asn Arg Pro Leu Asp Pro Ala Arg Cys Ala Leu Phe
 195 200 205
 Ser Leu Asp Ala Leu Ala Arg Ala Pro Tyr Asn Arg Ala Tyr Phe Val
 210 215 220
 Phe Ala Ala Pro Glu Pro Glu Ile Trp Ala Phe Glu Asn Glu His Val
 225 230 235 240
 His Ala Pro Asp Leu Arg Ala Tyr Leu Gln Ala Arg Leu Ser Thr
 245 250 255

<210> 2259

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXA01474

<400> 2259

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ttggccctac tcgacactat aacgcaccga ggaaactgca ttg gtg gga att gct 115
 Leu Val Gly Ile Ala
 1 5

tac gcc cgt ttc cct gat acc cgc gac gat tcc atc agc cgc ggc aaa 163
 Tyr Ala Arg Phe Pro Asp Thr Arg Asp Asp Ser Ile Ser Arg Gly Lys
 10 15 20

gca cga tca gcg ttg gag aaa tcc acg ggc ctt aaa gag cgt ttc gcg 211
 Ala Arg Ser Ala Leu Glu Lys Ser Thr Gly Leu Lys Glu Arg Phe Ala

25	30	35	
cg t cat ttt cct gca att tcc ata cct gtc gat acg ggt gat gct gca			259
Arg His Phe Pro Ala Ile Ser Ile Pro Val Asp Thr Gly Asp Ala Ala			
40	45	50	
gat att ctc gta tcg ggt tgg tgg ctt tca ggt tct aaa aag aag atc			307
Asp Ile Leu Val Ser Gly Trp Trp Leu Ser Gly Ser Lys Lys Lys Ile			
55	60	65	
ctg act gca gcg gaa atc cag acc tta ttt atc aac cga ttg gcc aca			355
Leu Thr Ala Ala Glu Ile Gln Thr Leu Phe Ile Asn Arg Leu Ala Thr			
70	75	80	85
ggt cca ttg agc act caa ttg gaa act gct acc ggg ttg aaa ctg cag			403
Gly Pro Leu Ser Thr Gln Leu Glu Thr Ala Thr Gly Leu Lys Leu Gln			
90	95	100	
gtg gtg acc aat cga gag cgt atg aag atc act ctc att gaa ccc aaa			451
Val Val Thr Asn Arg Glu Arg Met Lys Ile Thr Leu Ile Glu Pro Lys			
105	110	115	
ggc aca tca gga cat gcc atc gac ccc caa gct ggc aag ggt tca agg			499
Gly Thr Ser Gly His Ala Ile Asp Pro Gln Ala Gly Lys Gly Ser Arg			
120	125	130	
ggt ggc ttc ctc ctg gac aat ggc caa gaa gat gaa tac gac gat gtc			547
Gly Gly Phe Leu Leu Asp Asn Gly Gln Glu Asp Glu Tyr Asp Asp Val			
135	140	145	
gac acc gtc aca atc ccc gat gca ctc aat gtc atc ggt tac att ctt			595
Asp Thr Val Thr Ile Pro Asp Ala Leu Asn Val Ile Gly Tyr Ile Leu			
150	155	160	165
acc cat gga act cca cct caa gaa ggc tgg aag gta gac gtg ttg gag			643
Thr His Gly Thr Pro Pro Gln Glu Gly Trp Lys Val Asp Val Leu Glu			
170	175	180	
cg t tagtcctcga tgaattcttc tcc			669
Arg			

<210> 2260

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 2260

Leu Val Gly Ile Ala Tyr Ala Arg Phe Pro Asp Thr Arg Asp Asp Ser			
1	5	10	15
Ile Ser Arg Gly Lys Ala Arg Ser Ala Leu Glu Lys Ser Thr Gly Leu			
20	25	30	
Lys Glu Arg Phe Ala Arg His Phe Pro Ala Ile Ser Ile Pro Val Asp			
35	40	45	
Thr Gly Asp Ala Ala Asp Ile Leu Val Ser Gly Trp Trp Leu Ser Gly			
50	55	60	

Ser Lys Lys Lys Ile Leu Thr Ala Ala Glu Ile Gln Thr Leu Phe Ile
65 70 75 80

Asn Arg Leu Ala Thr Gly Pro Leu Ser Thr Gln Leu Glu Thr Ala Thr
85 90 95

Gly Leu Lys Leu Gln Val Val Thr Asn Arg Glu Arg Met Lys Ile Thr
100 105 110

Leu Ile Glu Pro Lys Gly Thr Ser Gly His Ala Ile Asp Pro Gln Ala
115 120 125

Gly Lys Gly Ser Arg Gly Gly Phe Leu Leu Asp Asn Gly Gln Glu Asp
130 135 140

Glu Tyr Asp Asp Val Asp Thr Val Thr Ile Pro Asp Ala Leu Asn Val
145 150 155 160

Ile Gly Tyr Ile Leu Thr His Gly Thr Pro Pro Gln Glu Gly Trp Lys
165 170 175

Val Asp Val Leu Glu Arg
180

<210> 2261
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA01475

<400> 2261
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cgtgcacatt ggattcacac ccgtagtagt ttttggggga atg agc atc caa ggg 115
Met Ser Ile Gln Gly
1 5

ttt tcc gca ggt gac tat tct gca tgt ttt gaa ccg cgc atc gat gcg 163
Phe Ser Ala Gly Asp Tyr Ser Ala Cys Phe Glu Pro Arg Ile Asp Ala
10 15 20

tgg gtt gat att cgc ggt ccg cgg aag ccc gag tgg ttg gcg gaa aat 211
Trp Val Asp Ile Arg Gly Pro Arg Lys Pro Glu Trp Leu Ala Glu Asn
25 30 35

atc gat aat ccg ctg aga cac tgg ggc gat aat cct cat atc ccg gtg 259
Ile Asp Asn Pro Leu Arg His Trp Gly Asp Asn Pro His Ile Pro Val
40 45 50

tct gct gcg aaa aag gct gga aat att tac aaa gag acc ctt cga acc 307
Ser Ala Ala Lys Lys Ala Gly Asn Ile Tyr Lys Glu Thr Leu Arg Thr
55 60 65

atg aga gcc tca aca aag acc cca gac cag gat ccc tta aaa gaa acc 355
Met Arg Ala Ser Thr Lys Thr Pro Asp Gln Asp Pro Leu Lys Glu Thr
70 75 80 85

ctg cgc agc ttc atc gca agc atc aac cag ctc gcc gca aag aag aat 403
 Leu Arg Ser Phe Ile Ala Ser Ile Asn Gln Leu Ala Ala Lys Lys Asn
 90 95 100

ttc att gat gcc ggg gtg cgc gaa gat atc gtt gtt gcg ctg gaa aaa 451
 Phe Ile Asp Ala Gly Val Arg Glu Asp Ile Val Val Ala Leu Glu Lys
 105 110 115

cta tgc gaa gca gca gaa gct agc cca gaa gaa att cag cag gcg atc 499
 Leu Cys Glu Ala Ala Glu Ala Ser Pro Glu Glu Ile Gln Gln Ala Ile
 120 125 130

gtg atg gga gaa gaa ttc atc gag gac taacgctcca acacgtctac 546
 Val Met Gly Glu Glu Phe Ile Glu Asp
 135 140

ctt 549

<210> 2262

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 2262

Met Ser Ile Gln Gly Phe Ser Ala Gly Asp Tyr Ser Ala Cys Phe Glu
 1 5 10 15

Pro Arg Ile Asp Ala Trp Val Asp Ile Arg Gly Pro Arg Lys Pro Glu
 20 25 30

Trp Leu Ala Glu Asn Ile Asp Asn Pro Leu Arg His Trp Gly Asp Asn
 35 40 45

Pro His Ile Pro Val Ser Ala Ala Lys Lys Ala Gly Asn Ile Tyr Lys
 50 55 60

Glu Thr Leu Arg Thr Met Arg Ala Ser Thr Lys Thr Pro Asp Gln Asp
 65 70 75 80

Pro Leu Lys Glu Thr Leu Arg Ser Phe Ile Ala Ser Ile Asn Gln Leu
 85 90 95

Ala Ala Lys Lys Asn Phe Ile Asp Ala Gly Val Arg Glu Asp Ile Val
 100 105 110

Val Ala Leu Glu Lys Leu Cys Glu Ala Ala Glu Ala Ser Pro Glu Glu
 115 120 125

Ile Gln Gln Ala Ile Val Met Gly Glu Glu Phe Ile Glu Asp
 130 135 140

<210> 2263

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(442)

<223> RXA01476

<400> 2263

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gccacatgac gttgatcgac ctcaactgctg gagtgagcgc atg agc gat tca ccg 115
                                   Met Ser Asp Ser Pro
                                   1 5

tgc acc gtc gtc atc ctg aac cgc aca gct act gcg act tcc atc ctg 163
Cys Thr Val Val Ile Leu Asn Arg Thr Ala Thr Ala Thr Ser Ile Leu
              10              15              20

aga gat att aaa gcc ctc acc ggt tac ggc ctg tct gag atc agg tcg 211
Arg Asp Ile Lys Ala Leu Thr Gly Tyr Gly Leu Ser Glu Ile Arg Ser
              25              30              35

cgc atc gtt gcg gga ctt ccc gtc gtg atc gag gag atg ttc tca aac 259
Arg Ile Val Ala Gly Leu Pro Val Val Ile Glu Glu Met Phe Ser Asn
              40              45              50

gcc tgg tac gac gaa cgc gca caa ctg ttg ctg gca ctg ctg acc aaa 307
Ala Trp Tyr Asp Glu Arg Ala Gln Leu Leu Leu Ala Leu Leu Thr Lys
              55              60              65

tgg cag aac gaa gga atc aca ttc gag att cgg gaa gtc gct gag gat 355
Trp Gln Asn Glu Gly Ile Thr Phe Glu Ile Arg Glu Val Ala Glu Asp
              70              75              80              85

gat ccc atc gaa gca ggg gca ttg atc tct cta gaa gtg ctg cga aac 403
Asp Pro Ile Glu Ala Gly Ala Leu Ile Ser Leu Glu Val Leu Arg Asn
              90              95              100

atc att gag cca gac gat aat gaa tcg agg gac ggt atc tagtggtgaa 452
Ile Ile Glu Pro Asp Asp Asn Glu Ser Arg Asp Gly Ile
              105              110

cgtaaaccgcc cgg 465

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<210> 2264

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 2264

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Met Ser Asp Ser Pro Cys Thr Val Val Ile Leu Asn Arg Thr Ala Thr
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Ala Thr Ser Ile Leu Arg Asp Ile Lys Ala Leu Thr Gly Tyr Gly Leu
  20 25 30

Ser Glu Ile Arg Ser Arg Ile Val Ala Gly Leu Pro Val Val Ile Glu
  35 40 45

Glu Met Phe Ser Asn Ala Trp Tyr Asp Glu Arg Ala Gln Leu Leu Leu
  50 55 60

Ala Leu Leu Thr Lys Trp Gln Asn Glu Gly Ile Thr Phe Glu Ile Arg
  65 70 75 80

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Asp Pro Asp Ala Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr
 135 140 145
 atg atc ggt ctt gat gtc acc ctg cag acc ctt ctt acc aag aag cac 595
 Met Ile Gly Leu Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His
 150 155 160 165
 act gcg cag tgg cgc gaa ctg ggc act cca gct gct atc gca ctg gcc 643
 Thr Ala Gln Trp Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala
 170 175 180
 gac atg act gat tac tac atc aag gca tat gag acc acc gca cca cac 691
 Asp Met Thr Asp Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His
 185 190 195
 ctg ggc ggt tgc ggc ctg cac gac cca ctg gca gta ggc gtt gca gtg 739
 Leu Gly Gly Cys Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val
 200 205 210
 gac cca agc ctg gtc act ttg ctc ccc atc aac ctc aag gta gac att 787
 Asp Pro Ser Leu Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile
 215 220 225
 gag ggc gag acc cgt gga cgc acc att ggc gat gaa gtc cgc ctc aac 835
 Glu Gly Glu Thr Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn
 230 235 240 245
 gat cca gtg cgc acc tcc cgc gca gct gtc gcc gta gac gtg gat cgt 883
 Asp Pro Val Arg Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg
 250 255 260
 ttc ctt tct gaa ttc atg acc cgc atc ggc cga gtc gca gca cag cag 931
 Phe Leu Ser Glu Phe Met Thr Arg Ile Gly Arg Val Ala Ala Gln Gln
 265 270 275
 taaaagcagc tctggtgaag gtt 954

<210> 2266

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 2266

Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu Asp Leu
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 Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His Ala Gln
 20 25 30
 Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile His Gly
 35 40 45
 Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser Lys Ala
 50 55 60
 Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr His Gly
 65 70 75 80
 Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu Ser Ala
 85 90 95

Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val Val Ile
 100 105 110

Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp Ala Glu
 115 120 125

Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe Arg Ser
 130 135 140

Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln Thr Leu
 145 150 155 160

Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr Pro Ala
 165 170 175

Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala Tyr Glu
 180 185 190

Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro Leu Ala
 195 200 205

Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro Ile Asn
 210 215 220

Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile Gly Asp
 225 230 235 240

Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala Val Ala
 245 250 255

Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile Gly Arg
 260 265 270

Val Ala Ala Gln Gln
 275

<210> 2267

<211> 1119

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1096)

<223> RXA01494

<400> 2267

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acaagacttc atccaagtct gaatctgagg aataacacca gtg acg gat aat agt 115
 Val Thr Asp Asn Ser
 1 5

cag ttt cat gct gct tca gca tta gtc cag gca gct cac acg gtt agc 163
 Gln Phe His Ala Ala Ser Ala Leu Val Gln Ala Ala His Thr Val Ser
 10 15 20

gtt gtg ggg cat ctg cga ccc gat gct gat gca atc ggc agt gta gct 211
 Val Val Gly His Leu Arg Pro Asp Ala Asp Ala Ile Gly Ser Val Ala

25										30										35										
gcc	aca	gtg	gcg	gca	cta	cag	caa	ctt	ggt	aaa	gac	gcc	gta	ggt	gca	259														
Ala	Thr	Val	Ala	Ala	Leu	Gln	Gln	Leu	Gly	Lys	Asp	Ala	Val	Gly	Ala															
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atc	ggc	cag	cta	gat	tcg	atg	ccc	gag	aac	ttg	tac	acc	att	cct	ggg	307														
Ile	Gly	Gln	Leu	Asp	Ser	Met	Pro	Glu	Asn	Leu	Tyr	Thr	Ile	Pro	Gly															
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gca	tca	aac	att	aag	ttt	ggc	gat	tca	ctg	ccg	gaa	tct	gac	ctc	atc	355														
Ala	Ser	Asn	Ile	Lys	Phe	Gly	Asp	Ser	Leu	Pro	Glu	Ser	Asp	Leu	Ile															
70					75					80					85															
att	gtt	gtt	gat	tgt	ggg	tca	atc	gaa	cgc	acc	ggt	gcg	ttt	gaa	agc	403														
Ile	Val	Val	Asp	Cys	Gly	Ser	Ile	Glu	Arg	Thr	Gly	Ala	Phe	Glu	Ser															
90					95					100																				
atc	atc	gtc	aac	aat	cct	gac	aaa	gta	ttg	gtg	gtt	gat	cac	cac	gcc	451														
Ile	Ile	Val	Asn	Asn	Pro	Asp	Lys	Val	Leu	Val	Val	Asp	His	His	Ala															
105					110					115																				
acc	aat	cct	ggg	ttt	ggt	gcc	gtc	aac	tta	atc	gat	gtg	gag	gca	gaa	499														
Thr	Asn	Pro	Gly	Phe	Gly	Ala	Val	Asn	Leu	Ile	Asp	Val	Glu	Ala	Glu															
120					125					130																				
tcc	acc	acc	acg	att	tta	tat	gac	tgg	ttt	gat	gcg	atg	tcg	gtg	caa	547														
Ser	Thr	Thr	Thr	Ile	Leu	Tyr	Asp	Trp	Phe	Asp	Ala	Met	Ser	Val	Gln															
135					140					145																				
att	act	ccc	gat	atc	gcc	cac	ggc	ctt	tat	gct	gga	ctg	ctc	acc	gat	595														
Ile	Thr	Pro	Asp	Ile	Ala	His	Gly	Leu	Tyr	Ala	Gly	Leu	Leu	Thr	Asp															
150					155					160					165															
acc	ggg	tgc	ttc	agg	tgg	ggt	cga	cca	gtc	atg	cat	gac	atg	gct	aaa	643														
Thr	Gly	Cys	Phe	Arg	Trp	Gly	Arg	Pro	Val	Met	His	Asp	Met	Ala	Lys															
170					175					180																				
gaa	ctc	atg	gag	ttc	ggt	cta	gac	att	cgt	gcc	att	tca	tca	gca	ttg	691														
Glu	Leu	Met	Glu	Phe	Gly	Leu	Asp	Ile	Arg	Ala	Ile	Ser	Ser	Ala	Leu															
185					190					195																				
ctt	gat	caa	acc	tcc	gtg	gat	gat	ttg	cgt	ctt	gtt	ggc	cag	att	gtc	739														
Leu	Asp	Gln	Thr	Ser	Val	Asp	Asp	Leu	Arg	Leu	Val	Gly	Gln	Ile	Val															
200					205					210																				
tct	cgg	atc	gag	ctg	cgg	gaa	gca	ggg	cca	tat	act	ctt	gct	gtt	ctc	787														
Ser	Arg	Ile	Glu	Leu	Arg	Glu	Ala	Gly	Pro	Tyr	Thr	Leu	Ala	Val	Leu															
215					220					225																				
gtg	gca	gac	ttc	gat	acc	atc	aac	ggc	cgt	tca	cgc	gcc	gtt	gtg	gaa	835														
Val	Ala	Asp	Phe	Asp	Thr	Ile	Asn	Gly	Arg	Ser	Arg	Ala	Val	Val	Glu															
230					235					240					245															
ggc	ttg	atc	gaa	atg	gtt	cgc	gct	gtg	gaa	ggc	gca	gac	ttc	gga	gca	883														
Gly	Leu	Ile	Glu	Met	Val	Arg	Ala	Val	Glu	Gly	Ala	Asp	Phe	Gly	Ala															
250					255					260																				
gta	ttc	aaa	gaa	tat	gaa	cgt	ggc	gtc	tat	acc	gtg	tca	ctg	cgt	tcc	931														
Val	Phe	Lys	Glu	Tyr	Glu	Arg	Gly	Val	Tyr	Thr	Val	Ser	Leu	Arg	Ser															
265					270					275																				

tcc aat ttg agt gtc gct tcc ttg gca gtg cat ctt ggc ggt ggc gga 979
 Ser Asn Leu Ser Val Ala Ser Leu Ala Val His Leu Gly Gly Gly Gly
 280 285 290
 cac att cct gct gca ggc tat acc gct cgt ggt acg gaa atc gaa gcc 1027
 His Ile Pro Ala Ala Gly Tyr Thr Ala Arg Gly Thr Glu Ile Glu Ala
 295 300 305
 ctc gat acg ttg att gaa gca acc gtt acc ttg ggg gag tct ttg cga 1075
 Leu Asp Thr Leu Ile Glu Ala Thr Val Thr Leu Gly Glu Ser Leu Arg
 310 315 320 325
 agc tcg gcg cat gtc gat gtc taacaacgac tttgagcatg agt 1119
 Ser Ser Ala His Val Asp Val
 330

<210> 2268

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 2268

Val Thr Asp Asn Ser Gln Phe His Ala Ala Ser Ala Leu Val Gln Ala
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Ala His Thr Val Ser Val Val Gly His Leu Arg Pro Asp Ala Asp Ala
 20 25 30

Ile Gly Ser Val Ala Ala Thr Val Ala Ala Leu Gln Gln Leu Gly Lys
 35 40 45

Asp Ala Val Gly Ala Ile Gly Gln Leu Asp Ser Met Pro Glu Asn Leu
 50 55 60

Tyr Thr Ile Pro Gly Ala Ser Asn Ile Lys Phe Gly Asp Ser Leu Pro
 65 70 75 80

Glu Ser Asp Leu Ile Ile Val Val Asp Cys Gly Ser Ile Glu Arg Thr
 85 90 95

Gly Ala Phe Glu Ser Ile Ile Val Asn Asn Pro Asp Lys Val Leu Val
 100 105 110

Val Asp His His Ala Thr Asn Pro Gly Phe Gly Ala Val Asn Leu Ile
 115 120 125

Asp Val Glu Ala Glu Ser Thr Thr Thr Ile Leu Tyr Asp Trp Phe Asp
 130 135 140

Ala Met Ser Val Gln Ile Thr Pro Asp Ile Ala His Gly Leu Tyr Ala
 145 150 155 160

Gly Leu Leu Thr Asp Thr Gly Cys Phe Arg Trp Gly Arg Pro Val Met
 165 170 175

His Asp Met Ala Lys Glu Leu Met Glu Phe Gly Leu Asp Ile Arg Ala
 180 185 190

Ile Ser Ser Ala Leu Leu Asp Gln Thr Ser Val Asp Asp Leu Arg Leu

195	200	205
Val Gly Gln Ile Val Ser Arg Ile Glu Leu Arg Glu Ala Gly Pro Tyr 210 215 220		
Thr Leu Ala Val Leu Val Ala Asp Phe Asp Thr Ile Asn Gly Arg Ser 225 230 235 240		
Arg Ala Val Val Glu Gly Leu Ile Glu Met Val Arg Ala Val Glu Gly 245 250 255		
Ala Asp Phe Gly Ala Val Phe Lys Glu Tyr Glu Arg Gly Val Tyr Thr 260 265 270		
Val Ser Leu Arg Ser Ser Asn Leu Ser Val Ala Ser Leu Ala Val His 275 280 285		
Leu Gly Gly Gly Gly His Ile Pro Ala Ala Gly Tyr Thr Ala Arg Gly 290 295 300		
Thr Glu Ile Glu Ala Leu Asp Thr Leu Ile Glu Ala Thr Val Thr Leu 305 310 315 320		
Gly Glu Ser Leu Arg Ser Ser Ala His Val Asp Val 325 330		

<210> 2269

<211> 1041

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1018)

<223> RXA01497

<400> 2269

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gccaccagaa agacgccct ttggcaccgc gaattagtca atg gtg ggt aaa ctt	115
Met Val Gly Lys Leu	
1 5	

ccc atc atg gct gaa acc aac gaa aat gat ctt cca gtt atc gac ctt	163
Pro Ile Met Ala Glu Thr Asn Glu Asn Asp Leu Pro Val Ile Asp Leu	
10 15 20	

gcc caa atc gaa ggc tat gtt gta gat gac tcg gat gaa gat gat cca	211
Ala Gln Ile Glu Gly Tyr Val Val Asp Asp Ser Asp Glu Asp Asp Pro	
25 30 35	

gta ctt ctg cgt cca gat gga acc ccc att gaa acc tgg cgc gaa gac	259
Val Leu Leu Arg Pro Asp Gly Thr Pro Ile Glu Thr Trp Arg Glu Asp	
40 45 50	

ttc cct tat gaa gag cgc gtc acc cgc gaa gac tat gag aag gtc aag	307
Phe Pro Tyr Glu Glu Arg Val Thr Arg Glu Asp Tyr Glu Lys Val Lys	
55 60 65	

cgc tcc ctc cag atc gag ctg ctg aag tgg cag aac tgg acc aag gaa	355
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<210> 2270

<211> 306

<212> PRT

<213> Corynebacterium glutamicum

<400> 2270

Met Val Gly Lys Leu Pro Ile Met Ala Glu Thr Asn Glu Asn Asp Leu
1 5 10 15
Pro Val Ile Asp Leu Ala Gln Ile Glu Gly Tyr Val Val Asp Asp Ser
20 25 30
Asp Glu Asp Asp Pro Val Leu Leu Arg Pro Asp Gly Thr Pro Ile Glu
35 40 45
Thr Trp Arg Glu Asp Phe Pro Tyr Glu Glu Arg Val Thr Arg Glu Asp
50 55 60
Tyr Glu Lys Val Lys Arg Ser Leu Gln Ile Glu Leu Leu Lys Trp Gln
65 70 75 80
Asn Trp Thr Lys Glu Thr Gly Gln Arg His Ile Ile Leu Phe Glu Gly
85 90 95
Arg Asp Ala Ala Gly Lys Gly Gly Thr Ile Lys Arg Phe Asn Glu His
100 105 110
Leu Asn Pro Arg Gly Ala Arg Thr Val Ala Leu Glu Lys Pro Ser Pro
115 120 125
Arg Glu Ser Thr Ser Trp Tyr Phe Gln Arg Tyr Ile Gln His Phe Pro
130 135 140
Ala Ala Gly Glu Ile Val Phe Phe Asp Arg Ser Trp Tyr Asn Arg Ser
145 150 155 160
Gly Val Glu Arg Val Met Gly Phe Cys Thr Glu Ser Gln His Ala Glu
165 170 175
Phe Leu Arg Glu Val Pro Met Leu Glu Asn Met Ile Leu Gly Ser Gly
180 185 190
Ile Ser Leu Thr Lys Phe Trp Phe Ser Val Thr Arg Lys Glu Gln Arg
195 200 205
Thr Arg Phe Ala Ile Arg Gln Val Asp Pro Val Arg Gln Trp Lys Leu
210 215 220
Ser Pro Met Asp Leu Ala Ser Leu Asp Arg Trp Asp Asp Tyr Thr Arg
225 230 235 240
Ala Lys Glu Glu Gln Phe Arg Tyr Thr Asp Thr Asp Glu Ser Pro Trp
245 250 255
Ile Thr Ile Lys Ser Asn Asp Lys Lys Arg Ala Arg Ile Asn Ala Met
260 265 270
Arg Tyr Val Leu Ser Lys Phe Asp Tyr Thr Asp Lys Asp Tyr Glu Leu
275 280 285

20	25	30
Val Asn Ile Pro Met Ser Glu Phe Val Gly Arg Ile Asp Glu Ile Asp		
35	40	45
Leu Asp Arg Asp Ile Tyr Val Ile Cys Lys Leu Gly Gly Arg Ser Ala		
50	55	60
Gln Val Ala Glu Tyr Leu Glu Gln Arg Gly Ile Glu Ala Ile Asn Val		
65	70	75
Asn Gly Gly Thr Asp Gly Trp Val Ala Ala Gly Leu Pro Thr Glu Ala		
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<210> 2273

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXA01504

<400> 2273

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ttggctcgta ccgaacttag aaaactcatg ggagtttcgc atg aat atc acg tgg 115
                                   Met Asn Ile Thr Trp
                                   1 5

ctt atc ctg gcc ggt gtt tta gcc atc atc gct gtc gtg ttc ttt tat 163
Leu Ile Leu Ala Gly Val Leu Ala Ile Ile Ala Val Val Phe Phe Tyr
                10                15                20

ctt tca gca cag aag aaa aag agc gaa ccg cag cct cct cgt cag cgt 211
Leu Ser Ala Gln Lys Lys Lys Ser Glu Pro Gln Pro Pro Arg Gln Arg
                25                30                35

caa gat cct ctg aaa ttt gcc gac gga tcc gac act ttt aat gcc cgc 259
Gln Asp Pro Leu Lys Phe Ala Asp Gly Ser Asp Thr Phe Asn Ala Arg
                40                45                50

att ttg ggt cct gga gca att att tcc cgc ggt ggc gtg gat tat gtc 307
Ile Leu Gly Pro Gly Ala Ile Ile Ser Arg Gly Gly Val Asp Tyr Val
                55                60                65

tgc cgc gga gcc atc cag ttc cgt caa ggc caa tac att tgg cac gag 355
Cys Arg Gly Ala Ile Gln Phe Arg Gln Gly Gln Tyr Ile Trp His Glu
                70                75                80                85

tat cta ctc gac ggt ggc aaa ggc agt gag tac ctg agc gtg gaa tac 403
Tyr Leu Leu Asp Gly Gly Lys Gly Ser Glu Tyr Leu Ser Val Glu Tyr
                90                95                100

gat gag ggc caa ctc aac ctc gga tgg tgg att acc cgc cct gac ctg 451
Asp Glu Gly Gln Leu Asn Leu Gly Trp Trp Ile Thr Arg Pro Asp Leu
                105                110                115

gca caa cag ccc gca cat gat gtc acc gtg gag ggc gtt cgc tac cgt 499

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Ala Gln Gln Pro Ala His Asp Val Thr Val Glu Gly Val Arg Tyr Arg
120 125 130

aaa acc gaa tct ggc gtg ggc acc ttc acc tcc gaa ggc acc acc ggc 547
Lys Thr Glu Ser Gly Val Gly Thr Phe Thr Ser Glu Gly Thr Thr Gly
135 140 145

gtg gct gat caa ggt gaa ttt gaa tac tgg gat ctc gcc gaa gtt ggc 595
Val Ala Asp Gln Gly Glu Phe Glu Tyr Trp Asp Leu Ala Glu Val Gly
150 155 160 165

gga aac agg ttg ctc agt ttt gaa cgc tac ggc aaa gac agt cca ttt 643
Gly Asn Arg Leu Leu Ser Phe Glu Arg Tyr Gly Lys Asp Ser Pro Phe
170 175 180

gaa gta tcg ctc ggg tgg acg gtg ctg ccc ggc gaa ctc acc gtt tac 691
Glu Val Ser Leu Gly Trp Thr Val Leu Pro Gly Glu Leu Thr Val Tyr
185 190 195

cca gca cca gag gcc tca tgattcatca catcgattgc atg 732
Pro Ala Pro Glu Ala Ser
200

<210> 2274
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 2274
Met Asn Ile Thr Trp Leu Ile Leu Ala Gly Val Leu Ala Ile Ile Ala
1 5 10 15

Val Val Phe Phe Tyr Leu Ser Ala Gln Lys Lys Lys Ser Glu Pro Gln
20 25 30

Pro Pro Arg Gln Arg Gln Asp Pro Leu Lys Phe Ala Asp Gly Ser Asp
35 40 45

Thr Phe Asn Ala Arg Ile Leu Gly Pro Gly Ala Ile Ile Ser Arg Gly
50 55 60

Gly Val Asp Tyr Val Cys Arg Gly Ala Ile Gln Phe Arg Gln Gly Gln
65 70 75 80

Tyr Ile Trp His Glu Tyr Leu Leu Asp Gly Gly Lys Gly Ser Glu Tyr
85 90 95

Leu Ser Val Glu Tyr Asp Glu Gly Gln Leu Asn Leu Gly Trp Trp Ile
100 105 110

Thr Arg Pro Asp Leu Ala Gln Gln Pro Ala His Asp Val Thr Val Glu
115 120 125

Gly Val Arg Tyr Arg Lys Thr Glu Ser Gly Val Gly Thr Phe Thr Ser
130 135 140

Glu Gly Thr Thr Gly Val Ala Asp Gln Gly Glu Phe Glu Tyr Trp Asp
145 150 155 160

Leu Ala Glu Val Gly Gly Asn Arg Leu Leu Ser Phe Glu Arg Tyr Gly

	165		170		175
Lys Asp Ser Pro Phe Glu Val Ser Leu Gly Trp Thr Val Leu Pro Gly					
	180		185		190
Glu Leu Thr Val Tyr Pro Ala Pro Glu Ala Ser					
	195		200		

<210> 2275
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>.
 <221> CDS
 <222> (101)..(598)
 <223> RXA01505

<400> 2275
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 tgccccggcga actcaccggt taccacgac cagaggcctc atg att cat cac atc 115
 Met Ile His His Ile
 1 5
 gat tgc atg cct aca gat gtc tcc gcc gaa gcg ctc ggc gtg agc tgg 163
 Asp Cys Met Pro Thr Asp Val Ser Ala Glu Ala Leu Gly Val Ser Trp
 10 15 20
 aat ggg gaa tcg ccg gag gtg ctc gtc gat aag ctt atc gac gca tcc 211
 Asn Gly Glu Ser Pro Glu Val Leu Val Asp Lys Leu Ile Asp Ala Ser
 25 30 35
 cca cac ccc agc acc tgc cat tta gcg gtg att ggc ggc tcg cat gtg 259
 Pro His Pro Ser Thr Cys His Leu Ala Val Ile Gly Gly Ser His Val
 40 45 50
 gtt acc gtt gaa acg ccc gat ggg cgt ttc cgg gaa gaa att tcc tgc 307
 Val Thr Val Glu Thr Pro Asp Gly Arg Phe Arg Glu Glu Ile Ser Cys
 55 60 65
 cat gca caa gaa gcg gaa gat tcc cgc tgg ccg ctg ccc gac agc atc 355
 His Ala Gln Glu Ala Glu Asp Ser Arg Trp Pro Leu Pro Asp Ser Ile
 70 75 80 85
 acg cgg gaa aac tac ctg ctg caa acc aac gtc gcc gtg ctg tct gag 403
 Thr Arg Glu Asn Tyr Leu Leu Gln Thr Asn Val Ala Val Leu Ser Glu
 90 95 100
 gaa gat ttt gcc cgc gca gcc gaa gaa atc tcc aac ggc gac gac gac 451
 Glu Asp Phe Ala Arg Ala Ala Glu Glu Ile Ser Asn Gly Asp Asp Asp
 105 110 115
 tgg ttg atc gcc agt ttc ccc ggc gcc ggc gaa cac cac ctc acc gcg 499
 Trp Leu Ile Ala Ser Phe Pro Gly Ala Gly Glu His His Leu Thr Ala
 120 125 130
 ctg acc gca gaa ttt ctg gaa gac gta tgg gaa tgg ttt agc cac cac 547
 Leu Thr Ala Glu Phe Leu Glu Asp Val Trp Glu Trp Phe Ser His His
 135 140 145

ctc tac cca gaa gag ctc acc atc gtg agc acg agg agc att tac aaa 595
Leu Tyr Pro Glu Glu Leu Thr Ile Val Ser Thr Arg Ser Ile Tyr Lys
150 155 160 165

cca tgagctcccg aaactaccga agc 621
Pro

<210> 2276

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 2276

Met Ile His His Ile Asp Cys Met Pro Thr Asp Val Ser Ala Glu Ala
1 5 10 15

Leu Gly Val Ser Trp Asn Gly Glu Ser Pro Glu Val Leu Val Asp Lys
20 25 30

Leu Ile Asp Ala Ser Pro His Pro Ser Thr Cys His Leu Ala Val Ile
35 40 45

Gly Gly Ser His Val Val Thr Val Glu Thr Pro Asp Gly Arg Phe Arg
50 55 60

Glu Glu Ile Ser Cys His Ala Gln Glu Ala Glu Asp Ser Arg Trp Pro
65 70 75 80

Leu Pro Asp Ser Ile Thr Arg Glu Asn Tyr Leu Leu Gln Thr Asn Val
85 90 95

Ala Val Leu Ser Glu Glu Asp Phe Ala Arg Ala Ala Glu Glu Ile Ser
100 105 110

Asn Gly Asp Asp Asp Trp Leu Ile Ala Ser Phe Pro Gly Ala Gly Glu
115 120 125

His His Leu Thr Ala Leu Thr Ala Glu Phe Leu Glu Asp Val Trp Glu
130 135 140

Trp Phe Ser His His Leu Tyr Pro Glu Glu Leu Thr Ile Val Ser Thr
145 150 155 160

Arg Ser Ile Tyr Lys Pro
165

<210> 2277

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> RXA01506

<400> 2277

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aagagctcac catcgtgagc acgaggagca tttaaaacc atg agc tcc cga aac 115
Met Ser Ser Arg Asn
1 5
tac cga agc ata gga ttc atc ctg ctg ttt tta gca gtg ttg tgc ctg 163
Tyr Arg Ser Ile Gly Phe Ile Leu Leu Phe Leu Ala Val Leu Cys Leu
10 15 20
ttc gct gcg gtt ttt gcc aag cct gcg gtg gga agc caa gtc tcc gac 211
Phe Ala Ala Val Phe Ala Lys Pro Ala Val Gly Ser Gln Val Ser Asp
25 30 35
cgc tgg ccc gga aac aac ggc acc tac tca tgc gct ggc gaa agt ggg 259
Arg Trp Pro Gly Asn Asn Gly Thr Tyr Ser Cys Ala Gly Glu Ser Gly
40 45 50
gtg gtg gat gaa atc gtg aac atg tcc acc cca acc gac cgc gcc acc 307
Val Val Asp Glu Ile Val Asn Met Ser Thr Pro Thr Asp Arg Ala Thr
55 60 65
gac ccc gca act ggc gat act tac ctg cga tac agc aaa aac ctg atc 355
Asp Pro Ala Thr Gly Asp Thr Tyr Leu Arg Tyr Ser Lys Asn Leu Ile
70 75 80 85
atc atc tca ggt gaa ggc acg ccg gaa tgc acc atc acc gtc gaa ggc 403
Ile Ile Ser Gly Glu Gly Thr Pro Glu Cys Thr Ile Thr Val Glu Gly
90 95 100
ctt gac cgc gtc aac agt ggt gcg ttc atc tgg ctc ggc ggc ggt ttc 451
Leu Asp Arg Val Asn Ser Gly Ala Phe Ile Trp Leu Gly Gly Gly Phe
105 110 115
ggc cca tcc tca cca agc agt tcc agc ggc gga tcc tcc ggt tcc ggc 499
Gly Pro Ser Ser Pro Ser Ser Ser Ser Gly Gly Ser Ser Gly Ser Gly
120 125 130
ggt ggc gtg aaa tagaaagaac actatgagtc aat 534
Gly Gly Val Lys
135

<210> 2278

<211> 137

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2278

Met Ser Ser Arg Asn Tyr Arg Ser Ile Gly Phe Ile Leu Leu Phe Leu
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20 25 30
Ser Gln Val Ser Asp Arg Trp Pro Gly Asn Asn Gly Thr Tyr Ser Cys
35 40 45
Ala Gly Glu Ser Gly Val Val Asp Glu Ile Val Asn Met Ser Thr Pro
50 55 60

Thr Asp Arg Ala Thr Asp Pro Ala Thr Gly Asp Thr Tyr Leu Arg Tyr
 65 70 75 80

Ser Lys Asn Leu Ile Ile Ile Ser Gly Glu Gly Thr Pro Glu Cys Thr
 85 90 95

Ile Thr Val Glu Gly Leu Asp Arg Val Asn Ser Gly Ala Phe Ile Trp
 100 105 110

Leu Gly Gly Gly Phe Gly Pro Ser Ser Pro Ser Ser Ser Ser Gly Gly
 115 120 125

Ser Ser Gly Ser Gly Gly Gly Val Lys
 130 135

<210> 2279

<211> 546

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(523)

<223> RXA01507

<400> 2279

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tcctccggtt ccggcgggtgg cgtgaaatag aaagaacact atg agt caa tat ctt 115
 Met Ser Gln Tyr Leu
 1 5

gtc gac gga gtg ctc ggc acc ctt tca tat ttc gtg ttg gcc gca gtg 163
 Val Asp Gly Val Leu Gly Thr Leu Ser Tyr Phe Val Leu Ala Ala Val
 10 15 20

atc ctc gtg gtc ggt ttt gtg att ttg gac ttg atc acc cca ggt aaa 211
 Ile Leu Val Val Gly Phe Val Ile Leu Asp Leu Ile Thr Pro Gly Lys
 25 30 35

ctg cat gaa ctc gtg ttt gtg cac cat ctg ccc aac gcc gct gtg atc 259
 Leu His Glu Leu Val Phe Val His His Leu Pro Asn Ala Ala Val Ile
 40 45 50

acc gtg gcg cag cag gtt tcc atc gga atc atc gtg gtc act gct gtg 307
 Thr Val Ala Gln Gln Val Ser Ile Gly Ile Ile Val Val Thr Ala Val
 55 60 65

ctg acc tcc tca gat att ttg agt gaa ggt ttg ctg gag act gca gtg 355
 Leu Thr Ser Ser Asp Ile Leu Ser Glu Gly Leu Leu Glu Thr Ala Val
 70 75 80 85

ttc ggt gcc ctt ggt ctg gtt atc caa gtg gtg gtc atg gcg gtg ttg 403
 Phe Gly Ala Leu Gly Leu Val Ile Gln Val Val Val Met Ala Val Leu
 90 95 100

gaa gct gtc att ccg gga cgt ttc cgt gat ctc gtg gaa gat ccc aaa 451
 Glu Ala Val Ile Pro Gly Arg Phe Arg Asp Leu Val Glu Asp Pro Lys
 105 110 115

<210> 2282

<211> 249

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2282

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Asp Arg Gly Gln Ile Leu Leu Ala Val Leu Ile Gly Leu Ala Leu Ile
20 25 30
Ala Ser Val Ile Met Leu Leu Ala Asn Ser Asp Gly Ala Met Lys Ile
35 40 45
Ala Leu Leu Ala Ala Leu Trp Ala Ala Ile Ile Gly Phe Phe Leu Val
50 55 60
Tyr Arg Ser Arg Lys Gln Val Glu Ala Ala Ala Arg Glu Lys Glu Thr
65 70 75 80
Leu Glu Tyr Ala His Gln Ser Glu Leu Asn Arg Leu Glu Ala Glu Leu
85 90 95
Val Gln Glu Lys Met Glu Ile Ser Glu Ser Arg Arg Ala Arg Asp Gln
100 105 110
Glu Thr Leu Glu Glu Ile Lys Leu Gln Leu Glu Glu Met Arg Thr Gln
115 120 125
Leu Ser Glu Leu Ser Gly Arg Glu Trp Gly Tyr Glu Pro Thr Met Leu
130 135 140
Arg Ala Glu Ala Arg Arg Ile Leu Glu Leu Glu Ser Gln Gln Leu Ser
145 150 155 160
Gln Gln Phe Gln Ala Pro Gln Pro Glu Val Pro Glu Pro Val Ala Val
165 170 175
Pro Glu Pro Met Pro Glu Pro Ala Pro Val Pro Glu Pro Val Pro Glu
180 185 190
Pro Glu Pro Val Glu Val Ala Val Glu Ala Glu Glu Glu Pro Ala Pro
195 200 205
Gly Arg Arg Arg Arg Arg His Ala Ala Pro Glu Glu Thr Gly Gly Arg
210 215 220
Arg Arg Lys Asp Glu Arg Gln Gly Gly Leu Ser Val Ala Asp Leu Leu
225 230 235 240
Ala Ala Ala Arg Lys Lys Glu Asn Asn
245

<210> 2283

<211> 507

<212> DNA

Ala Gln Leu Ala Ala Ala Leu Thr Tyr Ala Gly Phe Leu Ser Thr Leu
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Gln Arg Asp Ala Ser Tyr Phe Leu Asp Glu Phe Leu Gly Asp Pro Asp
50 55 60

Val Thr Ser Asp Ile Val Met Asp Ser Ala Gln Gln Phe Gln Ala Leu
65 70 75 80

Pro Ser Leu Asp Glu Val Ile Ala Gln Tyr Asp Ser Ile Asn Asn Pro
85 90 95

Gly Arg Gln Arg Leu Phe Arg Asp Leu Ala Arg Arg Gln Ala Glu Ile
100 105 110

Ser Arg Ala Gln Asp Ile Glu Leu Trp Ala Ile Gln Lys Glu Asp Arg
115 120 125

<210> 2285

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA01523

<400> 2285

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Met Lys Asn Trp Gln
1 5

gaa gaa ttc caa cta gtc aat ctc acg aaa ctt ctg cat agc gat acc 163
Glu Glu Phe Gln Leu Val Asn Leu Thr Lys Leu Leu His Ser Asp Thr
10 15 20

gag act tct gcg gca atc agt aat ggt caa atg att aaa ctc act cat 211
Glu Thr Ser Ala Ala Ile Ser Asn Gly Gln Met Ile Lys Leu Thr His
25 30 35

gaa gtc gca atc aat gct gaa aag tac cga agc ctt cct gca tgg gat 259
Glu Val Ala Ile Asn Ala Glu Lys Tyr Arg Ser Leu Pro Ala Trp Asp
40 45 50

aaa gca gcc gcc cga gct ttt gca gtg ggt atg act gtg gac aaa gca 307
Lys Ala Ala Ala Arg Ala Phe Ala Val Gly Met Thr Val Asp Lys Ala
55 60 65

gtg gta gcg ggg cag tct gcg gcg agg tta tgg gga tac caa act ttg 355
Val Val Ala Gly Gln Ser Ala Ala Arg Leu Trp Gly Tyr Gln Thr Leu
70 75 80 85

act gtt gag aaa acc gtg ttg tgt ctg ttg ccg gaa agg cta cgt tca 403
Thr Val Glu Lys Thr Val Leu Cys Leu Leu Pro Glu Arg Leu Arg Ser
90 95 100

aaa tcc tcc aag cat tgg ccg tcc ggg atg cga tat aaa gat cgt tac 451

Lys	Ser	Ser	Lys	His	Trp	Pro	Ser	Gly	Met	Arg	Tyr	Lys	Asp	Arg	Tyr		
			105					110					115				
ctc	tcg	tcg	cgt	gat	att	cga	gag	gtt	cat	ggg	atc	cga	gtt	acg	gga	499	
Leu	Ser	Ser	Arg	Asp	Ile	Arg	Glu	Val	His	Gly	Ile	Arg	Val	Thr	Gly		
			120				125					130					
gcg	ttc	cgc	aca	ttt	ttg	gac	atc	gct	ttg	gat	gat	ggg	gtg	gtg	gcg	547	
Ala	Phe	Arg	Thr	Phe	Leu	Asp	Ile	Ala	Leu	Asp	Asp	Gly	Val	Val	Ala		
			135			140					145						
gct	gtg	gtc	act	att	gat	tca	gct	cga	aga	cag	aat	cca	tcg	ctt	acg	595	
Ala	Val	Val	Thr	Ile	Asp	Ser	Ala	Arg	Arg	Gln	Asn	Pro	Ser	Leu	Thr		
150					155					160					165		
cgt	gag	aag	tta	atg	cac	agt	gcg	gaa	agt	ttc	ccg	agg	cat	cgg	ggt	643	
Arg	Glu	Lys	Leu	Met	His	Ser	Ala	Glu	Ser	Phe	Pro	Arg	His	Arg	Gly		
				170					175					180			
gtg	aag	gcg	tat	cgg	cag	gcg	att	gag	ttg	tcg	att	ccc	aat	tcg	gat	691	
Val	Lys	Ala	Tyr	Arg	Gln	Ala	Ile	Glu	Leu	Ser	Ile	Pro	Asn	Ser	Asp		
			185					190					195				
agt	gct	cag	gag	acg	agg	gct	cgg	tta	atc	ctt	cgg	gag	gcc	aag	ctc	739	
Ser	Ala	Gln	Glu	Thr	Arg	Ala	Arg	Leu	Ile	Leu	Arg	Glu	Ala	Lys	Leu		
			200				205					210					
ccg	gaa	atc	cag	tca	gtg	aag	gtg	cag	gcc	cgt	ttc	gat	caa	tcg	cac	787	
Pro	Glu	Ile	Gln	Ser	Val	Lys	Val	Gln	Ala	Arg	Phe	Asp	Gln	Ser	His		
			215			220					225						
aac	aag	tat	ttc	ctc	gtc	gat	ttc	ttg	atc	aat	gag	tgg	atc	atc	gtg	835	
Asn	Lys	Tyr	Phe	Leu	Val	Asp	Phe	Leu	Ile	Asn	Glu	Trp	Ile	Ile	Val		
230					235				240					245			
gag	att	gat	gga	cgt	tcg	aaa	tat	gat	tcc	ccg	gag	ctc	aat	gag	gtg	883	
Glu	Ile	Asp	Gly	Arg	Ser	Lys	Tyr	Asp	Ser	Pro	Glu	Leu	Asn	Glu	Val		
				250				255					260				
ctc	atg	gct	gaa	cgc	gat	cgg	gag	aaa	ttc	ttc	ctc	aat	cag	ggc	tat	931	
Leu	Met	Ala	Glu	Arg	Asp	Arg	Glu	Lys	Phe	Phe	Leu	Asn	Gln	Gly	Tyr		
			265				270						275				
gcg	gtc	tta	aga	atc	gat	ccg	aaa	cag	tta	gac	ctc	aac	caa	gat	ggg	979	
Ala	Val	Leu	Arg	Ile	Asp	Pro	Lys	Gln	Leu	Asp	Leu	Asn	Gln	Asp	Gly		
			280				285					290					
gag	tgt	gag	ttc	atc	gga	atc	ctc	aaa	aac	act	ttg	cag	aag	acc	cca	1027	
Glu	Cys	Glu	Phe	Ile	Gly	Ile	Leu	Lys	Asn	Thr	Leu	Gln	Lys	Thr	Pro		
			295			300					305						
cct	gag	cac	ctc	aag	caa	gcc	gcc	taa	a	c	a	c	t	c	c	1074	
Pro	Glu	His	Leu	Lys	Gln	Ala	Ala										
310					315												

<210> 2286

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 2286

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Ile Lys Leu Thr His Glu Val Ala Ile Asn Ala Glu Lys Tyr Arg Ser
35 40 45
Leu Pro Ala Trp Asp Lys Ala Ala Ala Arg Ala Phe Ala Val Gly Met
50 55 60
Thr Val Asp Lys Ala Val Val Ala Gly Gln Ser Ala Ala Arg Leu Trp
65 70 75 80
Gly Tyr Gln Thr Leu Thr Val Glu Lys Thr Val Leu Cys Leu Leu Pro
85 90 95
Glu Arg Leu Arg Ser Lys Ser Ser Lys His Trp Pro Ser Gly Met Arg
100 105 110
Tyr Lys Asp Arg Tyr Leu Ser Ser Arg Asp Ile Arg Glu Val His Gly
115 120 125
Ile Arg Val Thr Gly Ala Phe Arg Thr Phe Leu Asp Ile Ala Leu Asp
130 135 140
Asp Gly Val Val Ala Ala Val Val Thr Ile Asp Ser Ala Arg Arg Gln
145 150 155 160
Asn Pro Ser Leu Thr Arg Glu Lys Leu Met His Ser Ala Glu Ser Phe
165 170 175
Pro Arg His Arg Gly Val Lys Ala Tyr Arg Gln Ala Ile Glu Leu Ser
180 185 190
Ile Pro Asn Ser Asp Ser Ala Gln Glu Thr Arg Ala Arg Leu Ile Leu
195 200 205
Arg Glu Ala Lys Leu Pro Glu Ile Gln Ser Val Lys Val Gln Ala Arg
210 215 220
Phe Asp Gln Ser His Asn Lys Tyr Phe Leu Val Asp Phe Leu Ile Asn
225 230 235 240
Glu Trp Ile Ile Val Glu Ile Asp Gly Arg Ser Lys Tyr Asp Ser Pro
245 250 255
Glu Leu Asn Glu Val Leu Met Ala Glu Arg Asp Arg Glu Lys Phe Phe
260 265 270
Leu Asn Gln Gly Tyr Ala Val Leu Arg Ile Asp Pro Lys Gln Leu Asp
275 280 285
Leu Asn Gln Asp Gly Glu Cys Glu Phe Ile Gly Ile Leu Lys Asn Thr
290 295 300
Leu Gln Lys Thr Pro Pro Glu His Leu Lys Gln Ala Ala
305 310 315

<210> 2287
<211> 1845
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1822)
<223> RXA01525

<400> 2287

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Met Arg Ser Phe Gln
1 5
tcg atc ctt gac ctg gta aat tca gca tcc gag gtg gct acc aaa att 163
Ser Ile Leu Asp Leu Val Asn Ser Ala Ser Glu Val Ala Thr Lys Ile
10 15 20
gtg ttg aag cgc ttc gaa aaa cgg ata acc agc gaa act gac tgg gta 211
Val Leu Lys Arg Phe Glu Lys Arg Ile Thr Ser Glu Thr Asp Trp Val
25 30 35
ccg tat cag cgg ttt agt ctt tgg tcg gtt ggt tct ccg cta acg atc 259
Pro Tyr Gln Arg Phe Ser Leu Trp Ser Val Gly Ser Pro Leu Thr Ile
40 45 50
gaa cgc aaa ggc ccc gat gtg cgt gtg agc aag gac aac act gcc gtt 307
Glu Arg Lys Gly Pro Asp Val Arg Val Ser Lys Asp Asn Thr Ala Val
55 60 65
ctt cag cgc tat caa aga ccg gaa gca gaa gga ctg atc agc tac ttc 355
Leu Gln Arg Tyr Gln Arg Pro Glu Ala Glu Gly Leu Ile Ser Tyr Phe
70 75 80 85
atg gat cca aag cca tgg ata act gaa ttg gca ggc ctg aat ctg gac 403
Met Asp Pro Lys Pro Trp Ile Thr Glu Leu Ala Gly Leu Asn Leu Asp
90 95 100
gat gtt tcc gaa gat aca gtt gca ggt cgg aca gta tta gtg gtt ccc 451
Asp Val Ser Glu Asp Thr Val Ala Gly Arg Thr Val Leu Val Val Pro
105 110 115
cta tcc aat gtc att ctc agc atc gat gcg gaa ttt ggg atg att cta 499
Leu Ser Asn Val Ile Leu Ser Ile Asp Ala Glu Phe Gly Met Ile Leu
120 125 130
act gcg gaa aac gac ata gaa aag atc cac gca ata tct gtc gaa ctc 547
Thr Ala Glu Asn Asp Ile Glu Lys Ile His Ala Ile Ser Val Glu Leu
135 140 145
tta gaa aaa tgg aga tca tcc cat tac cct gag ccg cat ttt cct gca 595
Leu Glu Lys Trp Arg Ser Ser His Tyr Pro Glu Pro His Phe Pro Ala
150 155 160 165
gcg gtt ctc cca cct gcg tcg act gga aac cgc aac ctc cga gtt cta 643
Ala Val Leu Pro Pro Ala Ser Thr Gly Asn Arg Asn Leu Arg Val Leu
170 175 180

tgc cct gag ttt tcc att cca agt gtc aac gtt ggt gat cag gtt tta Cys Pro Glu Phe Ser Ile Pro Ser Val Asn Val Gly Asp Gln Val Leu 185 190 195	691
cta ttt tta aca ttt gat caa acc ctg cca cca gta gat cag ctt gaa Leu Phe Leu Thr Phe Asp Gln Thr Leu Pro Pro Val Asp Gln Leu Glu 200 205 210	739
act act cgc cgc gga tac act gat cca atc cag ctt gac tac gac cac Thr Thr Arg Arg Gly Tyr Thr Asp Pro Ile Gln Leu Asp Tyr Asp His 215 220 225	787
cgc caa tac agg ttt cac gcc gac ggt tgg gat gcc atc atc tcc acg Arg Gln Tyr Arg Phe His Ala Asp Gly Trp Asp Ala Ile Ile Ser Thr 230 235 240 245	835
gtg gag cca cta cac gac gaa gaa gaa ctc aca ggt tac ttc ctg cac Val Glu Pro Leu His Asp Glu Glu Glu Leu Thr Gly Tyr Phe Leu His 250 255 260	883
cgc ctt gac cca gat agc gcg tac cca acc att gca gtc gtt aca gca Arg Leu Asp Pro Asp Ser Ala Tyr Pro Thr Ile Ala Val Val Thr Ala 265 270 275	931
gcg cac tac cac ggt acg gac gca att atc gac gtg acc cta gat ggt Ala His Tyr His Gly Thr Asp Ala Ile Ile Asp Val Thr Leu Asp Gly 280 285 290	979
gtg cat cca ccc aaa aac caa gaa act ctt gaa ggc atc agc act agt Val His Pro Pro Lys Asn Gln Glu Thr Leu Glu Gly Ile Ser Thr Ser 295 300 305	1027
acc agt gac ggt gac ata ttt tgg ctc tcc gat gaa agc ttg cct ttc Thr Ser Asp Gly Asp Ile Phe Trp Leu Ser Asp Glu Ser Leu Pro Phe 310 315 320 325	1075
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atc ccc acg ttc caa gag atc gtc ctc gat tcc gct aat aga gcc cgc Ile Pro Thr Phe Gln Glu Ile Val Leu Asp Ser Ala Asn Arg Ala Arg 345 350 355	1171
gta aaa caa aag caa tgg cct cac gat ttc agt gat tgc aag gga aaa Val Lys Gln Lys Gln Trp Pro His Asp Phe Ser Asp Cys Lys Gly Lys 360 365 370	1219
aca tgg gag ctt ccg gat ctt aaa gaa gta ttc gaa gct gtc cct tcg Thr Trp Glu Leu Pro Asp Leu Lys Glu Val Phe Glu Ala Val Pro Ser 375 380 385	1267
att cca gca ggt tgg aga ttg tta gac agc ttc ggg aaa aac ttg cac Ile Pro Ala Gly Trp Arg Leu Leu Asp Ser Phe Gly Lys Asn Leu His 390 395 400 405	1315
aat gtc aca cgc gaa aac cct cgt ctt aat gac aac ttt tgg ctt caa Asn Val Thr Arg Glu Asn Pro Arg Leu Asn Asp Asn Phe Trp Leu Gln 410 415 420	1363

aca atc ctt agg ctt aaa cca ttt aaa gca gta gat ctt gat atc ggc 1411
 Thr Ile Leu Arg Leu Lys Pro Phe Lys Ala Val Asp Leu Asp Ile Gly
 425 430 435

cga tcg ata atc aca gca att tac cca tac ggt gat cga att tac tta 1459
 Arg Ser Ile Ile Thr Ala Ile Tyr Pro Tyr Gly Asp Arg Ile Tyr Leu
 440 445 450

cgc gct agt aac cac cac atc acg ttt aac cag gac ctc gag att ctc 1507
 Arg Ala Ser Asn His His Ile Thr Phe Asn Gln Asp Leu Glu Ile Leu
 455 460 465

aac gta gaa gtc ttt ggc gac cct gag gtt ccc gaa tct ggt cta att 1555
 Asn Val Glu Val Phe Gly Asp Pro Glu Val Pro Glu Ser Gly Leu Ile
 470 475 480 485

tat ctt cca cct ggg gat tct cca aca ctc ggt ttt ccc acc gga aca 1603
 Tyr Leu Pro Pro Gly Asp Ser Pro Thr Leu Gly Phe Pro Thr Gly Thr
 490 495 500

ctc atg atg ttt cat gag caa gaa ggc aca tat gct ttc cac gac cct 1651
 Leu Met Met Phe His Glu Gln Glu Gly Thr Tyr Ala Phe His Asp Pro
 505 510 515

gaa aca aca gaa caa ata aca act gtg aac tta gac agg aat agt ttt 1699
 Glu Thr Thr Glu Gln Ile Thr Thr Val Asn Leu Asp Arg Asn Ser Phe
 520 525 530

tca gtg gca tat tct tcc cga acc aaa att gtt att tca ctg aaa aac 1747
 Ser Val Ala Tyr Ser Ser Arg Thr Lys Ile Val Ile Ser Leu Lys Asn
 535 540 545

cca gaa agc cga cct acc aac aag ctg ttg gtg tgg gaa cca caa acc 1795
 Pro Glu Ser Arg Pro Thr Asn Lys Leu Leu Val Trp Glu Pro Gln Thr
 550 555 560 565

ggg tgg cga gaa cag aac ctg gag cgc tgagcacgct taaggtgagg 1842
 Gly Trp Arg Glu Gln Asn Leu Glu Arg
 570

tgg 1845

<210> 2288
 <211> 574
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2288
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 Glu Thr Asp Trp Val Pro Tyr Gln Arg Phe Ser Leu Trp Ser Val Gly
 35 40 45
 Ser Pro Leu Thr Ile Glu Arg Lys Gly Pro Asp Val Arg Val Ser Lys
 50 55 60

Asp Asn Thr Ala Val Leu Gln Arg Tyr Gln Arg Pro Glu Ala Glu Gly
65 70 75 80

Leu Ile Ser Tyr Phe Met Asp Pro Lys Pro Trp Ile Thr Glu Leu Ala
85 90 95

Gly Leu Asn Leu Asp Asp Val Ser Glu Asp Thr Val Ala Gly Arg Thr
100 105 110

Val Leu Val Val Pro Leu Ser Asn Val Ile Leu Ser Ile Asp Ala Glu
115 120 125

Phe Gly Met Ile Leu Thr Ala Glu Asn Asp Ile Glu Lys Ile His Ala
130 135 140

Ile Ser Val Glu Leu Leu Glu Lys Trp Arg Ser Ser His Tyr Pro Glu
145 150 155 160

Pro His Phe Pro Ala Ala Val Leu Pro Pro Ala Ser Thr Gly Asn Arg
165 170 175

Asn Leu Arg Val Leu Cys Pro Glu Phe Ser Ile Pro Ser Val Asn Val
180 185 190

Gly Asp Gln Val Leu Leu Phe Leu Thr Phe Asp Gln Thr Leu Pro Pro
195 200 205

Val Asp Gln Leu Glu Thr Thr Arg Arg Gly Tyr Thr Asp Pro Ile Gln
210 215 220

Leu Asp Tyr Asp His Arg Gln Tyr Arg Phe His Ala Asp Gly Trp Asp
225 230 235 240

Ala Ile Ile Ser Thr Val Glu Pro Leu His Asp Glu Glu Glu Leu Thr
245 250 255

Gly Tyr Phe Leu His Arg Leu Asp Pro Asp Ser Ala Tyr Pro Thr Ile
260 265 270

Ala Val Val Thr Ala Ala His Tyr His Gly Thr Asp Ala Ile Ile Asp
275 280 285

Val Thr Leu Asp Gly Val His Pro Pro Lys Asn Gln Glu Thr Leu Glu
290 295 300

Gly Ile Ser Thr Ser Thr Ser Asp Gly Asp Ile Phe Trp Leu Ser Asp
305 310 315 320

Glu Ser Leu Pro Phe Val Arg Gly Phe Ser Val Ser Thr Gly Glu Leu
325 330 335

Leu His Glu Ile Ser Ile Pro Thr Phe Gln Glu Ile Val Leu Asp Ser
340 345 350

Ala Asn Arg Ala Arg Val Lys Gln Lys Gln Trp Pro His Asp Phe Ser
355 360 365

Asp Cys Lys Gly Lys Thr Trp Glu Leu Pro Asp Leu Lys Glu Val Phe
370 375 380

Glu Ala Val Pro Ser Ile Pro Ala Gly Trp Arg Leu Leu Asp Ser Phe

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<211> 2634
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(2611)  
<223> RXA01527
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Val Ile Pro Asn Pro
1 5

aac ccg aac ccc aaa gcc aaa act ctt cgc ctc gtt tca gcg ctg acc 163
Asn Pro Asn Pro Lys Ala Lys Thr Leu Arg Leu Val Ser Ala Leu Thr
10 15 20

gcc atc act gtg gtg ggt ttt agc gct tca cct gtt cat gcg ttg ccg 211
Ala Ile Thr Val Val Gly Phe Ser Ala Ser Pro Val His Ala Leu Pro
25 30 35

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att ccg ttg gat cct tct gat ccg gcg gtg tcg gag ttg tgg gtg aat Ile Pro Leu Asp Pro Ser Asp Pro Ala Val Ser Glu Leu Trp Val Asn 40 45 50	259
ccg aat gcg cgg gct gat gat gag ctt tct ggt gtg gat gta gag atc Pro Asn Ala Arg Ala Asp Asp Glu Leu Ser Gly Val Asp Val Glu Ile 55 60 65	307
tcg gat ttt gtc atg ccg aat agc aat cta act gtg cag gtg ggg gag Ser Asp Phe Val Met Pro Asn Ser Asn Leu Thr Val Gln Val Gly Glu 70 75 80 85	355
tct ttt aag gcg cag gtt cgg gtg act aat cgt tcg tcg gag acg ttg Ser Phe Lys Ala Gln Val Arg Val Thr Asn Arg Ser Ser Glu Thr Leu 90 95 100	403
agc aat att acg ttg cag gcg cgt cgt gcg gag gcg tcg ttt gat atg Ser Asn Ile Thr Leu Gln Ala Arg Arg Ala Glu Ala Ser Phe Asp Met 105 110 115	451
gcg agt gct cgg gtg gcg gcg acg gat aat aat tat ggc tac ttc ggc Ala Ser Ala Arg Val Ala Ala Thr Asp Asn Asn Tyr Gly Tyr Phe Gly 120 125 130	499
gcg atg gtg act ctt gat gat gag ttg gag ccg ggg gag agt gtt gag Ala Met Val Thr Leu Asp Asp Glu Leu Glu Pro Gly Glu Ser Val Glu 135 140 145	547
act gag gtg gag att tct acc gat agt ttg tcg att tct cag ccg ggt Thr Glu Val Glu Ile Ser Thr Asp Ser Leu Ser Ile Ser Gln Pro Gly 150 155 160 165	595
tct tat ccg acg atg ttg gcg ttg tcg ggg cag ctt gat ggg gtg gcg Ser Tyr Pro Thr Met Leu Ala Leu Ser Gly Gln Leu Asp Gly Val Ala 170 175 180	643
cag cat ttg gat tcg cag cgt ttc ctt ctg cca gtc ctc agc gat aca Gln His Leu Asp Ser Gln Arg Phe Leu Leu Pro Val Leu Ser Asp Thr 185 190 195	691
act gat aca gaa gac acc gcc acc ccc acg acg atg att tac ccg ata Thr Asp Thr Glu Asp Thr Ala Thr Pro Thr Thr Met Ile Tyr Pro Ile 200 205 210	739
tca gcc cag acg aat gtg ttg ggt ggt gag acc ggc gag gcg ccg gaa Ser Ala Gln Thr Asn Val Leu Gly Gly Glu Thr Gly Glu Ala Pro Glu 215 220 225	787
gag ccg cct ttg ctg gtc agt tcc gac gcg ctt gcg ggc gag ttg gat Glu Pro Pro Leu Leu Val Ser Ser Asp Ala Leu Ala Gly Glu Leu Asp 230 235 240 245	835
gag ggc ggt cgt ttg caa aag ctt atc gac gcc tac ctc cag tct tca Glu Gly Gly Arg Leu Gln Lys Leu Ile Asp Ala Tyr Leu Gln Ser Ser 250 255 260	883
ccc gcc gtg cag caa gcc acg tgc ctt gct att gat ccg cag ctt ctt Pro Ala Val Gln Gln Ala Thr Cys Leu Ala Ile Asp Pro Gln Leu Leu 265 270 275	931
gat gtg gtg gat cgc atg acc ggc ggt tac acc gtg acc gat act cgt	979

Asp Val Val Asp Arg Met Thr Gly Gly Tyr Thr Val Thr Asp Thr Arg	
280 285 290	
ccc agt acg gtg cgg cag aat cag cgg ctt cgt gag ttg tgg act gcc	1027
Pro Ser Thr Val Arg Gln Asn Gln Arg Leu Arg Glu Leu Trp Thr Ala	
295 300 305	
gat aat caa ccc acc aat ggt gtc gcg ggc acg ggt gcg gaa aac gct	1075
Asp Asn Gln Pro Thr Asn Gly Val Ala Gly Thr Gly Ala Glu Asn Ala	
310 315 320 325	
gcc att ttc ttg gag aaa ctc cga cag gcc aca gcc acc tcg tgc acc	1123
Ala Ile Phe Leu Glu Lys Leu Arg Gln Ala Thr Ala Thr Ser Cys Thr	
330 335 340	
gtg gcg ttg ccg tgg gcg aat gct gat cta aat gca gtg agc caa acc	1171
Val Ala Leu Pro Trp Ala Asn Ala Asp Leu Asn Ala Val Ser Gln Thr	
345 350 355	
ggt aat cag tgg ttg atg cgc gag gcg cta cag cga ggt gtc acc acc	1219
Gly Asn Gln Trp Leu Met Arg Glu Ala Leu Gln Arg Gly Val Thr Thr	
360 365 370	
ttt gaa gaa gtg ttg ggt gtt att ccg gaa tcc aat gtg gtg att cct	1267
Phe Glu Glu Val Leu Gly Val Ile Pro Glu Ser Asn Val Val Ile Pro	
375 380 385	
gga aat ggt ttt gtg gag ccc tcc acc gtg ggt gat ctc gga tgg gcg	1315
Gly Asn Gly Phe Val Glu Pro Ser Thr Val Gly Asp Leu Gly Trp Ala	
390 395 400 405	
gaa gta acg ctt aat ccg gat cag gcg tgg gag gtg cag tca gag gag	1363
Glu Val Thr Leu Asn Pro Asp Gln Ala Trp Glu Val Gln Ser Glu Glu	
410 415 420	
ttg gtt gct gcc cct gat gcc aca gag caa agc gca ttg gat aac cct	1411
Leu Val Ala Ala Pro Asp Ala Thr Glu Gln Ser Ala Leu Asp Asn Pro	
425 430 435	
aag cca acg cca ggc acg gtg acg ccg cca acc cct atg tca acg gtg	1459
Lys Pro Thr Pro Gly Thr Val Thr Pro Pro Thr Pro Met Ser Thr Val	
440 445 450	
tcc gtg ttg gtt tct gat aac acg gtg tgg cgc aca acg agc gcg gat	1507
Ser Val Leu Val Ser Asp Asn Thr Val Trp Arg Thr Thr Ser Ala Asp	
455 460 465	
cgg ttc cac tct ttg gct ccg gga ata act ggg gtg tcg tat cag gga	1555
Arg Phe His Ser Leu Ala Pro Gly Ile Thr Gly Val Ser Tyr Gln Gly	
470 475 480 485	
tcg tta tcg gca acc ttg gct acc ttg gga caa aac cct gag act gtg	1603
Ser Leu Ser Ala Thr Leu Ala Thr Leu Gly Gln Asn Pro Glu Thr Val	
490 495 500	
ggc tat tcc aat ccg gat tcg cgt tat gac tac gcc atg gat tct gag	1651
Gly Tyr Ser Asn Pro Asp Ser Arg Tyr Asp Tyr Ala Met Asp Ser Glu	
505 510 515	
agc gcc cgc aat ctc acc ggc cag gcg gcg ctg cgc ttg acg gtg gac	1699
Ser Ala Arg Asn Leu Thr Gly Gln Ala Ala Leu Arg Leu Thr Val Asp	

520	525	530	
aac ggc gat gaa gac tct ccc gtg ttg atc atg ccg agc gcg gtg ctg Asn Gly Asp Glu Asp Ser Pro Val Leu Ile Met Pro Ser Ala Val Leu 535	540	545	1747
ggc gcc gaa gac ggc gcg atg ttg ctt gag acc acc ggg gct ttg ctt Gly Ala Glu Asp Gly Ala Met Leu Leu Glu Thr Thr Gly Ala Leu Leu 550	555	560	1795
gcc gac ggc tcc gcc cga cct ttt tcc ctg cag caa tat gtc act gcc Ala Asp Gly Ser Ala Arg Pro Phe Ser Leu Gln Gln Tyr Val Thr Ala 570	575	580	1843
aat gcg gaa caa aga aat act ttg gcc aca gca aca act cca ccg gat Asn Ala Glu Gln Arg Asn Thr Leu Ala Thr Ala Thr Thr Pro Pro Asp 585	590	595	1891
gac act gct ttt ggt gca ccc tac gac gat cct gcg tca ttg acg gaa Asp Thr Ala Phe Gly Ala Pro Tyr Asp Asp Pro Ala Ser Leu Thr Glu 600	605	610	1939
acc gaa att ctg cga acc act cag cag gcg gag tac atc gat gat ctc Thr Glu Ile Leu Arg Thr Thr Gln Gln Ala Glu Tyr Ile Asp Asp Leu 615	620	625	1987
act ggc atc atg tcc aat gat ccc agc att gca ctg acc cgt tat ggg Thr Gly Ile Met Ser Asn Asp Pro Ser Ile Ala Leu Thr Arg Tyr Gly 630	635	640	2035
ttt aca gca ccg ctg cgg caa gat ctg ctg cgc gcg ttg agt atc agt Phe Thr Ala Pro Leu Arg Gln Asp Leu Leu Arg Ala Leu Ser Ile Ser 650	655	660	2083
gag cgt cgt tcg tta gct cgc cac acc cag gca acc tct gct gcc gat Glu Arg Arg Ser Leu Ala Arg His Thr Gln Ala Thr Ser Ala Ala Asp 665	670	675	2131
aaa tta ctt aat cgc aac cgc gat act ctg cag aag ctg cgt agc tct Lys Leu Leu Asn Arg Asn Arg Asp Thr Leu Gln Lys Leu Arg Ser Ser 680	685	690	2179
gtg gcg ttg ttg ccg ccg gga aat gtg tat acc cga acc tcg gaa tcg Val Ala Leu Leu Pro Pro Gly Asn Val Tyr Thr Arg Thr Ser Glu Ser 695	700	705	2227
tct ccg ttg ttg att gtg gcg caa aac ggt ttg cca ttg ccc gcg gag Ser Pro Leu Leu Ile Val Ala Gln Asn Gly Leu Pro Leu Pro Ala Glu 710	715	720	2275
act cag att ttg tat tcc gga aat cag gat gcg cac atc aat act ccg Thr Gln Ile Leu Tyr Ser Gly Asn Gln Asp Ala His Ile Asn Thr Pro 730	735	740	2323
ggg gtg gtt cgt att ccg gcg cag ggt tcc atc acc ttg cag atg act Gly Val Val Arg Ile Pro Ala Gln Gly Ser Ile Thr Leu Gln Met Thr 745	750	755	2371
gcg gat ttg ccc gat gac aat ctg cgc act gat ctc acg ttg tgg ttg Ala Asp Leu Pro Asp Asp Asn Leu Arg Thr Asp Leu Thr Trp Leu 760	765	770	2419

gca tcc cca gat ggg gcc acc att agt gaa cct gtg gaa att act gtc 2467
 Ala Ser Pro Asp Gly Ala Thr Ile Ser Glu Pro Val Glu Ile Thr Val
 775 780 785

cag cct cgc ccg aat ttg ggc acc acg ctg ttt ttc gtg gca gcg ggc 2515
 Gln Pro Arg Pro Asn Leu Gly Thr Thr Leu Phe Phe Val Ala Ala Gly
 790 795 800 805

att ctg gca gta gga ggg ttg ttg ttt ata cgg aag aaa cga aac gtc 2563
 Ile Leu Ala Val Gly Gly Leu Leu Phe Ile Arg Lys Lys Arg Asn Val
 810 815 820

gaa aag cgc tcg ccc ggt acg gga tcg ccc aaa ccg cca cca acc cac 2611
 Glu Lys Arg Ser Pro Gly Thr Gly Ser Pro Lys Pro Pro Pro Thr His
 825 830 835

taacgtatcg catagttatt ttc 2634

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Val His Ala Leu Pro Ile Pro Leu Asp Pro Ser Asp Pro Ala Val Ser
 35 40 45
 Glu Leu Trp Val Asn Pro Asn Ala Arg Ala Asp Asp Glu Leu Ser Gly
 50 55 60
 Val Asp Val Glu Ile Ser Asp Phe Val Met Pro Asn Ser Asn Leu Thr
 65 70 75 80
 Val Gln Val Gly Glu Ser Phe Lys Ala Gln Val Arg Val Thr Asn Arg
 85 90 95
 Ser Ser Glu Thr Leu Ser Asn Ile Thr Leu Gln Ala Arg Arg Ala Glu
 100 105 110
 Ala Ser Phe Asp Met Ala Ser Ala Arg Val Ala Ala Thr Asp Asn Asn
 115 120 125
 Tyr Gly Tyr Phe Gly Ala Met Val Thr Leu Asp Asp Glu Leu Glu Pro
 130 135 140
 Gly Glu Ser Val Glu Thr Glu Val Glu Ile Ser Thr Asp Ser Leu Ser
 145 150 155 160
 Ile Ser Gln Pro Gly Ser Tyr Pro Thr Met Leu Ala Leu Ser Gly Gln
 165 170 175
 Leu Asp Gly Val Ala Gln His Leu Asp Ser Gln Arg Phe Leu Leu Pro
 180 185 190

Val Leu Ser Asp Thr Thr Asp Thr Glu Asp Thr Ala Thr Pro Thr Thr
 195 200 205
 Met Ile Tyr Pro Ile Ser Ala Gln Thr Asn Val Leu Gly Gly Glu Thr
 210 215 220
 Gly Glu Ala Pro Glu Glu Pro Pro Leu Leu Val Ser Ser Asp Ala Leu
 225 230 235 240
 Ala Gly Glu Leu Asp Glu Gly Gly Arg Leu Gln Lys Leu Ile Asp Ala
 245 250 255
 Tyr Leu Gln Ser Ser Pro Ala Val Gln Gln Ala Thr Cys Leu Ala Ile
 260 265 270
 Asp Pro Gln Leu Leu Asp Val Val Asp Arg Met Thr Gly Gly Tyr Thr
 275 280 285
 Val Thr Asp Thr Arg Pro Ser Thr Val Arg Gln Asn Gln Arg Leu Arg
 290 295 300
 Glu Leu Trp Thr Ala Asp Asn Gln Pro Thr Asn Gly Val Ala Gly Thr
 305 310 315 320
 Gly Ala Glu Asn Ala Ala Ile Phe Leu Glu Lys Leu Arg Gln Ala Thr
 325 330 335
 Ala Thr Ser Cys Thr Val Ala Leu Pro Trp Ala Asn Ala Asp Leu Asn
 340 345 350
 Ala Val Ser Gln Thr Gly Asn Gln Trp Leu Met Arg Glu Ala Leu Gln
 355 360 365
 Arg Gly Val Thr Thr Phe Glu Glu Val Leu Gly Val Ile Pro Glu Ser
 370 375 380
 Asn Val Val Ile Pro Gly Asn Gly Phe Val Glu Pro Ser Thr Val Gly
 385 390 395 400
 Asp Leu Gly Trp Ala Glu Val Thr Leu Asn Pro Asp Gln Ala Trp Glu
 405 410 415
 Val Gln Ser Glu Glu Leu Val Ala Ala Pro Asp Ala Thr Glu Gln Ser
 420 425 430
 Ala Leu Asp Asn Pro Lys Pro Thr Pro Gly Thr Val Thr Pro Pro Thr
 435 440 445
 Pro Met Ser Thr Val Ser Val Leu Val Ser Asp Asn Thr Val Trp Arg
 450 455 460
 Thr Thr Ser Ala Asp Arg Phe His Ser Leu Ala Pro Gly Ile Thr Gly
 465 470 475 480
 Val Ser Tyr Gln Gly Ser Leu Ser Ala Thr Leu Ala Thr Leu Gly Gln
 485 490 495
 Asn Pro Glu Thr Val Gly Tyr Ser Asn Pro Asp Ser Arg Tyr Asp Tyr
 500 505 510

Ala Met Asp Ser Glu Ser Ala Arg Asn Leu Thr Gly Gln Ala Ala Leu
 515 520 525
 Arg Leu Thr Val Asp Asn Gly Asp Glu Asp Ser Pro Val Leu Ile Met
 530 535 540
 Pro Ser Ala Val Leu Gly Ala Glu Asp Gly Ala Met Leu Leu Glu Thr
 545 550 555 560
 Thr Gly Ala Leu Leu Ala Asp Gly Ser Ala Arg Pro Phe Ser Leu Gln
 565 570 575
 Gln Tyr Val Thr Ala Asn Ala Glu Gln Arg Asn Thr Leu Ala Thr Ala
 580 585 590
 Thr Thr Pro Pro Asp Asp Thr Ala Phe Gly Ala Pro Tyr Asp Asp Pro
 595 600 605
 Ala Ser Leu Thr Glu Thr Glu Ile Leu Arg Thr Thr Gln Gln Ala Glu
 610 615 620
 Tyr Ile Asp Asp Leu Thr Gly Ile Met Ser Asn Asp Pro Ser Ile Ala
 625 630 635 640
 Leu Thr Arg Tyr Gly Phe Thr Ala Pro Leu Arg Gln Asp Leu Leu Arg
 645 650 655
 Ala Leu Ser Ile Ser Glu Arg Arg Ser Leu Ala Arg His Thr Gln Ala
 660 665 670
 Thr Ser Ala Ala Asp Lys Leu Leu Asn Arg Asn Arg Asp Thr Leu Gln
 675 680 685
 Lys Leu Arg Ser Ser Val Ala Leu Leu Pro Pro Gly Asn Val Tyr Thr
 690 695 700
 Arg Thr Ser Glu Ser Ser Pro Leu Leu Ile Val Ala Gln Asn Gly Leu
 705 710 715 720
 Pro Leu Pro Ala Glu Thr Gln Ile Leu Tyr Ser Gly Asn Gln Asp Ala
 725 730 735
 His Ile Asn Thr Pro Gly Val Val Arg Ile Pro Ala Gln Gly Ser Ile
 740 745 750
 Thr Leu Gln Met Thr Ala Asp Leu Pro Asp Asp Asn Leu Arg Thr Asp
 755 760 765
 Leu Thr Leu Trp Leu Ala Ser Pro Asp Gly Ala Thr Ile Ser Glu Pro
 770 775 780
 Val Glu Ile Thr Val Gln Pro Arg Pro Asn Leu Gly Thr Thr Leu Phe
 785 790 795 800
 Phe Val Ala Ala Gly Ile Leu Ala Val Gly Gly Leu Leu Phe Ile Arg
 805 810 815
 Lys Lys Arg Asn Val Glu Lys Arg Ser Pro Gly Thr Gly Ser Pro Lys
 820 825 830
 Pro Pro Pro Thr His

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<211> 1365
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1342)
<223> RXA01536
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				Met Ala Phe Gly Phe	5													
				1														
ttt agt aga cgt aag aaa aag aac aaa gac aaa aac ccg aat gaa aat	163																	
Phe Ser Arg Arg Lys Lys Lys Asn Lys Asp Lys Asn Pro Asn Glu Asn	20																	
				10														
tca gca gtg ccc gca cac tct gaa gat tca cct cag gag gtt ttt gag	211																	
Ser Ala Val Pro Ala His Ser Glu Asp Ser Pro Gln Glu Val Phe Glu	35																	
				25														
ggg aat ggt cgt cag gta ggc gac ccc att gaa cag cag gtt gat cga	259																	
Gly Asn Gly Arg Gln Val Gly Asp Pro Ile Glu Gln Gln Val Asp Arg	50																	
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gat gct aaa ggt cgt ctc aca gcg gcg gat ttc ttg ccg gac gct gat	307																	
Asp Ala Lys Gly Arg Leu Thr Ala Ala Asp Phe Leu Pro Asp Ala Asp	65																	
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ctg cca cag ctg aat cgt tgc cgt gca aat atg ctg cgc cgt gaa ttg	355																	
Leu Pro Gln Leu Asn Arg Ser Arg Ala Asn Met Leu Arg Arg Glu Leu	85																	
				70														
gag tac cgt ttt tca ctc cag aat gcc cac att aat atc gat gga aac	403																	
Glu Tyr Arg Phe Ser Leu Gln Asn Ala His Ile Asn Ile Asp Gly Asn	100																	
				90														
acg gcc atg att cag cgt tca gat ggc ggg gca gca cat gtc tgc ttg	451																	
Thr Ala Met Ile Gln Arg Ser Asp Gly Gly Ala Ala His Val Ser Leu	115																	
				105														
cgc acc ctc gcg atg aat gca gct ggc ctt gat aac ttt gat caa ctc	499																	
Arg Thr Leu Ala Met Asn Ala Ala Gly Leu Asp Asn Phe Asp Gln Leu	130																	
				120														
cct gaa ctg gtg gaa agc ttc gtt cac ggc acg ctg gcc gat gca aca	547																	
Pro Glu Leu Val Glu Ser Phe Val His Gly Thr Leu Ala Asp Ala Thr	145																	
				135														
tta aac gat ctt tct act gct gac ctg tat aaa gca ctg cgc ctt cgc	595																	
Leu Asn Asp Leu Ser Thr Ala Asp Leu Tyr Lys Ala Leu Arg Leu Arg	165																	
				150														
ctg ctg cca aca cct ggc gaa ggc gac gat cta gtt gag cat qqa ctc	643																	

Leu Leu Pro Thr	Pro Gly Glu Gly Asp Asp Leu Val Glu His Gly Leu	
	170 175 180	
gac cgg gaa agc cag atc cgc gac gat tca atc ctg cgc acc ttc acc	691	
Asp Arg Glu Ser Gln Ile Arg Asp Asp Ser Ile Leu Arg Thr Phe Thr		
	185 190 195	
tct gac atg tcg atc gcg ctg gtg ctc gat acc gag cat gcc atc cgc	739	
Ser Asp Met Ser Ile Ala Leu Val Leu Asp Thr Glu His Ala Ile Arg		
	200 205 210	
atc cag cca ctc aaa gag ctc gag gag ttc gat gac ctc agc gcc cta	787	
Ile Gln Pro Leu Lys Glu Leu Glu Glu Phe Asp Asp Leu Ser Ala Leu		
	215 220 225	
gag cgg gct gcg gac cgc aat acc tgg caa gag ctt tac gac gca aac	835	
Glu Arg Ala Ala Asp Arg Asn Thr Trp Gln Glu Leu Tyr Asp Ala Asn		
	230 235 240 245	
gtt gac gct tcc ttc gtc gac gct gaa tca gac agc gaa ggg tca tca	883	
Val Asp Ala Ser Phe Val Asp Ala Glu Ser Asp Ser Glu Gly Ser Ser		
	250 255 260	
ttt tgg gct ttc gaa tct aac tcg tac tac ttg ggt agt gca cca ctg	931	
Phe Trp Ala Phe Glu Ser Asn Ser Tyr Tyr Leu Gly Ser Ala Pro Leu		
	265 270 275	
ttc ctc aac gat ctg ttg gca aag tgg gca cct gac ctg gac caa agt	979	
Phe Leu Asn Asp Leu Leu Ala Lys Trp Ala Pro Asp Leu Asp Gln Ser		
	280 285 290	
gat ggc gtc atc ttt gct gtc cct gat cgt gat ctg ttg att gcg cgt	1027	
Asp Gly Val Ile Phe Ala Val Pro Asp Arg Asp Leu Leu Ile Ala Arg		
	295 300 305	
cct gtg acc acc ggc gaa gat ctg atg aac gga atc acc gcg atg gtg	1075	
Pro Val Thr Thr Gly Glu Asp Leu Met Asn Gly Ile Thr Ala Met Val		
	310 315 320 325	
agg atc gcg atg cgc ttt ggc ctc ggg aac ccg acg tcg ata agc ccg	1123	
Arg Ile Ala Met Arg Phe Gly Leu Gly Asn Pro Thr Ser Ile Ser Pro		
	330 335 340	
cgc ctg cac ctg ctg cgc gac aac cag gtg acc acc ttc acc gac ttc	1171	
Arg Leu His Leu Leu Arg Asp Asn Gln Val Thr Thr Phe Thr Asp Phe		
	345 350 355	
cgc gtc gtc tct cct gaa atg gaa gct gaa tgg gaa gac agc gcg ttt	1219	
Arg Val Val Ser Pro Glu Met Glu Ala Glu Trp Glu Asp Ser Ala Phe		
	360 365 370	
gac gcg cca ccg gcc ggc gcg atc ggc att gag gtg cgc cca gat ccg	1267	
Asp Ala Pro Pro Ala Gly Ala Ile Gly Ile Glu Val Arg Pro Asp Pro		
	375 380 385	
tat ctg atg gag cgc ctc caa cag ggc ggc ttt ggt gat ttc gga gat	1315	
Tyr Leu Met Glu Arg Leu Gln Gln Gly Gly Phe Gly Asp Phe Gly Asp		
	390 395 400 405	
ttc ggc aag ccc cgc gat cta gat atg tagcgaaaaa gggaccttca	1362	
Phe Gly Lys Pro Arg Asp Leu Asp Met		

410

ctt

1365

<210> 2292

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 2292

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Asn Pro Asn Glu Asn Ser Ala Val Pro Ala His Ser Glu Asp Ser Pro
20 25 30

Gln Glu Val Phe Glu Gly Asn Gly Arg Gln Val Gly Asp Pro Ile Glu
35 40 45

Gln Gln Val Asp Arg Asp Ala Lys Gly Arg Leu Thr Ala Ala Asp Phe
50 55 60

Leu Pro Asp Ala Asp Leu Pro Gln Leu Asn Arg Ser Arg Ala Asn Met
65 70 75 80

Leu Arg Arg Glu Leu Glu Tyr Arg Phe Ser Leu Gln Asn Ala His Ile
85 90 95

Asn Ile Asp Gly Asn Thr Ala Met Ile Gln Arg Ser Asp Gly Gly Ala
100 105 110

Ala His Val Ser Leu Arg Thr Leu Ala Met Asn Ala Ala Gly Leu Asp
115 120 125

Asn Phe Asp Gln Leu Pro Glu Leu Val Glu Ser Phe Val His Gly Thr
130 135 140

Leu Ala Asp Ala Thr Leu Asn Asp Leu Ser Thr Ala Asp Leu Tyr Lys
145 150 155 160

Ala Leu Arg Leu Arg Leu Leu Pro Thr Pro Gly Glu Gly Asp Asp Leu
165 170 175

Val Glu His Gly Leu Asp Arg Glu Ser Gln Ile Arg Asp Asp Ser Ile
180 185 190

Leu Arg Thr Phe Thr Ser Asp Met Ser Ile Ala Leu Val Leu Asp Thr
195 200 205

Glu His Ala Ile Arg Ile Gln Pro Leu Lys Glu Leu Glu Glu Phe Asp
210 215 220

Asp Leu Ser Ala Leu Glu Arg Ala Ala Asp Arg Asn Thr Trp Gln Glu
225 230 235 240

Leu Tyr Asp Ala Asn Val Asp Ala Ser Phe Val Asp Ala Glu Ser Asp
245 250 255

Ser Glu Gly Ser Ser Phe Trp Ala Phe Glu Ser Asn Ser Tyr Tyr Leu
260 265 270

Gly Ser Ala Pro Leu Phe Leu Asn Asp Leu Leu Ala Lys Trp Ala Pro
 275 280 285
 Asp Leu Asp Gln Ser Asp Gly Val Ile Phe Ala Val Pro Asp Arg Asp
 290 295 300
 Leu Leu Ile Ala Arg Pro Val Thr Thr Gly Glu Asp Leu Met Asn Gly
 305 310 315 320
 Ile Thr Ala Met Val Arg Ile Ala Met Arg Phe Gly Leu Gly Asn Pro
 325 330 335
 Thr Ser Ile Ser Pro Arg Leu His Leu Leu Arg Asp Asn Gln Val Thr
 340 345 350
 Thr Phe Thr Asp Phe Arg Val Val Ser Pro Glu Met Glu Ala Glu Trp
 355 360 365
 Glu Asp Ser Ala Phe Asp Ala Pro Pro Ala Gly Ala Ile Gly Ile Glu
 370 375 380
 Val Arg Pro Asp Pro Tyr Leu Met Glu Arg Leu Gln Gln Gly Gly Phe
 385 390 395 400
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<211> 825

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(802)

<223> RXA01540

<400> 2293

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 Met Thr Phe Ala Glu
 1 5
 ctt agc tca ccg cgt acc atc atc gct ttt aat ggc cgt gcc gaa tct 163
 Leu Ser Ser Pro Arg Thr Ile Ile Ala Phe Asn Gly Arg Ala Glu Ser
 10 15 20
 ggc aaa gat act gca gca cag tat ctc acc cat atg cac agt ttt cac 211
 Gly Lys Asp Thr Ala Ala Gln Tyr Leu Thr His Met His Ser Phe His
 25 30 35
 cgc atc gcc ttt gcc gat ggt gtc cgt gac gca ctc tat gcg ctt aac 259
 Arg Ile Ala Phe Ala Asp Gly Val Arg Asp Ala Leu Tyr Ala Leu Asn
 40 45 50
 cca ctg gtc tgt gtg gag cag gct atc acc aca cat ggt gcc att tat 307
 Pro Leu Val Cys Val Glu Gln Ala Ile Thr Thr His Gly Ala Ile Tyr
 55 60 65

gac cgc gtg gcc act gtt gtg gac aca ctt ggt tgg gat acc gca aag 355
 Asp Arg Val Ala Thr Val Val Asp Thr Leu Gly Trp Asp Thr Ala Lys
 70 75 80 85
 caa atc ccc gac atc cgc gca ctt atg cag cgt att ggt acc gaa gct 403
 Gln Ile Pro Asp Ile Arg Ala Leu Met Gln Arg Ile Gly Thr Glu Ala
 90 95 100
 ggt tgg cgc atc cac ggc gag cat ctg tgg gtc aat ctt gct atc aaa 451
 Gly Trp Arg Ile His Gly Glu His Leu Trp Val Asn Leu Ala Ile Lys
 105 110 115
 aag atc aat gaa ctg ccc gct gac cac gcc att gtc atc act gat ttg 499
 Lys Ile Asn Glu Leu Pro Ala Asp His Ala Ile Val Ile Thr Asp Leu
 120 125 130
 cga ttc ccc aat gag att gag tgg ttg aac agc ctc aaa gcc aac ccg 547
 Arg Phe Pro Asn Glu Ile Glu Trp Leu Asn Ser Leu Lys Ala Asn Pro
 135 140 145
 atg aac acc att cag acc gtc aaa gtc atc cga cca gat cat gaa tcg 595
 Met Asn Thr Ile Gln Thr Val Lys Val Ile Arg Pro Asp His Glu Ser
 150 155 160 165
 acc ttg act gca gga tca ttc ggt act acc tca cat att tcc gaa agc 643
 Thr Leu Thr Ala Gly Ser Phe Gly Thr Thr Ser His Ile Ser Glu Ser
 170 175 180
 ttt aat ctc act acc gac act gtg ctc cgc aac gat ggc acc att gac 691
 Phe Asn Leu Thr Thr Asp Thr Val Leu Arg Asn Asp Gly Thr Ile Asp
 185 190 195
 gat ttg cac tca aag ctg gct gat ttt ttg agc act tcc ccg cag ccc 739
 Asp Leu His Ser Lys Leu Ala Asp Phe Leu Ser Thr Ser Pro Gln Pro
 200 205 210
 gtg ctc tct cgt aac gcc cct gta cca aaa cac aac gca ccg gca cca 787
 Val Leu Ser Arg Asn Ala Pro Val Pro Lys His Asn Ala Pro Ala Pro
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 acc act gat gcc atg taaataaccc ccgtatcaag atc 825
 Thr Thr Asp Ala Met
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<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 2294

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 20 25 30
 Met His Ser Phe His Arg Ile Ala Phe Ala Asp Gly Val Arg Asp Ala
 35 40 45

Leu Tyr Ala Leu Asn Pro Leu Val Cys Val Glu Gln Ala Ile Thr Thr
 50 55 60
 His Gly Ala Ile Tyr Asp Arg Val Ala Thr Val Val Asp Thr Leu Gly
 65 70 75 80
 Trp Asp Thr Ala Lys Gln Ile Pro Asp Ile Arg Ala Leu Met Gln Arg
 85 90 95
 Ile Gly Thr Glu Ala Gly Trp Arg Ile His Gly Glu His Leu Trp Val
 100 105 110
 Asn Leu Ala Ile Lys Lys Ile Asn Glu Leu Pro Ala Asp His Ala Ile
 115 120 125
 Val Ile Thr Asp Leu Arg Phe Pro Asn Glu Ile Glu Trp Leu Asn Ser
 130 135 140
 Leu Lys Ala Asn Pro Met Asn Thr Ile Gln Thr Val Lys Val Ile Arg
 145 150 155 160
 Pro Asp His Glu Ser Thr Leu Thr Ala Gly Ser Phe Gly Thr Thr Ser
 165 170 175
 His Ile Ser Glu Ser Phe Asn Leu Thr Thr Asp Thr Val Leu Arg Asn
 180 185 190
 Asp Gly Thr Ile Asp Asp Leu His Ser Lys Leu Ala Asp Phe Leu Ser
 195 200 205
 Thr Ser Pro Gln Pro Val Leu Ser Arg Asn Ala Pro Val Pro Lys His
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 Asn Ala Pro Ala Pro Thr Thr Asp Ala Met
 225 230

<210> 2295

<211> 2889

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(2866)

<223> RXA01543

<400> 2295

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 Met Ser Leu Lys Gln
 1 5

gcc att atc gtg cgc aat gaa tat acg att aag cag gca aat ggc aaa 163
 Ala Ile Ile Val Arg Asn Glu Tyr Thr Ile Lys Gln Ala Asn Gly Lys
 10 15 20

ggt tca cga gga tca tcg cca ggt aaa tat atc tct ggc tat atg gca 211
 Gly Ser Arg Gly Ser Ser Pro Gly Lys Tyr Ile Ser Gly Tyr Met Ala
 25 30 35

cgc agc gat gcg gta gaa gca gta gca cct att gtg cgc aat aaa tta	259
Arg Ser Asp Ala Val Glu Ala Val Ala Pro Ile Val Arg Asn Lys Leu	
40 45 50	
gat gat ttc atc atg cgg tat atg gca cgt gat agt gcc gtg gag cag	307
Asp Asp Phe Ile Met Arg Tyr Met Ala Arg Asp Ser Ala Val Glu Gln	
55 60 65	
ctc acc acg gac agt aac gca gac tat gac cag caa cct gaa atg aac	355
Leu Thr Thr Asp Ser Asn Ala Asp Tyr Asp Gln Gln Pro Glu Met Asn	
70 75 80 85	
tct cgt cgt ggc cgg caa ggt cgc cgc gcg acc ttg aaa caa cgt cgt	403
Ser Arg Arg Gly Arg Gln Gly Arg Arg Ala Thr Leu Lys Gln Arg Arg	
90 95 100	
gca gaa cgc agc gcc cgg cga gca gca ttg cga gcg ggc gtg aat aca	451
Ala Glu Arg Ser Ala Arg Arg Ala Ala Leu Arg Ala Gly Val Asn Thr	
105 110 115	
gac tcc gac acc acc aac cca tca caa cct gtg cac ccg agg gaa ctc	499
Asp Ser Asp Thr Thr Asn Pro Ser Gln Pro Val His Pro Arg Glu Leu	
120 125 130	
gcg gaa ttt act acc cag gat ggg cag cgc gtt cat gat ctc atg ctg	547
Ala Glu Phe Thr Thr Gln Asp Gly Gln Arg Val His Asp Leu Met Leu	
135 140 145	
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Arg Ala Gln Gly Asn Gly Gly Val Ala Phe Gly Tyr Gly Asp Val Ser	
150 155 160 165	
ctg tca cat gat gat ctt cat gca gca agt aat aac gtc caa gag ctc	643
Leu Ser His Asp Asp Leu His Ala Ala Ser Asn Asn Val Gln Glu Leu	
170 175 180	
tat gaa aat agg cat acc gtg atg aaa gtg gtc cta tct ttt acc cag	691
Tyr Glu Asn Arg His Thr Val Met Lys Val Val Leu Ser Phe Thr Gln	
185 190 195	
gat tac ctg acc gcg cat ggc ctt att cca gag gat ctc gat att aag	739
Asp Tyr Leu Thr Ala His Gly Leu Ile Pro Glu Asp Leu Asp Ile Lys	
200 205 210	
cgt gct ggt gat tat cgc ggc cag gtt gac caa atg aag cta cgc atg	787
Arg Ala Gly Asp Tyr Arg Gly Gln Val Asp Gln Met Lys Leu Arg Met	
215 220 225	
gct gtc atg cat ggt gtg gat cgt cta gcc cag cgt cat tat gat gat	835
Ala Val Met His Gly Val Asp Arg Leu Ala Gln Arg His Tyr Asp Asp	
230 235 240 245	
ttg cgc tat gtc ggc gtg att cag gtt gat acg aag cat gtg cac gcc	883
Leu Arg Tyr Val Gly Val Ile Gln Val Asp Thr Lys His Val His Ala	
250 255 260	
cac ttg acc atg gtg gat gct ggt tat gga cac cgg gct gct gat ggt	931
His Leu Thr Met Val Asp Ala Gly Tyr Gly His Arg Ala Ala Asp Gly	
265 270 275	

acg caa aaa ggc aaa atc aat aag cca ggt aag gct att ttg cgg cgt	979
Thr Gln Lys Gly Lys Ile Asn Lys Pro Gly Lys Ala Ile Leu Arg Arg	
280 285 290	
ggg att gac gcc tgg ctt gat cag cat cag cat atg gcg cac ttg tca	1027
Gly Ile Asp Ala Trp Leu Asp Gln His Gln His Met Ala His Leu Ser	
295 300 305	
gca gca gtg ggg tat gaa aaa cgc aat gtc acc agc tac gtc aag cgc	1075
Ala Ala Val Gly Tyr Glu Lys Arg Asn Val Thr Ser Tyr Val Lys Arg	
310 315 320 325	
tgg gcg ttt cat cag ctc acc caa gaa agt gct gcg caa ttt gtg gtc	1123
Trp Ala Phe His Gln Leu Thr Gln Glu Ser Ala Ala Gln Phe Val Val	
330 335 340	
gct tgt ttg cca gag gat aag cga ctg tgg cgt gca tcg acc aat gcc	1171
Ala Cys Leu Pro Glu Asp Lys Arg Leu Trp Arg Ala Ser Thr Asn Ala	
345 350 355	
aag gaa atg gat aag ccg aat aga tta gtg cgc gag ttg gtg gag gcg	1219
Lys Glu Met Asp Lys Pro Asn Arg Leu Val Arg Glu Leu Val Glu Ala	
360 365 370	
cga ctt ggt gag act gat tca ccg atg ccg gca gca ctg tcg cag gtc	1267
Arg Leu Gly Glu Thr Asp Ser Pro Met Pro Ala Ala Leu Ser Gln Val	
375 380 385	
tat cag tat gcg caa aaa cgc cgc gtt aaa gaa ggt tta agc aag cag	1315
Tyr Gln Tyr Ala Gln Lys Arg Arg Val Lys Glu Gly Leu Ser Lys Gln	
390 395 400 405	
gac acc cag cgt ttg att gat aat ggc cgc gaa aag atc att gag cag	1363
Asp Thr Gln Arg Leu Ile Asp Asn Gly Arg Glu Lys Ile Ile Glu Gln	
410 415 420	
gcc atg aac ggt gtc tac agt gtc cta tcc gcg att tcc gat gag caa	1411
Ala Met Asn Gly Val Tyr Ser Val Leu Ser Ala Ile Ser Asp Glu Gln	
425 430 435	
cgc gat gtc tct acg gcc atg ttg aca gtc atg cgt caa gac tat gag	1459
Arg Asp Val Ser Thr Ala Met Leu Thr Val Met Arg Gln Asp Tyr Glu	
440 445 450	
gat ttg ctc gat ggt att gcg cgg aag aag agc aag gat cta gac gag	1507
Asp Leu Leu Asp Gly Ile Ala Arg Lys Lys Ser Lys Asp Leu Asp Glu	
455 460 465	
cag ggt agt agt gga tca caa gag gtg ggg aaa gaa gag cct gag cca	1555
Gln Gly Ser Ser Gly Ser Gln Glu Val Gly Lys Glu Glu Pro Glu Pro	
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agt att gag gaa ttt ggg ctg cgt ttg cgg tcg tat tca gca cgc ttg	1603
Ser Ile Glu Glu Phe Gly Leu Arg Leu Arg Ser Tyr Ser Ala Arg Leu	
490 495 500	
aat cat cac cga gaa caa cga gaa gcc ttt gcc gtg aaa aaa cgc tcg	1651
Asn His His Arg Glu Gln Arg Glu Ala Phe Ala Val Lys Lys Arg Ser	
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Trp	Glu	Asp	Ala	Asn	Ser	Gln	Gly	Leu	Ala	Asp	Pro	Thr	Ser	Gln	Val		
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Met	Trp	Ser	Phe	Tyr	Asp	Thr	Glu	Glu	Gln	Tyr	His	Ala	Met	Cys	Gln		
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Ser	Lys	Tyr	Gln	His	Phe	Leu	Thr	Phe	Ala	Pro	Pro	Val	Gly	Gln	Trp		
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gag	aag	caa	tgg	gct	gag	gtt	gct	gat	tac	ggg	aaa	agg	gtt	gtg	ggg	1843	
Glu	Lys	Gln	Trp	Ala	Glu	Val	Ala	Asp	Tyr	Gly	Lys	Arg	Val	Val	Gly		
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ctg	cgt	gca	ctg	cgg	gca	gat	cgt	tct	ttg	gca	cgc	atg	agc	gat	gaa	1891	
Leu	Arg	Ala	Leu	Arg	Ala	Asp	Arg	Ser	Leu	Ala	Arg	Met	Ser	Asp	Glu		
			585					590					595				
cgt	gca	gct	gaa	gct	ttg	ggg	cgg	caa	ctt	tat	gac	caa	ccc	ggg	ggg	1939	
Arg	Ala	Ala	Glu	Ala	Leu	Gly	Arg	Gln	Leu	Tyr	Asp	Gln	Pro	Gly	Gly		
		600					605					610					
ggg	tta	ttg	gct	cga	aca	ggc	gct	gag	ggg	aaa	gct	ggg	cgt	gcg	gtc	1987	
Gly	Leu	Leu	Ala	Arg	Thr	Gly	Ala	Glu	Gly	Lys	Ala	Gly	Arg	Ala	Val		
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ctg	gat	ggc	cga	att	gag	cgc	atg	atg	gtg	acc	tat	cag	caa	aaa	att	2035	
Leu	Asp	Gly	Arg	Ile	Glu	Arg	Met	Met	Val	Thr	Tyr	Gln	Gln	Lys	Ile		
	630				635				640						645		
gat	gat	ttg	cga	cga	gaa	tgg	gca	cag	ctc	ggg	gca	cgt	tta	gag	gtt	2083	
Asp	Asp	Leu	Arg	Arg	Glu	Trp	Ala	Gln	Leu	Gly	Ala	Arg	Leu	Glu	Val		
				650				655						660			
gaa	ggg	gat	gct	gta	ttg	atg	gat	gca	gca	gat	cta	cgt	gaa	tct	ggg	2131	
Glu	Gly	Asp	Ala	Val	Leu	Met	Asp	Ala	Ala	Asp	Leu	Arg	Glu	Ser	Gly		
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gga	gag	ggg	gca	gat	gaa	cgc	cag	ata	cag	cag	caa	aca	att	gag	ttg	2179	
Gly	Glu	Gly	Ala	Asp	Glu	Arg	Gln	Ile	Gln	Gln	Gln	Thr	Ile	Glu	Leu		
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ccg	gtc	gct	gat	gta	tct	gat	tct	gtg	cgc	aca	tac	ctt	gac	gaa	gag	2227	
Pro	Val	Ala	Asp	Val	Ser	Asp	Ser	Val	Arg	Thr	Tyr	Leu	Asp	Glu	Glu		
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Leu	Arg	Asp	Ser	Arg	Asp	Val	Ser	Ala	His	Asp	Pro	Val	His	Thr	Leu		
	710				715				720						725		
cgt	ggc	agg	ttt	cag	gtc	gtg	ttt	cga	ccg	gag	cat	gat	ttt	gag	cag	2323	
Arg	Gly	Arg	Phe	Gln	Val	Val	Phe	Arg	Pro	Glu	His	Asp	Phe	Glu	Gln		
				730				735						740			
gtg	ggg	ggc	cct	gac	ctg	cgc	gat	ctt	cac	tat	gcc	tgg	ttt	agc	gat	2371	
Val	Gly	Gly	Pro	Asp	Leu	Arg	Asp	Leu	His	Tyr	Ala	Trp	Phe	Ser	Asp		
			745					750					755				
cag	aag	gtc	agt	cag	ccc	att	gtg	tgt	agt	tac	ggg	gag	tta	gtc	acc	2419	
Gln	Lys	Val	Ser	Gln	Pro	Ile	Val	Cys	Ser	Tyr	Gly	Glu	Leu	Val	Thr		

760	765	770	
cag cga cgt tat gct ttt gaa cgc gct cgg gag tgg atg atc agt tcg			2467
Gln Arg Arg Tyr Ala Phe Glu Arg Ala Arg Glu Trp Met Ile Ser Ser			
775	780	785	
cag cag gaa cca gaa gca gtg gca gaa gag ctt gat cat gcc ggc gcg			2515
Gln Gln Glu Pro Glu Ala Val Ala Glu Glu Leu Asp His Ala Gly Ala			
790	795	800	805
gac ata act cgc atg gaa gca acc agt agt gag gta tcc cgt aca ggt			2563
Asp Ile Thr Arg Met Glu Ala Thr Ser Ser Glu Val Ser Arg Thr Gly			
	810	815	820
att ttg cgt agt gcc atg ctt gcc aga att aga gag cag gcg cga caa			2611
Ile Leu Arg Ser Ala Met Leu Ala Arg Ile Arg Glu Gln Ala Arg Gln			
	825	830	835
cgc gct cag cgt gca gcg gaa gag cag gct cgt cgt gag cgt gag ttg			2659
Arg Ala Gln Arg Ala Ala Glu Glu Gln Ala Arg Arg Glu Arg Glu Leu			
	840	845	850
gta gca cag cga caa caa gaa att gat cag gag acc acg caa cca gcg			2707
Val Ala Gln Arg Gln Gln Glu Ile Asp Gln Glu Thr Thr Gln Pro Ala			
	855	860	865
ttc gag gtg gtg caa cga cat gta caa ccg gag tcg gtg cag att aag			2755
Phe Glu Val Val Gln Arg His Val Gln Pro Glu Ser Val Gln Ile Lys			
870	875	880	885
cgg ggt aga aca gtt gcg cta gat aag cga gtg cag cca ctg att cgt			2803
Arg Gly Arg Thr Val Ala Leu Asp Lys Arg Val Gln Pro Leu Ile Arg			
	890	895	900
gat gct gtg gat cga gct gtg ctg gat tca cag ctg cgg agt acc cgt			2851
Asp Ala Val Asp Arg Ala Val Leu Asp Ser Gln Leu Arg Ser Thr Arg			
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<211> 922

<212> PRT

<213> Corynebacterium glutamicum

<400> 2296

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Ser	Gly	Tyr	Met	Ala	Arg	Ser	Asp	Ala	Val	Glu	Ala	Val	Ala	Pro	Ile
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Val	Arg	Asn	Lys	Leu	Asp	Asp	Phe	Ile	Met	Arg	Tyr	Met	Ala	Arg	Asp
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Ser Ala Val Glu Gln Leu Thr Thr Asp Ser Asn Ala Asp Tyr Asp Gln
65 70 75 80

Gln Pro Glu Met Asn Ser Arg Arg Gly Arg Gln Gly Arg Arg Ala Thr
85 90 95

Leu Lys Gln Arg Arg Ala Glu Arg Ser Ala Arg Arg Ala Ala Leu Arg
100 105 110

Ala Gly Val Asn Thr Asp Ser Asp Thr Thr Asn Pro Ser Gln Pro Val
115 120 125

His Pro Arg Glu Leu Ala Glu Phe Thr Thr Gln Asp Gly Gln Arg Val
130 135 140

His Asp Leu Met Leu Arg Ala Gln Gly Asn Gly Gly Val Ala Phe Gly
145 150 155 160

Tyr Gly Asp Val Ser Leu Ser His Asp Asp Leu His Ala Ala Ser Asn
165 170 175

Asn Val Gln Glu Leu Tyr Glu Asn Arg His Thr Val Met Lys Val Val
180 185 190

Leu Ser Phe Thr Gln Asp Tyr Leu Thr Ala His Gly Leu Ile Pro Glu
195 200 205

Asp Leu Asp Ile Lys Arg Ala Gly Asp Tyr Arg Gly Gln Val Asp Gln
210 215 220

Met Lys Leu Arg Met Ala Val Met His Gly Val Asp Arg Leu Ala Gln
225 230 235 240

Arg His Tyr Asp Asp Leu Arg Tyr Val Gly Val Ile Gln Val Asp Thr
245 250 255

Lys His Val His Ala His Leu Thr Met Val Asp Ala Gly Tyr Gly His
260 265 270

Arg Ala Ala Asp Gly Thr Gln Lys Gly Lys Ile Asn Lys Pro Gly Lys
275 280 285

Ala Ile Leu Arg Arg Gly Ile Asp Ala Trp Leu Asp Gln His Gln His
290 295 300

Met Ala His Leu Ser Ala Ala Val Gly Tyr Glu Lys Arg Asn Val Thr
305 310 315 320

Ser Tyr Val Lys Arg Trp Ala Phe His Gln Leu Thr Gln Glu Ser Ala
325 330 335

Ala Gln Phe Val Val Ala Cys Leu Pro Glu Asp Lys Arg Leu Trp Arg
340 345 350

Ala Ser Thr Asn Ala Lys Glu Met Asp Lys Pro Asn Arg Leu Val Arg
355 360 365

Glu Leu Val Glu Ala Arg Leu Gly Glu Thr Asp Ser Pro Met Pro Ala
370 375 380

Ala Leu Ser Gln Val Tyr Gln Tyr Ala Gln Lys Arg Arg Val Lys Glu

385		390		395		400
Gly Leu Ser Lys	Gln Asp Thr Gln Arg Leu Ile Asp Asn Gly Arg Glu					
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Lys Ile Ile Glu Gln Ala Met Asn Gly Val Tyr Ser Val Leu Ser Ala						
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Ile Ser Asp Glu Gln Arg Asp Val Ser Thr Ala Met Leu Thr Val Met						
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Arg Gln Asp Tyr Glu Asp Leu Leu Asp Gly Ile Ala Arg Lys Lys Ser						
	450			455		460
Lys Asp Leu Asp Glu Gln Gly Ser Ser Gly Ser Gln Glu Val Gly Lys						
	465			470		480
Glu Glu Pro Glu Pro Ser Ile Glu Glu Phe Gly Leu Arg Leu Arg Ser						
		485		490		495
Tyr Ser Ala Arg Leu Asn His His Arg Glu Gln Arg Glu Ala Phe Ala						
	500			505		510
Val Lys Lys Arg Ser Trp Glu Asp Ala Asn Ser Gln Gly Leu Ala Asp						
	515			520		525
Pro Thr Ser Gln Val Met Trp Ser Phe Tyr Asp Thr Glu Glu Gln Tyr						
	530			535		540
His Ala Met Cys Gln Ser Lys Tyr Gln His Phe Leu Thr Phe Ala Pro						
	545			550		555
Pro Val Gly Gln Trp Glu Lys Gln Trp Ala Glu Val Ala Asp Tyr Gly						
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Lys Arg Val Val Gly Leu Arg Ala Leu Arg Ala Asp Arg Ser Leu Ala						
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Arg Met Ser Asp Glu Arg Ala Ala Glu Ala Leu Gly Arg Gln Leu Tyr						
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Asp Gln Pro Gly Gly Gly Leu Leu Ala Arg Thr Gly Ala Glu Gly Lys						
	610			615		620
Ala Gly Arg Ala Val Leu Asp Gly Arg Ile Glu Arg Met Met Val Thr						
	625			630		635
Tyr Gln Gln Lys Ile Asp Asp Leu Arg Arg Glu Trp Ala Gln Leu Gly						
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Ala Arg Leu Glu Val Glu Gly Asp Ala Val Leu Met Asp Ala Ala Asp						
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Leu Arg Glu Ser Gly Gly Glu Gly Ala Asp Glu Arg Gln Ile Gln Gln						
	675			680		685
Gln Thr Ile Glu Leu Pro Val Ala Asp Val Ser Asp Ser Val Arg Thr						
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Tyr Leu Asp Glu Glu Leu Arg Asp Ser Arg Asp Val Ser Ala His Asp						
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						720

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                                         Val Lys Leu Asp Asp
                                           1             5

gct atg gtc atg atc gaa cag cgc ctg gtc aaa ggt cgc ggc gca acc 163
Ala Met Val Met Ile Glu Gln Arg Leu Val Lys Gly Arg Gly Ala Thr
          10              15              20
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aag acg caa cta gca ccc tat gag cat atc cag cgc aat att gca gcc 211
Lys Thr Gln Leu Ala Pro Tyr Glu His Ile Gln Arg Asn Ile Ala Ala
25 30 35

cga ggg ttg aga gcc gat gac gga ggc tcg tgc ttc ggt tat ggg gat 259
Arg Gly Leu Arg Ala Asp Asp Gly Gly Ser Cys Phe Gly Tyr Gly Asp
40 45 50

gcg tcg ctg agt aat gac gat gta gca act gct gca gaa gat att cag 307
Ala Ser Leu Ser Asn Asp Asp Val Ala Thr Ala Ala Glu Asp Ile Gln
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gat ttg ttt gcg tgc ggg cat acg gtt atc tca gcg att gtc gtt ttt 355
Asp Leu Phe Ala Cys Gly His Thr Val Ile Ser Ala Ile Val Val Phe
70 75 80 85

gat aag agc tat ctc agt gag cat gga atc atg agc ttt gat ccg aac 403
Asp Lys Ser Tyr Leu Ser Glu His Gly Ile Met Ser Phe Asp Pro Asn
90 95 100

tat ttt ggt cag gat att tat gcg gac acc cat cca gag att gat ctc 451
Tyr Phe Gly Gln Asp Ile Tyr Ala Asp Thr His Pro Glu Ile Asp Leu
105 110 115

atg gaa ttg cgt tta gcc gtg atg aat ggg ctc ttg ggg ctt gag gga 499
Met Glu Leu Arg Leu Ala Val Met Asn Gly Leu Leu Gly Leu Glu Gly
120 125 130

acg ttt ttt gag gat atg cgt tat gtc gca tct atc gag gtg agc cgg 547
Thr Phe Phe Glu Asp Met Arg Tyr Val Ala Ser Ile Glu Val Ser Arg
135 140 145

agc tat gtc tat gcg cac ata atg atg gcg gat gca ggc gtt gac gat 595
Ser Tyr Val Tyr Ala His Ile Met Met Ala Asp Ala Gly Val Asp Asp
150 155 160 165

gca cgc ggt aat gca cag gtg aag att acg gac acc gaa cga gtg ctg 643
Ala Arg Gly Asn Ala Gln Val Lys Ile Thr Asp Thr Glu Arg Val Leu
170 175 180

ttt aga cgt ggt gtt gaa tcc cgg ttt gtg gag caa gag gca cgc aac 691
Phe Arg Arg Gly Val Glu Ser Arg Phe Val Glu Gln Glu Ala Arg Asn
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Val Val Leu
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<213> Corynebacterium glutamicum

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 35 40 45
 Phe Gly Tyr Gly Asp Ala Ser Leu Ser Asn Asp Asp Val Ala Thr Ala
 50 55 60
 Ala Glu Asp Ile Gln Asp Leu Phe Ala Cys Gly His Thr Val Ile Ser
 65 70 75 80
 Ala Ile Val Val Phe Asp Lys Ser Tyr Leu Ser Glu His Gly Ile Met
 85 90 95
 Ser Phe Asp Pro Asn Tyr Phe Gly Gln Asp Ile Tyr Ala Asp Thr His
 100 105 110
 Pro Glu Ile Asp Leu Met Glu Leu Arg Leu Ala Val Met Asn Gly Leu
 115 120 125
 Leu Gly Leu Glu Gly Thr Phe Phe Glu Asp Met Arg Tyr Val Ala Ser
 130 135 140
 Ile Glu Val Ser Arg Ser Tyr Val Tyr Ala His Ile Met Met Ala Asp
 145 150 155 160
 Ala Gly Val Asp Asp Ala Arg Gly Asn Ala Gln Val Lys Ile Thr Asp
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<222> (101)..(1351)

<223> RXA01545

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 Met Lys Leu Ala Gly
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 Phe Asn Thr Asn Ser Pro Ala Ala Gln Arg Val Ala Glu Gln Gly Glu
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 Lys Val Gln Leu Asp Ala Pro Val Tyr Ala Val Phe Thr Pro Asp Val
 25 30 35

gtt gaa gtt gag ttt att ggc acg cag cat gag ccg gta ttg cac gtt 259

Val	Glu	Val	Glu	Phe	Ile	Gly	Thr	Gln	His	Glu	Pro	Val	Leu	His	Val		
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Glu	Gly	Ala	Ile	Asp	Ser	Val	Thr	Ala	Leu	Ser	Gln	Leu	Pro	Tyr	Asp		
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Ile	Gln	Lys	Ile	Thr	Phe	Asp	Ser	Glu	Asn	Gln	Gln	Arg	Phe	Ser	Gly		
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Phe	Tyr	Lys	Phe	Ser	Pro	Gln	Gln	His	Lys	Glu	Leu	Ile	Asp	Lys	Gly		
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Ser	Gln	Asp	Ala	Pro	Pro	Ile	Val	Leu	Val	Gly	Leu	Ser	Glu	Ile	His		
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Gly	Val	Asp	Phe	Ser	Gln	Glu	Ser	Ser	Gly	Tyr	Glu	Leu	Thr	Ser	Met		
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Phe	Glu	Asp	Tyr	Arg	Ser	Gln	Arg	Glu	Ala	Gly	Glu	Ala	Asp	Lys	Asp		
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Leu	Glu	Gln	Glu	Arg	Ala	Leu	Ser	Ala	Ala	Gln	Leu	Met	Ala	Lys	Leu		
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Gly	Met	Ser	Glu	Trp	Glu	Arg	Glu	Val	Thr	Glu	Phe	Tyr	Asn	Glu	Lys		
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Ile	Arg	Ala	Gln	Glu	Pro	Val	Val	Glu	Arg	Glu	Ala	Glu	Arg	Asp	Ser		

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gtt gca cag aag att cag act caa gaa tct gtg cgt gag gca tat att Val Ala Gln Lys Ile Gln Thr Gln Glu Ser Val Arg Glu Ala Tyr Ile 375 380 385			1267
cgc gag caa aag cat ggc tat gac gca tca cct gcg gag ggg cgc aag Arg Glu Gln Lys His Gly Tyr Asp Ala Ser Pro Ala Glu Gly Arg Lys 390 395 400 405			1315
ttt gat gag aaa att gca gaa cgc ggg cta gat cta taacgaggat Phe Asp Glu Lys Ile Ala Glu Arg Gly Leu Asp Leu 410 415			1361
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<400> 2300

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Phe	Thr	Pro	Asp	Val	Val	Glu	Val	Glu	Phe	Ile	Gly	Thr	Gln	His	Glu
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Pro	Val	Leu	His	Val	Glu	Gly	Ala	Ile	Asp	Ser	Val	Thr	Ala	Leu	Ser
	50					55					60				

Gln	Leu	Pro	Tyr	Asp	Ile	Gln	Lys	Ile	Thr	Phe	Asp	Ser	Glu	Asn	Gln
65					70				75					80	

Gln	Arg	Phe	Ser	Gly	Phe	Tyr	Lys	Phe	Ser	Pro	Gln	Gln	His	Lys	Glu
				85					90					95	

Leu Ile Asp Lys Gly Leu Tyr Leu Glu Gly Phe Gln Pro Pro Arg Glu
100 105 110

Met Met Thr Ser Leu Pro Trp Glu Leu Pro Met Asn Ala Asp Val Thr
115 120 125

Val Val Ala Pro Glu Ser Gln Asp Ala Pro Pro Ile Val Leu Val Gly
130 135 140

Leu Ser Glu Ile His Gly Val Asp Phe Ser Gln Glu Ser Ser Gly Tyr
145 150 155 160

Glu Leu Thr Ser Met Phe Glu Asp Tyr Arg Ser Gln Arg Glu Ala Gly
165 170 175

Glu Ala Asp Lys Asp Phe Ser Glu Ser Ile Ser Arg Ala Glu Ile Glu
180 185 190

Gly Lys Asp Ile Phe Ala Asp Ala Asn Arg Thr Arg Thr Gly Val Ser
195 200 205

Ala His Ala Gln Arg Leu Glu Gln Glu Arg Ala Leu Ser Ala Ala Gln
210 215 220

Leu Met Ala Lys Leu Ala Gly Ile Ser Phe Gln Thr Glu Pro Val Leu
225 230 235 240

Val Gly Ala Glu Glu Ser Phe Asp Ala Glu Gln Phe Leu Ala His Asp
245 250 255

Leu Asp Asp Thr Ala Gly Met Ser Glu Trp Glu Arg Glu Val Thr Glu
260 265 270

Phe Tyr Asn Glu Lys Ile Arg Ala Gln Glu Pro Val Val Glu Arg Glu
275 280 285

Ala Glu Arg Asp Ser Asp Ile Glu Thr Glu Val Asp Ala Ala Pro Thr
290 295 300

Val Ser Ala Ala Glu Ile Asn Asp Val Ile His Asp Leu Asp Glu Leu
305 310 315 320

Glu Phe Asp Asp Val Ile Asp Leu Asp Ala Asp Asp Val Val Asn Thr
325 330 335

Ala Glu Val Glu Ala Pro Ala Ser Val Ser Ala Ala Glu Ile Ser Ala
340 345 350

Thr Glu Leu Asp Phe Asp Arg Glu Ser Arg Ala Lys Thr Ala Gln Arg
355 360 365

Glu Ala Ser Arg Arg Val Ala Gln Lys Ile Gln Thr Gln Glu Ser Val
370 375 380

Arg Glu Ala Tyr Ile Arg Glu Gln Lys His Gly Tyr Asp Ala Ser Pro
385 390 395 400

Ala Glu Gly Arg Lys Phe Asp Glu Lys Ile Ala Glu Arg Gly Leu Asp
405 410 415

Leu

Asp Ala Lys Arg Ala Arg Ala Glu Lys Lys Leu Thr Lys Gln Gln Ala
 170 175 180
 aaa gaa gcc aaa aag cag cgc aaa ctt gat gcc att tac tcg gct caa 691
 Lys Glu Ala Lys Lys Gln Arg Lys Leu Asp Ala Ile Tyr Ser Ala Gln
 185 190 195
 cag gct gaa gag act ctg gcg caa cag gca cag tct gag cca gaa gag 739
 Gln Ala Glu Glu Thr Leu Ala Gln Gln Ala Gln Ser Glu Pro Glu Glu
 200 205 210
 tca gac gat aag aac cga cac gac gcc ctc aac gac gct gtt gca gca 787
 Ser Asp Asp Lys Asn Arg His Asp Ala Leu Asn Asp Ala Val Ala Ala
 215 220 225
 gct cgc aac tagctagtta ccacgcctga cac 819
 Ala Arg Asn
 230
 <210> 2302
 <211> 232
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 2302
 Met Ala Arg Ala Lys Asn Lys Lys Gln Arg Gln Leu Gln His Ala His
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 Asp Ala Ala Gln Ala Glu Ile Ala Glu Ala Val Ala Val Asn Thr Val
 20 25 30
 Glu Pro Ile Asn Ala Arg Thr Gly Gly Trp Pro Ser Trp Val Asp Lys
 35 40 45
 Val Trp Lys Leu Thr Gly Ser Leu Gly Gly Trp Phe Ala Phe Leu Val
 50 55 60
 Phe Ala Ile Ala Val Trp Pro Val Ala Ile Leu Ala Ala Gly Thr Val
 65 70 75 80
 Val Thr Ile Ile Gly Thr Trp Gly Val Ser Val Leu Pro Ser Leu Val
 85 90 95
 Ile Ser Ser Ile Gly Ala Ser Ala Gly Val Ile Ile Ser Thr Thr Asp
 100 105 110
 Gly Phe Leu Phe Ser Trp Val Ile Pro Val Leu Phe Leu Met Ile Val
 115 120 125
 Leu Ala Leu Val Val Met Lys Val Leu Asn Leu Ile Phe Gly Ala Leu
 130 135 140
 Trp Arg Phe Thr Met Thr Leu Arg Gln Gly Leu Tyr Ala Gly Arg Glu
 145 150 155 160
 Lys Ile Ser Arg Asp Asp Ala Lys Arg Ala Arg Ala Glu Lys Lys Leu
 165 170 175
 Thr Lys Gln Gln Ala Lys Glu Ala Lys Lys Gln Arg Lys Leu Asp Ala
 180 185 190

Gly Ile Ala Arg Thr Asp Pro Thr Gly Glu Val His Tyr Ala Tyr Asp
 135 140 145

gca gat ctg tcc aac cgc ttt agc agc tta gaa tcc gtg gtt act cgc 595
 Ala Asp Leu Ser Asn Arg Phe Ser Ser Leu Glu Ser Val Val Thr Arg
 150 155 160 165

att aat ggt aca gag tac agc tat gta tcc acg gtg acg atg aag tcg 643
 Ile Asn Gly Thr Glu Tyr Ser Tyr Val Ser Thr Val Thr Met Lys Ser
 170 175 180

aag cgc tct ggt ggt gag gca gaa aca acc tct acc tca cgc ctt gcc 691
 Lys Arg Ser Gly Gly Glu Ala Glu Thr Thr Ser Thr Ser Arg Leu Ala
 185 190 195

tat gac gtg atc gac ggc aaa att cgt aac ctc gaa gca cgt act gtc 739
 Tyr Asp Val Ile Asp Gly Lys Ile Arg Asn Leu Glu Ala Arg Thr Val
 200 205 210

ccc ggt ggt gtg aaa tac tcg ggc taaaagtttc tggggcaacc ccc 786
 Pro Gly Gly Val Lys Tyr Ser Gly
 215 220

<210> 2304

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 2304

Met Phe Asp Gln Val Lys Arg Phe Phe Val Arg Asn Ile Val Met Ile
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Ile Ala Leu Ile Leu Ala Val Val Val Ile Ile Val Ala Thr Ser Thr
 20 25 30

Ser Ala Asp Arg His Ala Val Leu Lys Arg Gln Thr Gly Glu Ile Met
 35 40 45

Ala Leu Gln Gln Glu Arg Asp Ala Leu Asn Ser Lys Leu Glu Gly Gln
 50 55 60

Leu Glu Gln Val Val Arg Asp Ala Thr Gly Gly Met Asp Ile Glu His
 65 70 75 80

Lys Ala Ala Asp Asp Ala Val Val Arg Glu Phe Leu Ser Met Ala Leu
 85 90 95

Thr Trp Asp Ser Val Arg Asp Tyr Leu Asp Val Arg Glu Gln Val Met
 100 105 110

Arg Val Tyr Asp Leu Asp Glu Glu Ser Gln Phe Met Ser Val Phe Met
 115 120 125

Pro Gly Glu Met Ala Gly Ile Ala Arg Thr Asp Pro Thr Gly Glu Val
 130 135 140

His Tyr Ala Tyr Asp Ala Asp Leu Ser Asn Arg Phe Ser Ser Leu Glu
 145 150 155 160

Ser Val Val Thr Arg Ile Asn Gly Thr Glu Tyr Ser Tyr Val Ser Thr

165	170	175
Val Thr Met Lys Ser Lys Arg Ser Gly Gly Glu Ala Glu Thr Thr Ser		
180	185	190
Thr Ser Arg Leu Ala Tyr Asp Val Ile Asp Gly Lys Ile Arg Asn Leu		
195	200	205
Glu Ala Arg Thr Val Pro Gly Gly Val Lys Tyr Ser Gly		
210	215	220

<210> 2305
 <211> 1131
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1108)
 <223> RXA01548

 <400> 2305
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 agaaaacttca ataacttagt aacttttaaaa ggggtttaat atg gct gag aat aat 115
Met Ala Glu Asn Asn
1 5

 ggc ggg tcg gat gac ctt aag ccc atc tct gtc gat ggg gtc gtc aat 163
 Gly Gly Ser Asp Asp Leu Lys Pro Ile Ser Val Asp Gly Val Val Asn
10 15 20

 ggg gaa gtg cgc agc gac aaa gaa aag cag gcg ttc gag aag att acc 211
 Gly Glu Val Arg Ser Asp Lys Glu Lys Gln Ala Phe Glu Lys Ile Thr
25 30 35

 ggt gat gat ctg cgt cgt cgt gca gaa caa atc cgt aaa cgt cgt tta 259
 Gly Asp Asp Leu Arg Arg Arg Ala Glu Gln Ile Arg Lys Arg Arg Leu
40 45 50

 gca aaa gcg caa gaa gat gca cgt aag cgt aag cca ttg ttt ggt ttg 307
 Ala Lys Ala Gln Glu Asp Ala Arg Lys Arg Lys Pro Leu Phe Gly Leu
55 60 65

 ggt cgt atc gct gtc aca gta ctg gct ggc gcc gta ttt att ggt aca 355
 Gly Arg Ile Ala Val Thr Val Leu Ala Gly Ala Val Phe Ile Gly Thr
70 75 80 85

 acg ttg tgg atc agt acc acc tcg ggc ggc ttt gac gac aag gtg agt 403
 Thr Leu Trp Ile Ser Thr Thr Ser Gly Gly Phe Asp Asp Lys Val Ser
90 95 100

 gca aac aat gag cag att gtc act ctg cgt aat gaa gtc aac gac tta 451
 Ala Asn Asn Glu Gln Ile Val Thr Leu Arg Asn Glu Val Asn Asp Leu
105 110 115

 aaa aac act gca gag aca atg ccc aaa aaa gag act ctt gct agt caa 499
 Lys Asn Thr Ala Glu Thr Met Pro Lys Lys Glu Thr Leu Ala Ser Gln
120 125 130

ttt gac gca gca acc tca cgt gca cag aat gtg gct gac tta cag aat 547
 Phe Asp Ala Ala Thr Ser Arg Ala Gln Asn Val Ala Asp Leu Gln Asn
 135 140 145
 cag tta gcc ggc att att acc agt gtt gat gat gat gcc gcg acc gag 595
 Gln Leu Ala Gly Ile Ile Thr Ser Val Asp Asp Asp Ala Ala Thr Glu
 150 155 160 165
 cag ttc aag aca att gtt gat gag ctg aaa ccg aaa ttc acg gtc tct 643
 Gln Phe Lys Thr Ile Val Asp Glu Leu Lys Pro Lys Phe Thr Val Ser
 170 175 180
 gct ggt acg aca ggt gaa ttt cct gcg gcg ggt cgt tgg tac cag cca 691
 Ala Gly Thr Thr Gly Glu Phe Pro Ala Ala Gly Arg Trp Tyr Gln Pro
 185 190 195
 caa gaa gtt gtt gtc gga gat aac aac cga ccc acc tgg gcg ccg atg 739
 Gln Glu Val Val Val Gly Asp Asn Asn Arg Pro Thr Trp Ala Pro Met
 200 205 210
 ggg gct gag tcc tgg gga tgg act gtg acc cct acà ctg tcg atg tca 787
 Gly Ala Glu Ser Trp Gly Trp Thr Val Thr Pro Thr Leu Ser Met Ser
 215 220 225
 gat acc gag cac gtt gtg gtg atg tgg gag gcc cgc ttg acc gga ggt 835
 Asp Thr Glu His Val Val Met Trp Glu Ala Arg Leu Thr Gly Gly
 230 235 240 245
 gag cgt tac ggt gcg ctg ttg gcg tgg gtg aca gcc gat tac aac atc 883
 Glu Arg Tyr Gly Ala Leu Leu Ala Trp Val Thr Ala Asp Tyr Asn Ile
 250 255 260
 aac acc ggc gtg ttt agc tcg ctg gcg ttg gcg cat acc tat gaa gga 931
 Asn Thr Gly Val Phe Ser Ser Leu Ala Leu Ala His Thr Tyr Glu Gly
 265 270 275
 cac cag cgt att ggt gca acc acc tca cca agt gaa ttt ggt gcc cac 979
 His Gln Arg Ile Gly Ala Thr Thr Ser Pro Ser Glu Phe Gly Ala His
 280 285 290
 ggc aca aat gca gag gcg agc gct gca cgt gct ggc agt gaa ggc ggg 1027
 Gly Thr Asn Ala Glu Ala Ser Ala Ala Arg Ala Gly Ser Glu Gly Gly
 295 300 305
 ggg ctt gag ggc gag gct att ttc gtt gat gag ctg cag cgg gca cta 1075
 Gly Leu Glu Gly Glu Ala Ile Phe Val Asp Glu Leu Gln Arg Ala Leu
 310 315 320 325
 gag atc gct cag ctg aac aaa cag gag aac aga taatgacgac acgaaatgta 1128
 Glu Ile Ala Gln Leu Asn Lys Gln Glu Asn Arg
 330 335

gat 1131

<210> 2306

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 2306

Met Ala Glu Asn Asn Gly Gly Ser Asp Asp Leu Lys Pro Ile Ser Val
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 Asp Gly Val Val Asn Gly Glu Val Arg Ser Asp Lys Glu Lys Gln Ala
 20 25 30
 Phe Glu Lys Ile Thr Gly Asp Asp Leu Arg Arg Arg Ala Glu Gln Ile
 35 40 45
 Arg Lys Arg Arg Leu Ala Lys Ala Gln Glu Asp Ala Arg Lys Arg Lys
 50 55 60
 Pro Leu Phe Gly Leu Gly Arg Ile Ala Val Thr Val Leu Ala Gly Ala
 65 70 75 80
 Val Phe Ile Gly Thr Thr Leu Trp Ile Ser Thr Thr Ser Gly Gly Phe
 85 90 95
 Asp Asp Lys Val Ser Ala Asn Asn Glu Gln Ile Val Thr Leu Arg Asn
 100 105 110
 Glu Val Asn Asp Leu Lys Asn Thr Ala Glu Thr Met Pro Lys Lys Glu
 115 120 125
 Thr Leu Ala Ser Gln Phe Asp Ala Ala Thr Ser Arg Ala Gln Asn Val
 130 135 140
 Ala Asp Leu Gln Asn Gln Leu Ala Gly Ile Ile Thr Ser Val Asp Asp
 145 150 155 160
 Asp Ala Ala Thr Glu Gln Phe Lys Thr Ile Val Asp Glu Leu Lys Pro
 165 170 175
 Lys Phe Thr Val Ser Ala Gly Thr Thr Gly Glu Phe Pro Ala Ala Gly
 180 185 190
 Arg Trp Tyr Gln Pro Gln Glu Val Val Val Gly Asp Asn Asn Arg Pro
 195 200 205
 Thr Trp Ala Pro Met Gly Ala Glu Ser Trp Gly Trp Thr Val Thr Pro
 210 215 220
 Thr Leu Ser Met Ser Asp Thr Glu His Val Val Val Met Trp Glu Ala
 225 230 235 240
 Arg Leu Thr Gly Gly Glu Arg Tyr Gly Ala Leu Leu Ala Trp Val Thr
 245 250 255
 Ala Asp Tyr Asn Ile Asn Thr Gly Val Phe Ser Ser Leu Ala Leu Ala
 260 265 270
 His Thr Tyr Glu Gly His Gln Arg Ile Gly Ala Thr Thr Ser Pro Ser
 275 280 285
 Glu Phe Gly Ala His Gly Thr Asn Ala Glu Ala Ser Ala Ala Arg Ala
 290 295 300
 Gly Ser Glu Gly Gly Gly Leu Glu Gly Glu Ala Ile Phe Val Asp Glu
 305 310 315 320
 Leu Gln Arg Ala Leu Glu Ile Ala Gln Leu Asn Lys Gln Glu Asn Arg

335

<400> 2307

cgt tca aag ctt ttg gag ttt atc gat aac gac gaa gct ttc tcc ttc 643

Arg Ser Lys Leu Leu Glu Phe Ile Asp Asn Asp Glu Ala Phe Ser Phe
 170 175 180
 ggt aaa gat ttc ctt ttg ctc tct tcg gcg aag ttc act cca ggc cat 691
 Gly Lys Asp Phe Leu Leu Leu Ser Ser Ala Lys Phe Thr Pro Gly His
 185 190 195
 att gat ata agc cag cgc aag ggt gtt gat gtc ctc ctc ccg ttg gct 739
 Ile Asp Ile Ser Gln Arg Lys Gly Val Asp Val Leu Leu Pro Leu Ala
 200 205 210
 tgt gta ttg ccc atg caa cgc cat ttg tgg tgg cag gag ctg aaa gtt 787
 Cys Val Leu Pro Met Gln Arg His Leu Trp Trp Gln Glu Leu Lys Val
 215 220 225
 ttg cca att aac ctg gct gat ata ctt ttg gga aat gaa att gcc caa 835
 Leu Pro Ile Asn Leu Ala Asp Ile Leu Leu Gly Asn Glu Ile Ala Gln
 230 235 240 245
 atg ggt ttc aag atc gtt tcc aaa gtt ttg aaa aac aaa gta tct gga 883
 Met Gly Phe Lys Ile Val Ser Lys Val Leu Lys Asn Lys Val Ser Gly
 250 255 260
 aca aat aac aag gcg atg gcg gca ttg gtt ttc gct gaa ctt gtg agg 931
 Thr Asn Asn Lys Ala Met Ala Ala Leu Val Phe Ala Glu Leu Val Arg
 265 270 275
 gat atg gtt gat cag cca act gaa ttg ctt cag aag gct cgt gag gaa 979
 Asp Met Val Asp Gln Pro Thr Glu Leu Leu Gln Lys Ala Arg Glu Glu
 280 285 290
 gcc gtc gga agg cgt gaa ttc ctt aaa gcg att act gca gaa ttc acc 1027
 Ala Val Gly Arg Arg Glu Phe Leu Lys Ala Ile Thr Ala Glu Phe Thr
 295 300 305
 agg aag ctg aat caa gcc gaa gct gat cag gtt tta gtt cgg gac ttt 1075
 Arg Lys Leu Asn Gln Ala Glu Ala Asp Gln Val Leu Val Arg Asp Phe
 310 315 320 325
 gca tgacactcat gtgggcaacc cgt 1101
 Ala

<210> 2308

<211> 326

<212> PRT

<213> Corynebacterium glutamicum

<400> 2308

Met Tyr Leu Gly Met Lys Glu Asp Ser Leu Ala Pro Pro Gln Asn Arg
 1 5 10 15

Phe Glu Ser His Lys Thr Val Phe Ser Leu Lys Gln Lys Asn Ile Pro
 20 25 30

Ile Lys Asp Ala Ala Lys Ser Asp Gln Val Asn Leu Thr Trp His Asp
 35 40 45

Tyr Pro Gly Glu Trp Phe Glu Gly Gly Ala Val Thr Asp Ser Glu Lys
 50 55 60

Gln Asp Lys Val Glu Thr Phe Arg Asn Leu Leu Gly Ser Asp Val Ala
 65 70 75 80
 Leu Phe Leu Val Asp Gly Gln Lys Leu His Asp Tyr Ala Asn Glu Glu
 85 90 95
 Glu Arg Tyr Leu Ser Tyr Leu Phe Asp Gly Phe Ile Glu Asn Leu Asn
 100 105 110
 Gln Ile Lys Asp Ala Ile Leu Glu Gly Gly Lys Gln Leu Gln Gln Phe
 115 120 125
 Pro Arg Ile Trp Val Ile Ala Leu Ser Lys Ala Asp Leu Trp Pro Asp
 130 135 140
 Leu Gln Val Lys Asp Phe Glu Asn Leu Leu Asn Lys Lys Ala Gly Asn
 145 150 155 160
 Glu Ile Ile Ala Leu Arg Ser Lys Leu Leu Glu Phe Ile Asp Asn Asp
 165 170 175
 Glu Ala Phe Ser Phe Gly Lys Asp Phe Leu Leu Leu Ser Ser Ala Lys
 180 185 190
 Phe Thr Pro Gly His Ile Asp Ile Ser Gln Arg Lys Gly Val Asp Val
 195 200 205
 Leu Leu Pro Leu Ala Cys Val Leu Pro Met Gln Arg His Leu Trp Trp
 210 215 220
 Gln Glu Leu Lys Val Leu Pro Ile Asn Leu Ala Asp Ile Leu Leu Gly
 225 230 235 240
 Asn Glu Ile Ala Gln Met Gly Phe Lys Ile Val Ser Lys Val Leu Lys
 245 250 255
 Asn Lys Val Ser Gly Thr Asn Asn Lys Ala Met Ala Ala Leu Val Phe
 260 265 270
 Ala Glu Leu Val Arg Asp Met Val Asp Gln Pro Thr Glu Leu Leu Gln
 275 280 285
 Lys Ala Arg Glu Glu Ala Val Gly Arg Arg Glu Phe Leu Lys Ala Ile
 290 295 300
 Thr Ala Glu Phe Thr Arg Lys Leu Asn Gln Ala Glu Ala Asp Gln Val
 305 310 315 320
 Leu Val Arg Asp Phe Ala
 325

<210> 2309

<211> 2265

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2242)

<400> 2309

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Leu Lys Lys His Val
1 5

acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt 163
Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu
10 15 20

ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca 211
Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro
25 30 35

gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc 259
Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser
40 45 50

gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc 307
Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly
55 60 65

agc gac aaa gtt ctc tat acc gaa gat gct tta agt atc gaa gat ggc 355
 Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly
 70 75 80 85

aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg 403
Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala
90 95 100

atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa 451
Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln
105 110 115

gtt gaa cct tgt gct cca ggt cag ttt gaa aag ttc acc agt gcg cgc 499
Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg
120 125 130

atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act 547
Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr
135 140 145

gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg 595
Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp
150 155 160 165

atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc 643
Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu
170 175 180

tac	gga	gaa	cta	gac	ctg	gta	gag	cac	ttt	tct	tac	gat	ctt	cgc	tcg	691
Tyr	Gly	Glu	Leu	Asp	Leu	Val	Glu	His	Phe	Ser	Tyr	Asp	Leu	Arg	Ser	
			185					190					195			

cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc 739
Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val
200 205 210

aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu 215 220 225	787
gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val 230 235 240 245	835
gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn 250 255 260	883
gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala 265 270 275	931
cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn 280 285 290	979
caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu 295 300 305	1027
gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly 310 315 320 325	1075
tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu 330 335 340	1123
ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu 345 350 355	1171
cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser 360 365 370	1219
tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu 375 380 385	1267
caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val 390 395 400 405	1315
acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp Ile Ala Thr Pro Glu 410 415 420	1363
aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser 425 430 435	1411
tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu 440 445 450	1459
acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc	1507

Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg 455 460 465	
ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp 470 475 480 485	1555
gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg 490 495 500	1603
gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg 505 510 515	1651
cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly 520 525 530	1699
gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe 535 540 545	1747
acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly 550 555 560 565	1795
aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys 570 575 580	1843
ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu 585 590 595	1891
att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr 600 605 610	1939
gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp 615 620 625	1987
cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro 630 635 640 645	2035
gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp 650 655 660	2083
gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu 665 670 675	2131
acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe 680 685 690	2179
aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe	2227

695

700

705

atg aga cag ttc aag taatccttgt gggcgctttg tct
 Met Arg Gln Phe Lys
 710

2265

<210> 2310

<211> 714

<212> PRT

<213> Corynebacterium glutamicum

<400> 2310

Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe
 1 5 10 15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala
 20 25 30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val
 35 40 45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg
 50 55 60

Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu
 65 70 75 80

Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val
 85 90 95

Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn
 100 105 110

Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys
 115 120 125

Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe
 130 135 140

Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val
 145 150 155 160

Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala
 165 170 175

Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser
 180 185 190

Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys
 195 200 205

Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys
 210 215 220

Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr
 225 230 235 240

Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg
 245 250 255

Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp
 260 265 270
 Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp
 275 280 285
 Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro
 290 295 300
 Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg
 305 310 315 320
 Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro
 325 330 335
 Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg
 340 345 350
 Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp
 355 360 365
 Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln
 370 375 380
 Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
 385 390 395 400
 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
 405 410 415
 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
 420 425 430
 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
 435 440 445
 Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
 450 455 460
 Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
 465 470 475 480
 Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
 485 490 495
 Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
 500 505 510
 Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
 515 520 525
 Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
 530 535 540
 Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
 545 550 555 560
 Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
 565 570 575
 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly

Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser
 70 75 80 85
 ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac 403
 Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr
 90 95 100
 ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc 450
 Gly Val Asn Gly Pro Val Asp Ala Asn
 105 110
 ttt 453

<210> 2312
 <211> 110
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2312
 Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala
 1 5 10 15
 Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
 20 25 30
 Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
 35 40 45
 Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
 50 55 60
 His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
 65 70 75 80
 Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
 85 90 95
 Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
 100 105 110

<210> 2313
 <211> 1143
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1120)
 <223> RXA01575

<400> 2313
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 gttaggtgcc accgacccca gtgatgataa cttgattgtc atg aaa tcc att gat 115
 Met Lys Ser Ile Asp
 1 5
 ctt gag cag ctg gcg ggc acg caa tcg cgc acg tat caa tcg cga aag 163
 Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr Tyr Gln Ser Arg Lys

10	15	20	
atc acc gat gag atg gtc gcc cgg ccg	gtg cat gtg gcg atc gcg ctg		211
Ile Thr Asp Glu Met Val Ala Arg Pro	Val His Val Ala Ile Ala Leu		
25	30	35	
tgg gaa gtg ccg tgg gag tcg gca aaa	tcc ggc aag att gag ggt tgg		259
Trp Glu Val Pro Trp Glu Ser Ala Lys	Ser Gly Lys Ile Glu Gly Trp		
40	45	50	
gtc att gcc gtg gat tcg ccg cgt ggg	ccg ttt gtg cgc agc ggg cag		307
Val Ile Ala Val Asp Ser Pro Arg Gly	Arg Phe Val Arg Ser Gly Gln		
55	60	65	
acc aaa aat ggc gac gcc gtc aac cgg	act gtg tcg atg ctg aaa tca		355
Thr Lys Asn Gly Asp Ala Val Asn Arg	Thr Val Ser Met Leu Lys Ser		
70	75	80	85
gcg ttg aaa ggg gtc cgc ggg aag gcg	tgg att gta act ggg cgt cga		403
Ala Leu Lys Gly Val Arg Gly Lys Ala	Trp Ile Val Thr Gly Arg Arg		
90	95	100	
caa gca gct tta cgc gca gcc ctg gtg	cgc gaa aac tac ctg gtc acc		451
Gln Ala Ala Leu Arg Ala Ala Leu Val	Arg Glu Asn Tyr Leu Val Thr		
105	110	115	
gga agc ttc gcc gag caa aat agg gcc	ggc gtg aag gcg tcg gcg atc		499
Gly Ser Phe Ala Glu Gln Asn Arg Ala	Gly Val Lys Ala Ser Ala Ile		
120	125	130	
tcg cgc cgc gcc gaa caa tcc gcg ctc	tac aag gcg aaa aaa atc ggc		547
Ser Arg Arg Ala Glu Gln Ser Ala Leu	Tyr Lys Ala Lys Lys Ile Gly		
135	140	145	
gaa ttc gcc gag cgc gcc cca cgc gtc	aaa gag cgg caa gag gca cat		595
Glu Phe Ala Glu Arg Ala Pro Arg Val	Lys Glu Arg Gln Glu Ala His		
150	155	160	165
tgg tgg cca cgg ttg tca cgc acg caa	ggc acc gca ggc gtt tta cgc		643
Trp Trp Pro Arg Leu Ser Arg Thr Gln	Gly Thr Ala Gly Val Leu Arg		
170	175	180	
tta gcg acg gac gcc tct acc gat ggg	gtc ttc cgc ggc gcc atg tgc		691
Leu Ala Thr Asp Ala Ser Thr Asp Gly	Val Phe Arg Gly Ala Met Cys		
185	190	195	
ttc gta gcc tca aac ggc gac tac ctc	ctg gag acc caa gac acc acc		739
Phe Val Ala Ser Asn Gly Asp Tyr Leu	Leu Glu Thr Gln Asp Thr Thr		
200	205	210	
gca agc tcc gac gaa tta gaa ctc gaa	agc atc acc cac gcc ctg atc		787
Ala Ser Ser Asp Glu Leu Glu Leu Glu	Ser Ile Thr His Ala Leu Ile		
215	220	225	
tac ctc aaa acc atc ggc gcg acc caa	gcc atc atc gaa tcc gac agc		835
Tyr Leu Lys Thr Ile Gly Ala Thr Gln	Ala Ile Ile Glu Ser Asp Ser		
230	235	240	245
aaa gcc gca ctt gaa gcc atc gac ttc	atc ctc aac aac cga ccg cgc		883
Lys Ala Ala Leu Glu Ala Ile Asp Phe	Ile Leu Asn Asn Arg Pro Arg		
250	255	260	

cgg ggc agg tgg cgc ggc atc acc gca tgc gcc cgc aac cgg ttc cgg 931
 Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala Arg Asn Arg Phe Arg
 265 270 275

gat gcc tgg gaa gcg ctt atc gac gac tgc gtt gtg gaa tta tcc cgc 979
 Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val Val Glu Leu Ser Arg
 280 285 290

gta cta ggg cac gcc ggg gat cca ctg aac caa gca gcc gac caa atc 1027
 Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln Ala Ala Asp Gln Ile
 295 300 305

gca tac atg ggc atg cgc gcc gta att ttt gaa caa aaa tcc gca cac 1075
 Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu Gln Lys Ser Ala His
 310 315 320 325

ccc aca ttg ctc aaa gga att gac aag gcg ctt cgc aag gcc gag 1120
 Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu Arg Lys Ala Glu
 330 335 340

taagggtgggc aacgagtcgg tga 1143

<210> 2314
 <211> 340
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2314
 Met Lys Ser Ile Asp Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr
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Tyr Gln Ser Arg Lys Ile Thr Asp Glu Met Val Ala Arg Pro Val His
 20 25 30

Val Ala Ile Ala Leu Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly
 35 40 45

Lys Ile Glu Gly Trp Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe
 50 55 60

Val Arg Ser Gly Gln Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val
 65 70 75 80

Ser Met Leu Lys Ser Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile
 85 90 95

Val Thr Gly Arg Arg Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu
 100 105 110

Asn Tyr Leu Val Thr Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val
 115 120 125

Lys Ala Ser Ala Ile Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys
 130 135 140

Ala Lys Lys Ile Gly Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu
 145 150 155 160

Arg Gln Glu Ala His Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr

165	170	175
Ala Gly Val Leu Arg Leu Ala Thr Asp	Ala Ser Thr Asp Gly Val Phe	
180	185	190
Arg Gly Ala Met Cys Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu		
195	200	205
Thr Gln Asp Thr Thr Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile		
210	215	220
Thr His Ala Leu Ile Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile		
225	230	235
Ile Glu Ser Asp Ser Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu		
245	250	255
Asn Asn Arg Pro Arg Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala		
260	265	270
Arg Asn Arg Phe Arg Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val		
275	280	285
Val Glu Leu Ser Arg Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln		
290	295	300
Ala Ala Asp Gln Ile Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu		
305	310	315
Gln Lys Ser Ala His Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu		
325	330	335
Arg Lys Ala Glu		
340		

<210> 2315
 <211> 498
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(475)
 <223> RXA01577

<400> 2315
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 Met Thr Gln Thr Thr
 1 5
 acc caa atc atc atc cag ata ctg ctt ctc ctg gca acc gca gca ctg 163
 Thr Gln Ile Ile Ile Gln Ile Leu Leu Leu Leu Ala Thr Ala Ala Leu
 10 15 20
 gca cta tat ttc ctc cga aac cgc cgc aaa gcc cgc gcc aaa gca tgg 211
 Ala Leu Tyr Phe Leu Arg Asn Arg Arg Lys Ala Arg Ala Lys Ala Trp
 25 30 35

gtg aaa atc ggc ttc gta gta ttc att ttc gcc gca gta tgg gca gtg 259
Val Lys Ile Gly Phe Val Val Phe Ile Phe Ala Ala Val Trp Ala Val
40 45 50

ctc cgc ccc gat gac ctc acc caa cta gcc aac ttt gtg ggc gtg gac 307
Leu Arg Pro Asp Asp Leu Thr Gln Leu Ala Asn Phe Val Gly Val Asp
55 60 65

cgc ggc acc gac cta atg ctt tac gcc ctg gtt gtg gca ttt atg ttc 355
Arg Gly Thr Asp Leu Met Leu Tyr Ala Leu Val Val Ala Phe Met Phe
70 75 80 85

acc acg ctg tcc agt tat gtg cgt ttc cgt gaa caa gag ctg cgt tat 403
Thr Thr Leu Ser Ser Tyr Val Arg Phe Arg Glu Gln Glu Leu Arg Tyr
90 95 100

tcc aag ctg gcc cgc gct gtc gct ttg caa aat gtg gtg ctg ccg gag 451
Ser Lys Leu Ala Arg Ala Val Ala Leu Gln Asn Val Val Leu Pro Glu
105 110 115

gat tcc cag ggt tct gac ccc gct taggaaagcg cttggcctct gga 498
Asp Ser Gln Gly Ser Asp Pro Ala
120 125

<210> 2316

<211> 125

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2316

Met Thr Gln Thr Thr Thr Gln Ile Ile Ile Gln Ile Leu Leu Leu Leu
1 5 10 15

Ala Thr Ala Ala Leu Ala Leu Tyr Phe Leu Arg Asn Arg Arg Lys Ala
20 25 30

Arg Ala Lys Ala Trp Val Lys Ile Gly Phe Val Val Phe Ile Phe Ala
35 40 45

Ala Val Trp Ala Val Leu Arg Pro Asp Asp Leu Thr Gln Leu Ala Asn
50 55 60

Phe Val Gly Val Asp Arg Gly Thr Asp Leu Met Leu Tyr Ala Leu Val
65 70 75 80

Val Ala Phe Met Phe Thr Thr Leu Ser Ser Tyr Val Arg Phe Arg Glu
85 90 95

Gln Glu Leu Arg Tyr Ser Lys Leu Ala Arg Ala Val Ala Leu Gln Asn
100 105 110

Val Val Leu Pro Glu Asp Ser Gln Gly Ser Asp Pro Ala
115 120 125

<210> 2317

<211> 507

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) . . (484)

<223> RXA01579

<400> 2317

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ttgtgagaag ggtgctcagc agcaatgccc aggtgcgtcg ttg acc gag gta ttc 115
Leu Thr Glu Val Phe
1 5

aac act gac cag cgg gtg ctt aac gcg ctt ttc aat gtt gta gaa gaa 163
Asn Thr Asp Gln Arg Val Leu Asn Ala Leu Phe Asn Val Val Glu Glu
10 15 20

gat gac tcc ggc gat acc gat gat gaa cag cac aac cac cag aat cca 211
Asp Asp Ser Gly Asp Thr Asp Asp Glu Gln His Asn His Gln Asn Pro
25 30 35

gtt cgc ggc acc gag ttt gcc ggc ctc gtt gaa agc cat gag caa aga 259
Val Arg Gly Thr Glu Phe Ala Gly Leu Val Glu Ser His Glu Gln Arg
40 45 50

tcc aat gga cac cgc cag tgg cag cac acc aag cca gtc cat ctt cgg 307
Ser Asn Gly His Arg Gln Trp Gln His Thr Lys Pro Val His Leu Arg
55 60 65

ggt ttc ttc agc ggt gga ttc ctt cac gct gaa agg cag tgc gag ggc 355
Gly Phe Phe Ser Gly Gly Phe Leu His Ala Glu Arg Gln Cys Glu Gly
70 75 80 85

agc gac agc gca gaa agc agc cat gac cca gaa gat gga acg gaa acc 403
Ser Asp Ser Ala Glu Ser Ser His Asp Pro Glu Asp Gly Thr Glu Thr
90 95 100

aag tgt ttc agc caa cca gcc acc agc aag cgc gtc cac gcc gcc gat 451
Lys Cys Phe Ser Gln Pro Ala Thr Ser Lys Arg Val His Ala Ala Asp
105 110 115

acc acc gtt gac aga ggt aac aat tcc gag aag tagcgcatat tgcttttcat 504
Thr Thr Val Asp Arg Gly Asn Asn Ser Glu Lys
120 125

tgg 507

<210> 2318

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 2318

Leu Thr Glu Val Phe Asn Thr Asp Gln Arg Val Leu Asn Ala Leu Phe
1 5 10 15

Asn Val Val Glu Glu Asp Asp Ser Gly Asp Thr Asp Asp Glu Gln His
20 25 30

Asn His Gln Asn Pro Val Arg Gly Thr Glu Phe Ala Gly Leu Val Glu
35 40 45

Ser His Glu Gln Arg Ser Asn Gly His Arg Gln Trp Gln His Thr Lys
 50 55 60

Pro Val His Leu Arg Gly Phe Phe Ser Gly Gly Phe Leu His Ala Glu
 65 70 75 80

Arg Gln Cys Glu Gly Ser Asp Ser Ala Glu Ser Ser His Asp Pro Glu
 85 90 95

Asp Gly Thr Glu Thr Lys Cys Phe Ser Gln Pro Ala Thr Ser Lys Arg
 100 105 110

Val His Ala Ala Asp Thr Thr Val Asp Arg Gly Asn Asn Ser Glu Lys
 115 120 125

<210> 2319
 <211> 750
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(727)
 <223> RXA01585

<400> 2319
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ctactgatga ggtgcagtcg caggaagctc tagaaaagta gtg gtt gag act ctt 115
 Val Val Glu Thr Leu
 1 5

tct atc acc tca ggt gcg gct ggc ctg cag gcg ctt gtt gcg cgt gcg 163
 Ser Ile Thr Ser Gly Ala Ala Gly Leu Gln Ala Leu Val Ala Arg Ala
 10 15 20

gtt ggt ttg aat gag ttg gcg agc gcg cgt ttc cgc cag ctg acg cca 211
 Val Gly Leu Asn Glu Leu Ala Ser Ala Arg Phe Arg Gln Leu Thr Pro
 25 30 35

gag gtc gtt gat gtt ttt gtc acc act ccg ttc aac gtg acg gcg tcg 259
 Glu Val Val Asp Val Phe Val Thr Thr Pro Phe Asn Val Thr Ala Ser
 40 45 50

cgc cgg gta ttt ggt gtg gcg ggt cgc gat ggc gct gca gtt ggc gcg 307
 Arg Arg Val Phe Gly Val Ala Gly Arg Asp Gly Ala Ala Val Gly Ala
 55 60 65

aag gat ttg ctg cag gca ctg agc gag ggc cgg gaa gac gta ggc acc 355
 Lys Asp Leu Leu Gln Ala Leu Ser Glu Gly Arg Glu Asp Val Gly Thr
 70 75 80 85

tcc cgc gac gcc agc tgg ccg ggc tca ttg ccg cca gcc acg ggc ttt 403
 Ser Arg Asp Ala Ser Trp Pro Gly Ser Leu Pro Pro Ala Thr Gly Phe
 90 95 100

acg ctt gtc gac gaa ctg ccc acc cac gtg gtg cgc act ttg gct gat 451
 Thr Leu Val Asp Glu Leu Pro Thr His Val Val Arg Thr Leu Ala Asp
 105 110 115

cag ggt cag gca ttg gct cgc cag ttc tcc ggc ccg ctt ggc cct ccg 499
 Gln Gly Gln Ala Leu Ala Arg Gln Phe Ser Gly Pro Leu Gly Pro Pro
 120 125 130

gct tcg ttg atg gat cag gaa gtt att tca gca gaa ggc aat ggc aag 547
 Ala Ser Leu Met Asp Gln Glu Val Ile Ser Ala Glu Gly Asn Gly Lys
 135 140 145

aag gcc gga atc ccg atg cgc acg gta ttt acc tgc act tcg ctt ggt 595
 Lys Ala Gly Ile Pro Met Arg Thr Val Phe Thr Cys Thr Ser Leu Gly
 150 155 160 165

ttg atc cca ggt ttt gag gca gcc aat gat gtg ccg agg cac ctg ccg 643
 Leu Ile Pro Gly Phe Glu Ala Ala Asn Asp Val Pro Arg His Leu Arg
 170 175 180

gta tcg gtg aat ggt cgt tgg acc cgc gtt gat gct ccc tat ggc agt 691
 Val Ser Val Asn Gly Arg Trp Thr Arg Val Asp Ala Pro Tyr Gly Ser
 185 190 195

gtt tat cac tcg tca ggt ttg ggt ctg agc gtt ttc taaagcaaga 737
 Val Tyr His Ser Ser Gly Leu Gly Leu Ser Val Phe
 200 205

cccagcctgc aag 750

<210> 2320
 <211> 209
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2320
 Val Val Glu Thr Leu Ser Ile Thr Ser Gly Ala Ala Gly Leu Gln Ala
 1 5 10 15

Leu Val Ala Arg Ala Val Gly Leu Asn Glu Leu Ala Ser Ala Arg Phe
 20 25 30

Arg Gln Leu Thr Pro Glu Val Val Asp Val Phe Val Thr Thr Pro Phe
 35 40 45

Asn Val Thr Ala Ser Arg Arg Val Phe Gly Val Ala Gly Arg Asp Gly
 50 55 60

Ala Ala Val Gly Ala Lys Asp Leu Leu Gln Ala Leu Ser Glu Gly Arg
 65 70 75 80

Glu Asp Val Gly Thr Ser Arg Asp Ala Ser Trp Pro Gly Ser Leu Pro
 85 90 95

Pro Ala Thr Gly Phe Thr Leu Val Asp Glu Leu Pro Thr His Val Val
 100 105 110

Arg Thr Leu Ala Asp Gln Gly Gln Ala Leu Ala Arg Gln Phe Ser Gly
 115 120 125

Pro Leu Gly Pro Pro Ala Ser Leu Met Asp Gln Glu Val Ile Ser Ala
 130 135 140

Glu Gly Asn Gly Lys Lys Ala Gly Ile Pro Met Arg Thr Val Phe Thr
 145 150 155 160

Cys Thr Ser Leu Gly Leu Ile Pro Gly Phe Glu Ala Ala Asn Asp Val
 165 170 175

Pro Arg His Leu Arg Val Ser Val Asn Gly Arg Trp Thr Arg Val Asp
 180 185 190

Ala Pro Tyr Gly Ser Val Tyr His Ser Ser Gly Leu Gly Leu Ser Val
 195 200 205

Phe

<210> 2321

<211> 392

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(369)

<223> RXA01586

<400> 2321

aac aac gcg gcg ttc att gag atc gcg cag gaa gct cga ttg gcg ttt 48
 Asn Asn Ala Ala Phe Ile Glu Ile Ala Gln Glu Ala Arg Leu Ala Phe
 1 5 10 15

gcg gag gat cag ttc cgt gag cgt ggc tat gag atc cct gct gtg ttt 96
 Ala Glu Asp Gln Phe Arg Glu Arg Gly Tyr Glu Ile Pro Ala Val Phe
 20 25 30

gtg cgc cac ttg gaa gtt gat tat ttg cgt gcg atc ttg ccg gat acc 144
 Val Arg His Leu Glu Val Asp Tyr Leu Arg Ala Ile Leu Pro Asp Thr
 35 40 45

acc cag gct gtc gtg gag aca cag gtg acc aag atc ggt aat act tcc 192
 Thr Gln Ala Val Val Glu Thr Gln Val Thr Lys Ile Gly Asn Thr Ser
 50 55 60

ttc agc act cgt caa gag gtc aag gat cgt aac ggt cgt gtg tgc tgc 240
 Phe Ser Thr Arg Gln Glu Val Lys Asp Arg Asn Gly Arg Val Cys Cys
 65 70 75 80

gtg gtt gag tgc gtg cag gtg gct gtc aat gtg cag act gct gcg ccc 288
 Val Val Glu Cys Val Gln Val Ala Val Asn Val Gln Thr Ala Ala Pro
 85 90 95

cgt tcc atc agc aag gtg gag cgc aag gtg ctg acc gct gtc gct act 336
 Arg Ser Ile Ser Lys Val Glu Arg Lys Val Leu Thr Ala Val Ala Thr
 100 105 110

gat gag gtg cag tcg cag gaa gct cta gaa aag tagtggttga gactctttct 389
 Asp Glu Val Gln Ser Gln Glu Ala Leu Glu Lys
 115 120

atc

392

<210> 2322

<211> 123

<212> PRT

<213> Corynebacterium glutamicum

<400> 2322

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Asn Asn Ala Ala Phe Ile Glu Ile Ala Gln Glu Ala Arg Leu Ala Phe
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Ala Glu Asp Gln Phe Arg Glu Arg Gly Tyr Glu Ile Pro Ala Val Phe
                20             25             30
Val Arg His Leu Glu Val Asp Tyr Leu Arg Ala Ile Leu Pro Asp Thr
          35             40             45
Thr Gln Ala Val Val Glu Thr Gln Val Thr Lys Ile Gly Asn Thr Ser
 50             55             60
Phe Ser Thr Arg Gln Glu Val Lys Asp Arg Asn Gly Arg Val Cys Cys
 65             70             75             80
Val Val Glu Cys Val Gln Val Ala Val Asn Val Gln Thr Ala Ala Pro
          85             90             95
Arg Ser Ile Ser Lys Val Glu Arg Lys Val Leu Thr Ala Val Ala Thr
          100            105            110
Asp Glu Val Gln Ser Gln Glu Ala Leu Glu Lys
          115            120

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<210> 2323

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXA01595

<400> 2323

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cggcaatgat tgacacggct gtaaaggaag gtccgcaata atg act gca ccc acg      115
                                   Met Thr Ala Pro Thr
                                   1             5
aac gct ggg gaa ctc agg cga gtt ttg ctg gtt cca cac acc ggg cgt      163
Asn Ala Gly Glu Leu Arg Arg Val Leu Leu Val Pro His Thr Gly Arg
          10             15             20
tct tcc aat att gaa tcc gcc atc ttg gca gcc aag ctg ctc gac gat      211
Ser Ser Asn Ile Glu Ser Ala Ile Leu Ala Ala Lys Leu Leu Asp Asp
          25             30             35
gct gga atc gat gtg agg gtg ctg atc aat gat gca gat gat cca att      259
Ala Gly Ile Asp Val Arg Val Leu Ile Asn Asp Ala Asp Asp Pro Ile
          40             45             50

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gca gag cac tcc gtt tta ggc cgt ttc acc cat gtc agg cac gct gca	307
Ala Glu His Ser Val Leu Gly Arg Phe Thr His Val Arg His Ala Ala	
55 60 65	
gac gcc gct gac ggc gca gaa cta gtt ctg gtg ctg ggt gga gat ggc	355
Asp Ala Ala Asp Gly Ala Glu Leu Val Leu Val Leu Gly Gly Asp Gly	
70 75 80 85	
acc ttc ctc cgc gca gca gat atg gcc cac gct gtt gat ttg cct gtt	403
Thr Phe Leu Arg Ala Ala Asp Met Ala His Ala Val Asp Leu Pro Val	
90 95 100	
ctg ggc atc aac cta ggc cat gtg gga ttc ttg gct gaa tgg gag tct	451
Leu Gly Ile Asn Leu Gly His Val Gly Phe Leu Ala Glu Trp Glu Ser	
105 110 115	
gac tca ctt gaa gag gca ctc aaa cgt gtg atc gac cgc gat tac cgt	499
Asp Ser Leu Glu Glu Ala Leu Lys Arg Val Ile Asp Arg Asp Tyr Arg	
120 125 130	
att gaa gat cgc atg acc tta act gtc gtt gtc cta gac ggc ggt gga	547
Ile Glu Asp Arg Met Thr Leu Thr Val Val Val Leu Asp Gly Gly Gly	
135 140 145	
gaa gaa atc ggc cga ggc tgg gct ctc aat gag gtc agt att gaa aac	595
Glu Glu Ile Gly Arg Gly Trp Ala Leu Asn Glu Val Ser Ile Glu Asn	
150 155 160 165	
tta aac cgc agg gga gtg ctc gat gca acc ctc gag gta gat gca cga	643
Leu Asn Arg Arg Gly Val Leu Asp Ala Thr Leu Glu Val Asp Ala Arg	
170 175 180	
cca gtt gct tcc ttt ggt tgc gat ggc gtg ctg att tcc acc cca acc	691
Pro Val Ala Ser Phe Gly Cys Asp Gly Val Leu Ile Ser Thr Pro Thr	
185 190 195	
ggc tcc acc gct tat gca ttt tcc gcc ggt ggt cct gta ctg tgg cca	739
Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly Pro Val Leu Trp Pro	
200 205 210	
gaa ctc gat gcc atc ttg gtg gtt cct aat aac gcc cac gcg ctg ttt	787
Glu Leu Asp Ala Ile Leu Val Val Pro Asn Asn Ala His Ala Leu Phe	
215 220 225	
acc aaa ccg ctg gtt gtg agc cca aaa tcc acc gta gct gtg gaa tcc	835
Thr Lys Pro Leu Val Val Ser Pro Lys Ser Thr Val Ala Val Glu Ser	
230 235 240 245	
aat tca gat act tca gca gcg atg gcc gtc atg gat ggt ttc cgt ccc	883
Asn Ser Asp Thr Ser Ala Ala Met Ala Val Met Asp Gly Phe Arg Pro	
250 255 260	
att cct atg cct cca gga tcc cgt gtt gag gtc acc agg ggt gag cgt	931
Ile Pro Met Pro Pro Gly Ser Arg Val Glu Val Thr Arg Gly Glu Arg	
265 270 275	
ccc gtg cgt tgg gtg agg ctt gat tct tca ccg ttt acc gac cga ctt	979
Pro Val Arg Trp Val Arg Leu Asp Ser Ser Pro Phe Thr Asp Arg Leu	
280 285 290	
gtg agc aaa tta agg ctc ccc gtt acc ggt tgg cgg ggt ccg caa aaa	1027

Val Ser Lys Leu Arg Leu Pro Val Thr Gly Trp Arg Gly Pro Gln Lys
 295 300 305

cag gcg gaa aat aaa gat ccc agg tca gcg ggg taattcgaaa accattcgaa 1080
 Gln Ala Glu Asn Lys Asp Pro Arg Ser Ala Gly
 310 315 320

caa 1083

<210> 2324

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 2324

Met Thr Ala Pro Thr Asn Ala Gly Glu Leu Arg Arg Val Leu Leu Val
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Pro His Thr Gly Arg Ser Ser Asn Ile Glu Ser Ala Ile Leu Ala Ala
 20 25 30

Lys Leu Leu Asp Asp Ala Gly Ile Asp Val Arg Val Leu Ile Asn Asp
 35 40 45

Ala Asp Asp Pro Ile Ala Glu His Ser Val Leu Gly Arg Phe Thr His
 50 55 60

Val Arg His Ala Ala Asp Ala Ala Asp Gly Ala Glu Leu Val Leu Val
 65 70 75 80

Leu Gly Gly Asp Gly Thr Phe Leu Arg Ala Ala Asp Met Ala His Ala
 85 90 95

Val Asp Leu Pro Val Leu Gly Ile Asn Leu Gly His Val Gly Phe Leu
 100 105 110

Ala Glu Trp Glu Ser Asp Ser Leu Glu Glu Ala Leu Lys Arg Val Ile
 115 120 125

Asp Arg Asp Tyr Arg Ile Glu Asp Arg Met Thr Leu Thr Val Val Val
 130 135 140

Leu Asp Gly Gly Gly Glu Glu Ile Gly Arg Gly Trp Ala Leu Asn Glu
 145 150 155 160

Val Ser Ile Glu Asn Leu Asn Arg Arg Gly Val Leu Asp Ala Thr Leu
 165 170 175

Glu Val Asp Ala Arg Pro Val Ala Ser Phe Gly Cys Asp Gly Val Leu
 180 185 190

Ile Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
 195 200 205

Pro Val Leu Trp Pro Glu Leu Asp Ala Ile Leu Val Val Pro Asn Asn
 210 215 220

Ala His Ala Leu Phe Thr Lys Pro Leu Val Val Ser Pro Lys Ser Thr
 225 230 235 240

att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala
 120 125 130

 cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu
 135 140 145

 gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met
 150 155 160 165

 gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met
 170 175 180

 gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr
 185 190 195

 gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala
 200 205 210

 cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789
 His Gly Ile Val Pro Asp Met Lys Lys Leu
 215 220

 aaa 792

<210> 2326

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 2326

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr
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 20 25 30

 Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu
 35 40 45

 His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala
 50 55 60

 Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu
 65 70 75 80

 Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala
 85 90 95

 Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser
 100 105 110

 Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
 130 135 140
 Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
 145 150 155 160
 Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
 165 170 175
 Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
 180 185 190
 Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
 195 200 205
 Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
 210 215 220

<210> 2327

<211> 1653

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1630)

<223> RXA01602

<400> 2327

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 Met Ala Lys Thr His
 1 5
 att cgg tta cag gac ctt tcc ctg tca tac acc tca acc ccg tta att 163
 Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr Ser Thr Pro Leu Ile
 10 15 20
 acg aag ctc aat atc act gtt tct tct gga cag tgc gca gtg att gtt 211
 Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln Cys Ala Val Ile Val
 25 30 35
 ggt gag aat ggt cga ggt aaa acc aca ctt ctg cga gca ctg gct cga 259
 Gly Glu Asn Gly Arg Gly Lys Thr Thr Leu Leu Arg Ala Leu Ala Arg
 40 45 50
 gaa ttc ccg cca tct gca ggt gag att ctc act cat ggc acg gta gca 307
 Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr His Gly Thr Val Ala
 55 60 65
 att gct cat caa cac atg cct gca ggt gat ctg tcc gtc gga gag atc 355
 Ile Ala His Gln His Met Pro Ala Gly Asp Leu Ser Val Gly Glu Ile
 70 75 80 85
 tgt gat gag gca att cgt gat tca aag aat gct ctc gaa gag ctt gag 403
 Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala Leu Glu Glu Leu Glu
 90 95 100
 aga gct gga gct cta ctt gag aca aac act gcg cac gca ctt gat gga 451

Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala His Ala Leu Asp Gly	
105 110 115	
tat caa caa gcc ctt gat gcc gct gaa gtg ctt gac gca tgg aac gct	499
Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu Asp Ala Trp Asn Ala	
120 125 130	
gaa cat cga tta gaa aaa gct ctg cgc agc ttt ggc gcg atc acc gat	547
Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe Gly Ala Ile Thr Asp	
135 140 145	
aga tcc cgt gca ctc agt gag cta tcg atc ggg caa agg tat cgg gta	595
Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly Gln Arg Tyr Arg Val	
150 155 160 165	
cgg ctg gcc tgc ctc atc ggt ggc gat gct gat att ttg ctt ctc gat	643
Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp Ile Leu Leu Leu Asp	
170 175 180	
gaa ccc acc aat cat ctt gac cgg ggc gcg ctt aac tat ctc acc gaa	691
Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu Asn Tyr Leu Thr Glu	
185 190 195	
gcc ata acc tcc cac aaa ggt gtg gta ctt gtt gtt tct cat gat caa	739
Ala Ile Thr Ser His Lys Gly Val Val Leu Val Val Ser His Asp Gln	
200 205 210	
gca ctg atc aaa gat gtc gcg gat ttc atc atc gat att gat tca acc	787
Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile Asp Ile Asp Ser Thr	
215 220 225	
cca gac ggc cta cca cgg atc tat cat gag ggt ttt gat tct tat cga	835
Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly Phe Asp Ser Tyr Arg	
230 235 240 245	
cgc caa agg agt gcg ctt ctt gaa act tgg agg cag gat tat gcc gct	883
Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg Gln Asp Tyr Ala Ala	
250 255 260	
gca caa act gtg caa cag caa ttg cag gag gat cta gag cac gca cgc	931
Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp Leu Glu His Ala Arg	
265 270 275	
cag cgg gtg aat tct tcg tgg aaa cct cca aaa gga acg gga aaa cac	979
Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys Gly Thr Gly Lys His	
280 285 290	
act cgc gca tct cgg gct ccc gga gtg gtg cag gcc tta aag cga gca	1027
Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln Ala Leu Lys Arg Ala	
295 300 305	
cag gat gcg ttg gat agc aaa gcg ttg gac gtt ccc ccg gct ccg gcc	1075
Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val Pro Pro Ala Pro Ala	
310 315 320 325	
cca ttg ctt ctg cct acc ttg aaa gtg cga cca gat aaa ccc atg gtg	1123
Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro Asp Lys Pro Met Val	
330 335 340	
gac ttt tcg gac ctt ttt gta ccc cac cgc ttg cgt ctg cca ggc tca	1171
Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu Arg Leu Pro Gly Ser	

345 350 355
 cat tca gtg gta tca ggt gac aaa ata gtg atc act ggt gac aac ggc 1219
 His Ser Val Val Ser Gly Asp Lys Ile Val Ile Thr Gly Asp Asn Gly
 360 365 370
 gct ggc aaa tca acg ctc atc gaa gtc ttg tct ggg gtt ttg act ccg 1267
 Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser Gly Val Leu Thr Pro
 375 380 385
 gca agt ggt tcg gtt gca aac cat gcc cga act ggg gtt ctc ggc caa 1315
 Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr Gly Val Leu Gly Gln
 390 395 400 405
 gaa tca ctt gtc ggc gag gtg cca tca ata gca cga gat cac gca gtt 1363
 Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala Arg Asp His Ala Val
 410 415 420
 aag tgg gga ctt tta agt gtt gag gag agc cga ttt gcc cta cag gaa 1411
 Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg Phe Ala Leu Gln Glu
 425 430 435
 ttc tca att ggt caa cgc aga aga cta gat ttg gcc atg tcg tta gct 1459
 Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu Ala Met Ser Leu Ala
 440 445 450
 ggc aat cct gaa ctg ttg ctt ctc gat gaa cct tcg aac cat ctg tct 1507
 Gly Asn Pro Glu Leu Leu Leu Leu Asp Glu Pro Ser Asn His Leu Ser
 455 460 465
 atg cac ttg gtt tcc gca ctt aca gag tgg ctg gac acg acc gcg gct 1555
 Met His Leu Val Ser Ala Leu Thr Glu Trp Leu Asp Thr Thr Ala Ala
 470 475 480 485
 gca gtg atc atg gta acg cat gat cga cag cta ctc cgc gat acg gct 1603
 Ala Val Ile Met Val Thr His Asp Arg Gln Leu Leu Arg Asp Thr Ala
 490 495 500
 cat tgg agg cac atc gag ttg aaa tct taagaattcg caagggttt 1650
 His Trp Arg His Ile Glu Leu Lys Ser
 505 510
 cac 1653

<210> 2328

<211> 510

<212> PRT

<213> Corynebacterium glutamicum

<400> 2328

Met Ala Lys Thr His Ile Arg Leu Gln Asp Leu Ser Leu Ser Tyr Thr
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Ser Thr Pro Leu Ile Thr Lys Leu Asn Ile Thr Val Ser Ser Gly Gln
 20 25 30

Cys Ala Val Ile Val Gly Glu Asn Gly Arg Gly Lys Thr Leu Leu
 35 40 45

Arg Ala Leu Ala Arg Glu Phe Pro Pro Ser Ala Gly Glu Ile Leu Thr

50	55	60
His Gly Thr Val Ala Ile Ala His Gln His Met Pro Ala Gly Asp Leu 65 70 75 80		
Ser Val Gly Glu Ile Cys Asp Glu Ala Ile Arg Asp Ser Lys Asn Ala 85 90 95		
Leu Glu Glu Leu Glu Arg Ala Gly Ala Leu Leu Glu Thr Asn Thr Ala 100 105 110		
His Ala Leu Asp Gly Tyr Gln Gln Ala Leu Asp Ala Ala Glu Val Leu 115 120 125		
Asp Ala Trp Asn Ala Glu His Arg Leu Glu Lys Ala Leu Arg Ser Phe 130 135 140		
Gly Ala Ile Thr Asp Arg Ser Arg Ala Leu Ser Glu Leu Ser Ile Gly 145 150 155 160		
Gln Arg Tyr Arg Val Arg Leu Ala Cys Leu Ile Gly Gly Asp Ala Asp 165 170 175		
Ile Leu Leu Leu Asp Glu Pro Thr Asn His Leu Asp Arg Gly Ala Leu 180 185 190		
Asn Tyr Leu Thr Glu Ala Ile Thr Ser His Lys Gly Val Val Leu Val 195 200 205		
Val Ser His Asp Gln Ala Leu Ile Lys Asp Val Ala Asp Phe Ile Ile 210 215 220		
Asp Ile Asp Ser Thr Pro Asp Gly Leu Pro Arg Ile Tyr His Glu Gly 225 230 235 240		
Phe Asp Ser Tyr Arg Arg Gln Arg Ser Ala Leu Leu Glu Thr Trp Arg 245 250 255		
Gln Asp Tyr Ala Ala Ala Gln Thr Val Gln Gln Gln Leu Gln Glu Asp 260 265 270		
Leu Glu His Ala Arg Gln Arg Val Asn Ser Ser Trp Lys Pro Pro Lys 275 280 285		
Gly Thr Gly Lys His Thr Arg Ala Ser Arg Ala Pro Gly Val Val Gln 290 295 300		
Ala Leu Lys Arg Ala Gln Asp Ala Leu Asp Ser Lys Ala Leu Asp Val 305 310 315 320		
Pro Pro Ala Pro Ala Pro Leu Leu Leu Pro Thr Leu Lys Val Arg Pro 325 330 335		
Asp Lys Pro Met Val Asp Phe Ser Asp Leu Phe Val Pro His Arg Leu 340 345 350		
Arg Leu Pro Gly Ser His Ser Val Val Ser Gly Asp Lys Ile Val Ile 355 360 365		
Thr Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Glu Val Leu Ser 370 375 380		

Gly Val Leu Thr Pro Ala Ser Gly Ser Val Ala Asn His Ala Arg Thr
385 390 395 400

Gly Val Leu Gly Gln Glu Ser Leu Val Gly Glu Val Pro Ser Ile Ala
405 410 415

Arg Asp His Ala Val Lys Trp Gly Leu Leu Ser Val Glu Glu Ser Arg
420 425 430

Phe Ala Leu Gln Glu Phe Ser Ile Gly Gln Arg Arg Arg Leu Asp Leu
435 440 445

Ala Met Ser Leu Ala Gly Asn Pro Glu Leu Leu Leu Leu Asp Glu Pro
450 455 460

Ser Asn His Leu Ser Met His Leu Val Ser Ala Leu Thr Glu Trp Leu
465 470 475 480

Asp Thr Thr Ala Ala Ala Val Ile Met Val Thr His Asp Arg Gln Leu
485 490 495

Leu Arg Asp Thr Ala His Trp Arg His Ile Glu Leu Lys Ser
500 505 510

<210> 2329

<211> 1638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1615)

<223> RXA01605

<220>

<221> misc_feature

<222> (25, 31)

<223> n = a, t, c, or g

<400> 2329

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cattgaaatt ccgaagaact tcagcgattc tattgccage gtg acc agc gat tca 115
Val Thr Ser Asp Ser
1 5

ccc gcg cca gca acc gtc aac gcg gta ttc aac aac agc aac ggc ttc 163
Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn Asn Ser Asn Gly Phe
10 15 20

att gcc tcc atg ctg ggc aac cag gtg gtc aac act gtt gtg gag acc 211
Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn Thr Val Val Glu Thr
25 30 35

atg gac acg gaa ttc ggc gtc cgc att gtg gat aac atg ctc gtc ggt 259
Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp Asn Met Leu Val Gly
40 45 50

ttc tcc acc ttg ggc gac ggc atg aac caa gcc gcc gaa ggt gcc act 307

Phe	Ser	Thr	Leu	Gly	Asp	Gly	Met	Asn	Gln	Ala	Ala	Glu	Gly	Ala	Thr		
	55					60					65						
acg	ctc	agc	gat	ggc	gtc	ggt	tcc	gcc	aac	gac	ggt	gca	gtt	cag	ctt	355	
Thr	Leu	Ser	Asp	Gly	Val	Gly	Ser	Ala	Asn	Asp	Gly	Ala	Val	Gln	Leu		
	70				75				80					85			
gcc	gac	ggc	gcg	gtc	acc	ctg	cgc	gac	ggc	atc	gca	agt	gcc	aat	gag	403	
Ala	Asp	Gly	Ala	Val	Thr	Leu	Arg	Asp	Gly	Ile	Ala	Ser	Ala	Asn	Glu		
				90				95					100				
ggt	gcg	caa	tcg	ctt	gcc	gac	ggc	gcc	agc	cag	ctc	gac	acc	ggc	ctc	451	
Gly	Ala	Gln	Ser	Leu	Ala	Asp	Gly	Ala	Ser	Gln	Leu	Asp	Thr	Gly	Leu		
		105				110						115					
ggc	tcc	gcg	gct	aca	ggc	agc	caa	acg	ctc	gcc	gac	ggt	cta	tcc	agc	499	
Gly	Ser	Ala	Ala	Thr	Gly	Ser	Gln	Thr	Leu	Ala	Asp	Gly	Leu	Ser	Ser		
	120					125						130					
ctg	tct	gcg	ggc	acc	gcc	caa	cta	ggc	caa	ggc	gca	acc	cag	gtt	tca	547	
Leu	Ser	Ala	Gly	Thr	Ala	Gln	Leu	Gly	Gln	Gly	Ala	Thr	Gln	Val	Ser		
	135					140					145						
gat	ggc	gtg	ggc	caa	ctt	gtc	gac	caa	gta	gca	cca	ctg	acc	gcc	tat	595	
Asp	Gly	Val	Gly	Gln	Leu	Val	Asp	Gln	Val	Ala	Pro	Leu	Thr	Ala	Tyr		
	150				155				160					165			
gtt	cca	gac	atc	aac	tct	cag	ttg	atc	acc	ctg	cgc	gac	ggc	gca	gcc	643	
Val	Pro	Asp	Ile	Asn	Ser	Gln	Leu	Ile	Thr	Leu	Arg	Asp	Gly	Ala	Ala		
			170					175						180			
acc	att	gcc	tct	gaa	cta	tct	gat	ccc	tcc	agc	acc	tac	cgc	tcc	ggc	691	
Thr	Ile	Ala	Ser	Glu	Leu	Ser	Asp	Pro	Ser	Ser	Thr	Tyr	Arg	Ser	Gly		
			185					190					195				
gtg	gac	tcc	gct	gtg	agc	gca	tcc	cag	caa	cta	gca	gcc	ggc	ctg	caa	739	
Val	Asp	Ser	Ala	Val	Ser	Ala	Ser	Gln	Gln	Leu	Ala	Ala	Gly	Leu	Gln		
	200						205					210					
acc	ctg	aaa	gac	gga	tcc	agc	caa	ctc	agc	atc	ggt	gca	cgc	acc	ctc	787	
Thr	Leu	Lys	Asp	Gly	Ser	Ser	Gln	Leu	Ser	Ile	Gly	Ala	Arg	Thr	Leu		
	215					220					225						
gct	gat	ggc	acc	agc	caa	ttg	gcc	gca	ggt	tcc	gaa	cag	cta	gtt	gtt	835	
Ala	Asp	Gly	Thr	Ser	Gln	Leu	Ala	Ala	Gly	Ser	Glu	Gln	Leu	Val	Val		
	230				235				240					245			
ggc	gca	caa	gca	ctg	cgc	gac	ggc	acc	gtc	cag	ctt	gat	gaa	ggc	tcc	883	
Gly	Ala	Gln	Ala	Leu	Arg	Asp	Gly	Thr	Val	Gln	Leu	Asp	Glu	Gly	Ser		
				250					255					260			
agc	gaa	ctc	gcc	ctc	aaa	ctc	acc	gac	ggc	gca	agc	caa	gta	cca	acc	931	
Ser	Glu	Leu	Ala	Leu	Lys	Leu	Thr	Asp	Gly	Ala	Ser	Gln	Val	Pro	Thr		
			265					270					275				
ttc	gct	gac	ggc	gca	gac	acc	acc	atc	gca	acc	cca	gtt	gaa	aca	gaa	979	
Phe	Ala	Asp	Gly	Ala	Asp	Thr	Thr	Ile	Ala	Thr	Pro	Val	Glu	Thr	Glu		
		280					285					290					
caa	gca	gga	gac	acc	aca	ccg	ctc	ttc	ggt	att	ggt	ctc	gca	cca	ttc	1027	
Gln	Ala	Gly	Asp	Thr	Thr	Pro	Leu	Phe	Gly	Ile	Gly	Leu	Ala	Pro	Phe		

295	300	305	
ttc atg gct gtc ggc ctg ttc atg gga gca acc gtt gcc tgg atg atc			1075
Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr Val Ala Trp Met Ile			
310	315	320	325
ctg cac cca atc agt cgc cgc gca ctc gac tcc cgc atg gga ggc ttc			1123
Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser Arg Met Gly Gly Phe			
	330	335	340
cga ggc acc ctg gca agc tac ctt cca tca aca gtc tta ggc ctt ggc			1171
Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr Val Leu Gly Leu Gly			
	345	350	355
caa gca acc atc atg tgg gca gta ctg tac ttc ctg ctc gac ctc aat			1219
Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe Leu Leu Asp Leu Asn			
	360	365	370
cca gct cac cca gct gga ctg tgg atg gcg atg gtc gcc atc tca tgg			1267
Pro Ala His Pro Ala Gly Leu Trp Met Ala Met Val Ala Ile Ser Trp			
	375	380	385
gta ttc atc tcc att acc cat atg ttc aac aac gtg gca gga ccc tcc			1315
Val Phe Ile Ser Ile Thr His Met Phe Asn Asn Val Ala Gly Pro Ser			
	390	395	400
gca ggc cgt gtg ctg tcc atc gtg atg atg tcc ttc cag cta gtc tcc			1363
Ala Gly Arg Val Leu Ser Ile Val Met Met Ser Phe Gln Leu Val Ser			
	410	415	420
tcc ggt ggc cta tac cca cca gaa acc cag cca gca ttc ttc cac tgg			1411
Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro Ala Phe Phe His Trp			
	425	430	435
ttc cac acc tac gac ccg atc acc tac gca gtc aac ctc gtg cgc caa			1459
Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val Asn Leu Val Arg Gln			
	440	445	450
atg atc ttc aac gaa acc cca tcc aac gac cca cgc ttc ata caa gca			1507
Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro Arg Phe Ile Gln Ala			
	455	460	465
atc tgg gta ctg ctc ttc atc tgg gca ctg atg ctc gcc atc tcc acc			1555
Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met Leu Ala Ile Ser Thr			
	470	475	480
ctg gcg aat aga aca aac aag gtt ctt cgc atg aag gac tac cac cca			1603
Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met Lys Asp Tyr His Pro			
	490	495	500
gaa ctg aag gtc taaaagcttt tcccgcgcgg ttc			1638
Glu Leu Lys Val			
505			

<210> 2330

<211> 505

<212> PRT

<213> Corynebacterium glutamicum

<400> 2330

Val Thr Ser Asp Ser Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn
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Asn Ser Asn Gly Phe Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn
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Thr Val Val Glu Thr Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp
35 40 45
Asn Met Leu Val Gly Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala
50 55 60
Ala Glu Gly Ala Thr Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp
65 70 75 80
Gly Ala Val Gln Leu Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile
85 90 95
Ala Ser Ala Asn Glu Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln
100 105 110
Leu Asp Thr Gly Leu Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala
115 120 125
Asp Gly Leu Ser Ser Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly
130 135 140
Ala Thr Gln Val Ser Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala
145 150 155 160
Pro Leu Thr Ala Tyr Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu
165 170 175
Arg Asp Gly Ala Ala Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser
180 185 190
Thr Tyr Arg Ser Gly Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu
195 200 205
Ala Ala Gly Leu Gln Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile
210 215 220
Gly Ala Arg Thr Leu Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser
225 230 235 240
Glu Gln Leu Val Val Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln
245 250 255
Leu Asp Glu Gly Ser Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala
260 265 270
Ser Gln Val Pro Thr Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr
275 280 285
Pro Val Glu Thr Glu Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile
290 295 300
Gly Leu Ala Pro Phe Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr
305 310 315 320
Val Ala Trp Met Ile Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser

325	330	335
Arg Met Gly Gly Phe Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr		
340	345	350
Val Leu Gly Leu Gly Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe		
355	360	365
Leu Leu Asp Leu Asn Pro Ala His Pro Ala Gly Leu Trp Met Ala Met		
370	375	380
Val Ala Ile Ser Trp Val Phe Ile Ser Ile Thr His Met Phe Asn Asn		
385	390	400
Val Ala Gly Pro Ser Ala Gly Arg Val Leu Ser Ile Val Met Met Ser		
405	410	415
Phe Gln Leu Val Ser Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro		
420	425	430
Ala Phe Phe His Trp Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val		
435	440	445
Asn Leu Val Arg Gln Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro		
450	455	460
Arg Phe Ile Gln Ala Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met		
465	470	475
Leu Ala Ile Ser Thr Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met		
485	490	495
Lys Asp Tyr His Pro Glu Leu Lys Val		
500	505	

<210> 2331
 <211> 852
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(829)
 <223> RXA01610

<400> 2331
 cattaatcac atgtggttaa tgcctttttt gattgcgtag actaggaagg tacgtcaact 60
 tccatatctt tagtttgcca aagcgatcaa cttaaaacac gtg tcc ggt ttt ctt 115
 Val Ser Gly Phe Leu
 1 5
 act ccc cca gct aca ccc cat att cgg acg gca act gcc agt att gct 163
 Thr Pro Pro Ala Thr Pro His Ile Arg Thr Ala Thr Ala Ser Ile Ala
 10 15 20
 acc gca gtt gcc gta gca ctg tca gtg ttc gct gct gca ctc att cca 211
 Thr Ala Val Ala Val Ala Leu Ser Val Phe Ala Ala Ala Leu Ile Pro
 25 30 35

gga agc gct ctg tat tct gtg ctg acc gct gga ggg gtg gca ctt gga 259
 Gly Ser Ala Leu Tyr Ser Val Leu Thr Ala Gly Gly Val Ala Leu Gly
 40 45 50

gca gca tca ggc gtt gcc gcg tta cgc cat cgc gga ggg ctt cgc att 307
 Ala Ala Ser Gly Val Ala Ala Leu Arg His Arg Gly Gly Leu Arg Ile
 55 60 65

ttt caa tgg ctg tct gcg ctt ggt gga atc gtc att ttg ctg atc ggt 355
 Phe Gln Trp Leu Ser Ala Leu Gly Gly Ile Val Ile Leu Leu Ile Gly
 70 75 80 85

atc gta gtg gca gtt gca aag ttt ggg gcc tcg gca aaa ctt gcc acg 403
 Ile Val Val Ala Val Ala Lys Phe Gly Ala Ser Ala Lys Leu Ala Thr
 90 95 100

tta ggc ctg gtg acc tcg tat tat ctc atg ccg tct gcg gca ttg gcc 451
 Leu Gly Leu Val Thr Ser Tyr Tyr Leu Met Pro Ser Ala Ala Leu Ala
 105 110 115

tgt tat atc gga ggg ctt ggc cag cta cca gcc aaa tgg att gcg cca 499
 Cys Tyr Ile Gly Gly Leu Gly Gln Leu Pro Ala Lys Trp Ile Ala Pro
 120 125 130

gcg ttt atg gct acg gct ggt gca ggt gct gcg gga tgg ttt tca ttg 547
 Ala Phe Met Ala Thr Ala Gly Ala Gly Ala Ala Gly Trp Phe Ser Leu
 135 140 145

ggg gca ggc acc ggt ttt gaa cgg ttc ctc att gct gtt gca gcg gtg 595
 Gly Ala Gly Thr Gly Phe Glu Arg Phe Leu Ile Ala Val Ala Ala Val
 150 155 160 165

ttt tca ctg atg gga tgt gta tac cca gtg tgg gga tgc gtc gta aag 643
 Phe Ser Leu Met Gly Cys Val Tyr Pro Val Trp Gly Cys Val Val Lys
 170 175 180

cgt cca cgt caa gtg gct gca tgg ctg gtc gcg ctg gcg gcc ctg gtg 691
 Arg Pro Arg Gln Val Ala Ala Trp Leu Val Ala Leu Ala Ala Leu Val
 185 190 195

ctt ggg gcg ctc atg ctt ttt atg gtg agc atg gtg gtg gcg ccg ggt 739
 Leu Gly Ala Leu Met Leu Phe Met Val Ser Met Val Val Ala Pro Gly
 200 205 210

ttg ctg tgg ctg cag ccc acg acg gtc gca tgg ggt ttt atg att gcc 787
 Leu Leu Trp Leu Gln Pro Thr Thr Val Ala Trp Gly Phe Met Ile Ala
 215 220 225

ggg gtt ctt gcg acg gtc gca ggc ttg tgg cct agg cgt ttt 829
 Gly Val Leu Ala Thr Val Ala Gly Leu Trp Pro Arg Arg Phe
 230 235 240

tagacggaat cgtctgggag ggt 852

<210> 2332

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 2332

Val Ser Gly Phe Leu Thr Pro Pro Ala Thr Pro His Ile Arg Thr Ala
 1 5 10 15
 Thr Ala Ser Ile Ala Thr Ala Val Ala Val Ala Leu Ser Val Phe Ala
 20 25 30
 Ala Ala Leu Ile Pro Gly Ser Ala Leu Tyr Ser Val Leu Thr Ala Gly
 35 40 45
 Gly Val Ala Leu Gly Ala Ala Ser Gly Val Ala Ala Leu Arg His Arg
 50 55 60
 Gly Gly Leu Arg Ile Phe Gln Trp Leu Ser Ala Leu Gly Gly Ile Val
 65 70 75 80
 Ile Leu Leu Ile Gly Ile Val Val Ala Val Ala Lys Phe Gly Ala Ser
 85 90 95
 Ala Lys Leu Ala Thr Leu Gly Leu Val Thr Ser Tyr Tyr Leu Met Pro
 100 105 110
 Ser Ala Ala Leu Ala Cys Tyr Ile Gly Gly Leu Gly Gln Leu Pro Ala
 115 120 125
 Lys Trp Ile Ala Pro Ala Phe Met Ala Thr Ala Gly Ala Gly Ala Ala
 130 135 140
 Gly Trp Phe Ser Leu Gly Ala Gly Thr Gly Phe Glu Arg Phe Leu Ile
 145 150 155 160
 Ala Val Ala Ala Val Phe Ser Leu Met Gly Cys Val Tyr Pro Val Trp
 165 170 175
 Gly Cys Val Val Lys Arg Pro Arg Gln Val Ala Ala Trp Leu Val Ala
 180 185 190
 Leu Ala Ala Leu Val Leu Gly Ala Leu Met Leu Phe Met Val Ser Met
 195 200 205
 Val Val Ala Pro Gly Leu Leu Trp Leu Gln Pro Thr Thr Val Ala Trp
 210 215 220
 Gly Phe Met Ile Ala Gly Val Leu Ala Thr Val Ala Gly Leu Trp Pro
 225 230 235 240
 Arg Arg Phe

<210> 2333

<211> 480

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(457)

<223> RXA01611

<400> 2333

cccgc ttaca actacttggt ttacaccggt gttatcaagg gctaaatcgc ctaacctcta 60

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<400> 2334
Met Arg Lys Phe Arg Asn Thr Ala Ile Ala Leu Val Ser Ala Ala Ala
  1          5          10          15

Ile Thr Leu Gly Gly Val Thr Ala Ala Thr Ala Gln Glu Asp Glu Thr
      20          25          30

Pro Pro Ala Ala Glu Thr Glu Thr Thr Ser Pro Ser Gly Ser Ser Gly
      35          40          45

Ser Ser Trp Asn Asp Tyr Asn Glu Glu Tyr Glu Gly Asp Gln Glu Gly
      50          55          60

Tyr Gly Ile Asp Gly Phe Gly Ser Ser Arg Asp Asp Ser Gly Glu Glu
      65          70          75          80

Val Pro Arg Trp Leu Glu Thr Trp Gly Lys Val Phe Asp Ala Leu Thr
      85          90          95

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Ile Thr Ser Val Leu Gly Leu Val Val Phe Pro Val Val Asn Phe Leu
 100 105 110

Lys Tyr Asn Gly Leu Ile Lys
 115

<210> 2335

<211> 468

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(445)

<223> RXA01612

<400> 2335

gaaaaaacga cgttgggttcg tagtcgctgg aaattttaata attcctccgt ccccttcaac 60

taggggggtgg aaacccgact atttccgaag gactattctc atg cgt tct ttc cgt 115
 Met Arg Ser Phe Arg
 1 5

acc gcg gca gtt gca ggc ctt act gca gtt gca ctt tcc gta ggt tcc 163
 Thr Ala Ala Val Ala Gly Leu Thr Ala Val Ala Leu Ser Val Gly Ser
 10 15 20

gcc acc gtg gca act gcg gaa gaa tct gat caa aac ctc tca tcc ggc 211
 Ala Thr Val Ala Thr Ala Glu Glu Ser Asp Gln Asn Leu Ser Ser Gly
 25 30 35

ttc tca gca ctt tct tcc ggt ggc gca gcg gcc gta ggt gag gac tgg 259
 Phe Ser Ala Leu Ser Ser Gly Ala Ala Ala Val Gly Glu Asp Trp
 40 45 50

gat gca gac cag ccc gtc aca ggt gaa gac atc ttt ggt gaa gag cac 307
 Asp Ala Asp Gln Pro Val Thr Gly Glu Asp Ile Phe Gly Glu Glu His
 55 60 65

gag cgc gat aac gaa aac acc cca gcg tgg gct aag aac atg tac gat 355
 Glu Arg Asp Asn Glu Asn Thr Pro Ala Trp Ala Lys Asn Met Tyr Asp
 70 75 80 85

cta acc gtc ttg ggt ggc att gct tcc ctt ctc ggt gtc atc gta ttc 403
 Leu Thr Val Leu Gly Gly Ile Ala Ser Leu Leu Gly Val Ile Val Phe
 90 95 100

ccc gct tac aac tac ttg gtt tac acc ggt gtt atc aag ggc 445
 Pro Ala Tyr Asn Tyr Leu Val Tyr Thr Gly Val Ile Lys Gly
 105 110 115

taaatgcct aacctctatc ttc 468

<210> 2336

<211> 115

<212> PRT

<213> Corynebacterium glutamicum

<400> 2336

Met Arg Ser Phe Arg Thr Ala Ala Val Ala Gly Leu Thr Ala Val Ala
 1 5 10 15

Leu Ser Val Gly Ser Ala Thr Val Ala Thr Ala Glu Glu Ser Asp Gln
 20 25 30

Asn Leu Ser Ser Gly Phe Ser Ala Leu Ser Ser Gly Gly Ala Ala Ala
 35 40 45

Val Gly Glu Asp Trp Asp Ala Asp Gln Pro Val Thr Gly Glu Asp Ile
 50 55 60

Phe Gly Glu Glu His Glu Arg Asp Asn Glu Asn Thr Pro Ala Trp Ala
 65 70 75 80

Lys Asn Met Tyr Asp Leu Thr Val Leu Gly Gly Ile Ala Ser Leu Leu
 85 90 95

Gly Val Ile Val Phe Pro Ala Tyr Asn Tyr Leu Val Tyr Thr Gly Val
 100 105 110

Ile Lys Gly
 115

<210> 2337

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01619

<400> 2337

cctgcaagtt tactgctcgg ccgtcacggg ggaatggaaa aagtacgctt ggtgttcata 60

tagcgaaccc attttctatt gcgatgagag gaacaccacc atg cgc gca atc act 115
 Met Arg Ala Ile Thr
 1 5

cac aac act ttc ggc gac ccc gcc gac gtc cta cag att acc gag aag 163
 His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu Gln Ile Thr Glu Lys
 10 15 20

gaa att ccc act ccc ggc cca ggt cag gtt cgt att caa gtg acg ctg 211
 Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg Ile Gln Val Thr Leu
 25 30 35

gca acc atc cac aac cat gat ttg tgg acc gtg aag ggc tct tac ggc 259
 Ala Thr Ile His Asn His Asp Leu Trp Thr Val Lys Gly Ser Tyr Gly
 40 45 50

ttc gtc cca gat ctg ccg gcc gcc gca ggc acc gag gca gtc ggc atc 307
 Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr Glu Ala Val Gly Ile
 55 60 65

gtc gac gcc ctg ggc gag ggc gtc gaa ggt ttg cag gtc ggt cag cgt 355
 Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu Gln Val Gly Gln Arg

70	75	80	85	
gtt gcg tcc ggc acc agc ttt ggc atc tgg gcg gag tac gcg ctt gtc				403
Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala Glu Tyr Ala Leu Val	90	95	100	
gac gcc tcc ggc ctc att ccc gta cca gaa cag ctc tcc gac gaa agc				451
Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln Leu Ser Asp Glu Ser	105	110	115	
gca gct cag ctc gtc gca atg cct ttc agc gcc atc agc ctt ctt gat				499
Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala Ile Ser Leu Leu Asp	120	125	130	
ttc ctg gat atg aaa cca ggg gag tgg ctg atc caa aac tcc gca aac				547
Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile Gln Asn Ser Ala Asn	135	140	145	
ggg gcc gtc ggc cgc atg ctc gca cag ctg gca gaa tcc cgc gcc atc				595
Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala Glu Ser Arg Gly Ile	150	155	160	165
cat gtc gtt ggt ctc gtc cgc cgt gac gcc ggt gtc caa gaa ctc gct				643
His Val Val Gly Leu Val Arg Arg Asp Ala Gly Val Gln Glu Leu Ala	170	175	180	
gct caa aac atc agc ggc gtc gtt tcc act gag acc cca ggc tgg gaa				691
Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu Thr Pro Gly Trp Glu	185	190	195	
aag cag gtc gaa gac atc acc ggt ggc gca agc atc gcc gtc gca ctt				739
Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser Ile Ala Val Ala Leu	200	205	210	
gat tcc gtc ggt gga tcc tcc gca gct gac ctg gtg aaa ctg ctt ggc				787
Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu Val Lys Leu Leu Gly	215	220	225	
gaa ggc ggc acc ctc gtc tcc ttc ggc gcc atg ggc aac cca atc atg				835
Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met Gly Asn Pro Ile Met	230	235	240	245
gaa atc cca tcc ggc ccc gtc atc ttc aag cac atc acc gtc aag ggc				883
Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His Ile Thr Val Lys Gly	250	255	260	
ttc tgg gga agc aaa gtc agc cgc gaa atg cca gca gag aag aaa acc				931
Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro Ala Glu Lys Lys Thr	265	270	275	
cag ttg ttc ggc gag ctc att gcg cgc ata ctt gat gga aca ttg acc				979
Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu Asp Gly Thr Leu Thr	280	285	290	
ctt cca gtt gat tcc acc ttt gat gcc gct gac atc gtc tcg gcc gtg				1027
Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp Ile Val Ser Ala Val	295	300	305	
cgc gcc tcc agc gag cct ggc cgt gcc gga aaa gtg ctc att cgt ttc				1075
Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys Val Leu Ile Arg Phe	310	315	320	325

taaacgttta aggccccatta gac

1098

<210> 2338

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 2338

Met Arg Ala Ile Thr His Asn Thr Phe Gly Asp Pro Ala Asp Val Leu
1 5 10 15

Gln Ile Thr Glu Lys Glu Ile Pro Thr Pro Gly Pro Gly Gln Val Arg
20 25 30

Ile Gln Val Thr Leu Ala Thr Ile His Asn His Asp Leu Trp Thr Val
35 40 45

Lys Gly Ser Tyr Gly Phe Val Pro Asp Leu Pro Ala Ala Ala Gly Thr
50 55 60

Glu Ala Val Gly Ile Val Asp Ala Leu Gly Glu Gly Val Glu Gly Leu
65 70 75 80

Gln Val Gly Gln Arg Val Ala Ser Gly Thr Ser Phe Gly Ile Trp Ala
85 90 95

Glu Tyr Ala Leu Val Asp Ala Ser Gly Leu Ile Pro Val Pro Glu Gln
100 105 110

Leu Ser Asp Glu Ser Ala Ala Gln Leu Val Ala Met Pro Phe Ser Ala
115 120 125

Ile Ser Leu Leu Asp Phe Leu Asp Met Lys Pro Gly Glu Trp Leu Ile
130 135 140

Gln Asn Ser Ala Asn Gly Ala Val Gly Arg Met Leu Ala Gln Leu Ala
145 150 155 160

Glu Ser Arg Gly Ile His Val Val Gly Leu Val Arg Arg Asp Ala Gly
165 170 175

Val Gln Glu Leu Ala Ala Gln Asn Ile Ser Gly Val Val Ser Thr Glu
180 185 190

Thr Pro Gly Trp Glu Lys Gln Val Glu Asp Ile Thr Gly Gly Ala Ser
195 200 205

Ile Ala Val Ala Leu Asp Ser Val Gly Gly Ser Ser Ala Ala Asp Leu
210 215 220

Val Lys Leu Leu Gly Glu Gly Gly Thr Leu Val Ser Phe Gly Ala Met
225 230 235 240

Gly Asn Pro Ile Met Glu Ile Pro Ser Gly Pro Val Ile Phe Lys His
245 250 255

Ile Thr Val Lys Gly Phe Trp Gly Ser Lys Val Ser Arg Glu Met Pro
260 265 270

Ala Glu Lys Lys Thr Gln Leu Phe Gly Glu Leu Ile Ala Arg Ile Leu
 275 280 285

Asp Gly Thr Leu Thr Leu Pro Val Asp Ser Thr Phe Asp Ala Ala Asp
 290 295 300

Ile Val Ser Ala Val Arg Ala Ser Ser Glu Pro Gly Arg Ala Gly Lys
 305 310 315 320

Val Leu Ile Arg Phe
 325

<210> 2339

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> RXA01622

<400> 2339

aaggcgtggg cggtttttgaa ggagcttcgt ttggagcgcg gtcctttgga tcgtgaagtt 60

gccatcgcag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115
 Met Ser Asp Phe Tyr
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403
 Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val
 90 95 100

gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
 105 110 115

cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
 120 125 130

ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
135 140 145

aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
150 155 160 165

tgc	gac	att	atc	gcg	ccg	ggc	cgc	gtc	gat	att	tgg	ggc	gac	gtg	atg	643
Ser	Asp	Ile	Ile	Ala	Pro	Gly	Arg	Val	Asp	Ile	Trp	Gly	Asp	Val	Met	
				170				175						180		

cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
185 190 195

cct tca gat aat tagatgagtt ccgaaaattt aaa 726
Pro Ser Asp Asn
200

<210> 2340

<211> 201

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2340

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn
1 5 10 15

Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
20 25 30

Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
35 40 45

Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
50 55 60

Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
65 70 75 80

Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
85 90 95

Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
100 105 110

Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
145 · 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn
 195 200

<210> 2341

<211> 834

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(811)

<223> RXA01623

<400> 2341

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 gttgtattcc acgtttccgt cggacccttc agataattag atg agt tcc gaa aat 115
 Met Ser Ser Glu Asn
 1 5
 tta aaa gaa att cgc ggc gga atc ggt gag act tta acg gtc ggt ttg 163
 Leu Lys Glu Ile Arg Gly Gly Ile Gly Glu Thr Leu Thr Val Gly Leu
 10 15 20
 ggg ctg att ccg ctg ggt ttg gcc ttt ggg ctg ttg atg gtc cag aca 211
 Gly Leu Ile Pro Leu Gly Leu Ala Phe Gly Leu Leu Met Val Gln Thr
 25 30 35
 ggt ttc gcc tgg tgg tgg acg ccg att ttc tcc ttc gtg atc tat gcc 259
 Gly Phe Ala Trp Trp Trp Thr Pro Ile Phe Ser Phe Val Ile Tyr Ala
 40 45 50
 ggt tcg atg gaa ttt ctg gca atc ggc atg gtc acc gca ggt atc ggc 307
 Gly Ser Met Glu Phe Leu Ala Ile Gly Met Val Thr Ala Gly Ile Gly
 55 60 65
 ccg ttt tcg gcg gcg gtc gct ggt ttc atg gtg aat ttc cgc cac att 355
 Pro Phe Ser Ala Ala Val Ala Gly Phe Met Val Asn Phe Arg His Ile
 70 75 80 85
 ttc tac ggt ctc acc ttc cca cgc cac cgc atc aag tcc ggc gcc gcc 403
 Phe Tyr Gly Leu Thr Phe Pro Arg His Arg Ile Lys Ser Gly Ala Gly
 90 95 100
 cgc gcc tat tcc acc tac gcg ctt acc gac gag tcc tac gcc atc gtg 451
 Arg Ala Tyr Ser Thr Tyr Ala Leu Thr Asp Glu Ser Tyr Ala Ile Val
 105 110 115
 tca gcc cgc cca cct ggc gat atc agt ggc acg cgg gtg ctt acc gtt 499
 Ser Ala Arg Pro Pro Gly Asp Ile Ser Gly Thr Arg Val Leu Thr Val
 120 125 130
 caa att ttg tgc caa gct ctg tgg gtt atc cca gga att att ggc gcc 547
 Gln Ile Leu Cys Gln Ala Leu Trp Val Ile Pro Gly Ile Ile Gly Ala
 135 140 145
 ttg gtt ggt caa gtg ctg ccc gat gat cta aaa ggc atg gat ttt gcc 595

Leu Val Gly Gln Val Leu Pro Asp Asp Leu Lys Gly Met Asp Phe Ala
 150 155 160 165
 ctg acc gcg ctg ttt gtg gtg ctg gcg tgg gag gca ttc aaa aat aac 643
 Leu Thr Ala Leu Phe Val Val Leu Ala Trp Glu Ala Phe Lys Asn Asn
 170 175 180
 aag gat tat tcg ctg cca tta ttc gcg gtg gta ttg gct ctg gtt tcc 691
 Lys Asp Tyr Ser Leu Pro Leu Phe Ala Val Val Leu Ala Leu Val Ser
 185 190 195
 ggt ttt gtg gcg ccc gag cag atg ctg gtt atc gct ttg acc acg tac 739
 Gly Phe Val Ala Pro Glu Gln Met Leu Val Ile Ala Leu Thr Thr Tyr
 200 205 210
 ttt ttg atc ctt ctt ctc cgc gtc cgc ttc ccc aac ctg gac aag aaa 787
 Phe Leu Ile Leu Leu Leu Arg Val Arg Phe Pro Asn Leu Asp Lys Lys
 215 220 225
 ctg gag atc agg act tcc cat gag tgagtttggc ctgccagaag gcg 834
 Leu Glu Ile Arg Thr Ser His Glu
 230 235

<210> 2342

<211> 237

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2342

Met Ser Ser Glu Asn Leu Lys Glu Ile Arg Gly Gly Ile Gly Glu Thr
 1 5 10 15
 Leu Thr Val Gly Leu Gly Leu Ile Pro Leu Gly Leu Ala Phe Gly Leu
 20 25 30
 Leu Met Val Gln Thr Gly Phe Ala Trp Trp Trp Thr Pro Ile Phe Ser
 35 40 45
 Phe Val Ile Tyr Ala Gly Ser Met Glu Phe Leu Ala Ile Gly Met Val
 50 55 60
 Thr Ala Gly Ile Gly Pro Phe Ser Ala Ala Val Ala Gly Phe Met Val
 65 70 75 80
 Asn Phe Arg His Ile Phe Tyr Gly Leu Thr Phe Pro Arg His Arg Ile
 85 90 95
 Lys Ser Gly Ala Gly Arg Ala Tyr Ser Thr Tyr Ala Leu Thr Asp Glu
 100 105 110
 Ser Tyr Ala Ile Val Ser Ala Arg Pro Pro Gly Asp Ile Ser Gly Thr
 115 120 125
 Arg Val Leu Thr Val Gln Ile Leu Cys Gln Ala Leu Trp Val Ile Pro
 130 135 140
 Gly Ile Ile Gly Ala Leu Val Gly Gln Val Leu Pro Asp Asp Leu Lys
 145 150 155 160
 Gly Met Asp Phe Ala Leu Thr Ala Leu Phe Val Val Leu Ala Trp Glu

165	170	175
Ala Phe Lys Asn Asn Lys Asp Tyr Ser Leu Pro Leu Phe Ala Val Val		
180	185	190
Leu Ala Leu Val Ser Gly Phe Val Ala Pro Glu Gln Met Leu Val Ile		
195	200	205
Ala Leu Thr Thr Tyr Phe Leu Ile Leu Leu Leu Arg Val Arg Phe Pro		
210	215	220
Asn Leu Asp Lys Lys Leu Glu Ile Arg Thr Ser His Glu		
225	230	235

<210> 2343

<211> 468

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(445)

<223> RXA01624

<400> 2343

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                                         Met Ser Glu Phe Gly
                                         1 5

ctg cca gaa ggc gtc acg ctg ctc aac gtc gcc gcc gtg ttg atc ccc 163
Leu Pro Glu Gly Val Thr Leu Leu Asn Val Ala Ala Val Leu Ile Pro
                        10 15 20

atc gcg atc atc acc ttg ctg ctg cgc atc ttc ccc ttc gcc gcg atg 211
Ile Ala Ile Ile Thr Leu Leu Leu Arg Ile Phe Pro Phe Ala Ala Met
                        25 30 35

aaa cgc gtc aac agc aac caa ctc atg gga gtt ttg ggg cgc aca atg 259
Lys Arg Val Asn Ser Asn Gln Leu Met Gly Val Leu Gly Arg Thr Met
                        40 45 50

cca gtc gga gtg atg gtc gta ttg gtc att tac acg ctc ttt ggc cag 307
Pro Val Gly Val Met Val Val Leu Val Ile Tyr Thr Leu Phe Gly Gln
                        55 60 65

gtc agt gcg cca ggt ggt gtg ggt gct tca ctg atc gcg gtg gca ttc 355
Val Ser Ala Pro Gly Gly Val Gly Ala Ser Leu Ile Ala Val Ala Phe
                        70 75 80 85

acc gcg ctg ctg cac tgg ttg aaa ggc tcc gcc ggg ctg tcc atc gtc 403
Thr Ala Leu Leu His Trp Leu Lys Gly Ser Ala Gly Leu Ser Ile Val
                        90 95 100

ggt ggc acc ttg gcc tac atg ttt ctg gtc aac gtc gtt ttt 445
Gly Gly Thr Leu Ala Tyr Met Phe Leu Val Asn Val Val Phe
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taaaagatgc ttctcgacgc aaa 468

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<210> 2344

<211> 115

<212> PRT

<213> Corynebacterium glutamicum

<400> 2344

Met Ser Glu Phe Gly Leu Pro Glu Gly Val Thr Leu Leu Asn Val Ala
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Pro Phe Ala Ala Met Lys Arg Val Asn Ser Asn Gln Leu Met Gly Val
 35 40 45

Leu Gly Arg Thr Met Pro Val Gly Val Met Val Val Leu Val Ile Tyr
 50 55 60

Thr Leu Phe Gly Gln Val Ser Ala Pro Gly Gly Val Gly Ala Ser Leu
 65 70 75 80

Ile Ala Val Ala Phe Thr Ala Leu Leu His Trp Leu Lys Gly Ser Ala
 85 90 95

Gly Leu Ser Ile Val Gly Gly Thr Leu Ala Tyr Met Phe Leu Val Asn
 100 105 110

Val Val Phe
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<212> DNA

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<220>

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<222> (101)..(1114)

<223> RXA01628

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tttcttaagg aagctccgac ccattcacatg tagcctttcc ttg gtt ctc gta ggg 115
 Leu Val Leu Val Gly
 1 5

tgc agc aac acg gca gag tcc acg acc acc gat acg gca ggc tcc act 163
 Cys Ser Asn Thr Ala Glu Ser Thr Thr Asp Thr Ala Gly Ser Thr
 10 15 20

gaa act tca tca cag att tca ccc acc act cca gtc agc acc acc gaa 211
 Glu Thr Ser Ser Gln Ile Ser Pro Thr Thr Pro Val Ser Thr Thr Glu
 25 30 35

gca gcg ccg cct gaa gat cca agc gca aac gct ttg gaa gag tat gct 259
 Ala Ala Pro Pro Glu Asp Pro Ser Ala Asn Ala Leu Glu Glu Tyr Ala
 40 45 50

cag atc ctt gcc aat cca agc atc tac ccc tta acc gaa att tca caa	307
Gln Ile Leu Ala Asn Pro Ser Ile Tyr Pro Leu Thr Glu Ile Ser Gln	
55 60 65	
ttc gtc ccc aca ggc aca tat gcc tac aca ctt gtt gaa gca act tcc	355
Phe Val Pro Thr Gly Thr Tyr Ala Tyr Thr Leu Val Glu Ala Thr Ser	
70 75 80 85	
gat tcc atc cca gaa cta cta ctc cgc gcc gat agt cac gaa ttc gcg	403
Asp Ser Ile Pro Glu Leu Leu Leu Arg Ala Asp Ser His Glu Phe Ala	
90 95 100	
cca att ttg gtt ttc acc tat gac gaa aac aca caa tcc gca acc caa	451
Pro Ile Leu Val Phe Thr Tyr Asp Glu Asn Thr Gln Ser Ala Thr Gln	
105 110 115	
gct gga gga gtc cta att gac ggt gtc gcc agc gcc ggc ggt tca cga	499
Ala Gly Gly Val Leu Ile Asp Gly Val Ala Ser Ala Gly Gly Ser Arg	
120 125 130	
gtc aag gtc aga gct tca aat tca gga gca gga atc tac caa ttg aat	547
Val Lys Val Arg Ala Ser Asn Ser Gly Ala Gly Ile Tyr Gln Leu Asn	
135 140 145	
tgg tac tcg ata caa cca gtt ggc gaa agc tct ttg tac gga atc caa	595
Trp Tyr Ser Ile Gln Pro Val Gly Glu Ser Ser Leu Tyr Gly Ile Gln	
150 155 160 165	
gga aac tcc ctg aca caa atc gca gac ccc gag gat ttc atg gtc cgt	643
Gly Asn Ser Leu Thr Gln Ile Ala Asp Pro Glu Asp Phe Met Val Arg	
170 175 180	
gaa cta tta cct gac cac cac gaa att acc tgg gtt gat tcc aac gac	691
Glu Leu Leu Pro Asp His His Glu Ile Thr Trp Val Asp Ser Asn Asp	
185 190 195	
ccc tcc ggc cta tca acc gtt cag act ggt gga gcc aac att caa caa	739
Pro Ser Gly Leu Ser Thr Val Gln Thr Gly Gly Ala Asn Ile Gln Gln	
200 205 210	
gca gcc cca act ccc gtt caa cag cct gcg tca aac ctg cac tac ttc	787
Ala Ala Pro Thr Pro Val Gln Gln Pro Ala Ser Asn Leu His Tyr Phe	
215 220 225	
tct ggt gta gta acg atg cag acc gcc ggc gaa ctc atg cga ggt gaa	835
Ser Gly Val Val Thr Met Gln Thr Ala Gly Glu Leu Met Arg Gly Glu	
230 235 240 245	
cga act ccc aat ggt gag cct gcc act gat ctc tat ctc gta ctg gtc	883
Arg Thr Pro Asn Gly Glu Pro Ala Thr Asp Leu Tyr Leu Val Leu Val	
250 255 260	
ctt gat tcc cca att gaa atc aca gca cga aac gca gct aca gac cct	931
Leu Asp Ser Pro Ile Glu Ile Thr Ala Arg Asn Ala Ala Thr Asp Pro	
265 270 275	
cag act cgt acc att tcc gaa gtc agc ctc ggc cga tac atc ccc gct	979
Gln Thr Arg Thr Ile Ser Glu Val Ser Leu Gly Arg Tyr Ile Pro Ala	
280 285 290	

gat ggt gac aat gat tgg ata ggc tac ctc gac acc cac gtg gaa atc 1027
 Asp Gly Asp Asn Asp Trp Ile Gly Tyr Leu Asp Thr His Val Glu Ile
 295 300 305

act gca aca acg gat cag gtc tgg ttc cca acc gac acc ggt cta cct 1075
 Thr Ala Thr Thr Asp Gln Val Trp Phe Pro Thr Asp Thr Gly Leu Pro
 310 315 320 325

ctt gga atg ctt cgt cta gcg gac tac aaa agc atc tca taaaccgacg 1124
 Leu Gly Met Leu Arg Leu Ala Asp Tyr Lys Ser Ile Ser
 330 335

cagcactcgt cga 1137

<210> 2346

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 2346

Leu Val Leu Val Gly Cys Ser Asn Thr Ala Glu Ser Thr Thr Thr Asp
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Thr Ala Gly Ser Thr Glu Thr Ser Ser Gln Ile Ser Pro Thr Thr Pro
 20 25 30

Val Ser Thr Thr Glu Ala Ala Pro Pro Glu Asp Pro Ser Ala Asn Ala
 35 40 45

Leu Glu Glu Tyr Ala Gln Ile Leu Ala Asn Pro Ser Ile Tyr Pro Leu
 50 55 60

Thr Glu Ile Ser Gln Phe Val Pro Thr Gly Thr Tyr Ala Tyr Thr Leu
 65 70 75 80

Val Glu Ala Thr Ser Asp Ser Ile Pro Glu Leu Leu Leu Arg Ala Asp
 85 90 95

Ser His Glu Phe Ala Pro Ile Leu Val Phe Thr Tyr Asp Glu Asn Thr
 100 105 110

Gln Ser Ala Thr Gln Ala Gly Gly Val Leu Ile Asp Gly Val Ala Ser
 115 120 125

Ala Gly Gly Ser Arg Val Lys Val Arg Ala Ser Asn Ser Gly Ala Gly
 130 135 140

Ile Tyr Gln Leu Asn Trp Tyr Ser Ile Gln Pro Val Gly Glu Ser Ser
 145 150 155 160

Leu Tyr Gly Ile Gln Gly Asn Ser Leu Thr Gln Ile Ala Asp Pro Glu
 165 170 175

Asp Phe Met Val Arg Glu Leu Leu Pro Asp His His Glu Ile Thr Trp
 180 185 190

Val Asp Ser Asn Asp Pro Ser Gly Leu Ser Thr Val Gln Thr Gly Gly
 195 200 205

Ala Asn Ile Gln Gln Ala Ala Pro Thr Pro Val Gln Gln Pro Ala Ser

210	215	220
Asn Leu His Tyr Phe Ser Gly Val Val Thr Met Gln Thr Ala Gly Glu 225 230 235 240		
Leu Met Arg Gly Glu Arg Thr Pro Asn Gly Glu Pro Ala Thr Asp Leu 245 250 255		
Tyr Leu Val Leu Val Leu Asp Ser Pro Ile Glu Ile Thr Ala Arg Asn 260 265 270		
Ala Ala Thr Asp Pro Gln Thr Arg Thr Ile Ser Glu Val Ser Leu Gly 275 280 285		
Arg Tyr Ile Pro Ala Asp Gly Asp Asn Asp Trp Ile Gly Tyr Leu Asp 290 295 300		
Thr His Val Glu Ile Thr Ala Thr Thr Asp Gln Val Trp Phe Pro Thr 305 310 315 320		
Asp Thr Gly Leu Pro Leu Gly Met Leu Arg Leu Ala Asp Tyr Lys Ser 325 330 335		

Ile Ser

<210> 2347
 <211> 1200
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1177)
 <223> RXA01630

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 Met Ser Asp Gln Lys
 1 5
 att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg 163
 Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg
 10 15 20
 gtg cgt gcc ctc cgt gaa att gat ggg gta gag gtc gtc gcc gcc gcg 211
 Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu Val Val Ala Ala Ala
 25 30 35
 gat act gat tcc cgc ctc cag tac ttc acc gac aaa tat gat gtt gaa 259
 Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp Lys Tyr Asp Val Glu
 40 45 50
 ccc cgc gag atc gat gac gtc ttg aac gac gat cgc atc aac gcc atc 307
 Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp Arg Ile Asn Ala Ile
 55 60 65
 atg gtt cac tcc aag agc aag gac atg gtc cct cac gcc aag cgc gcg 355

Met	Val	His	Ser	Lys	Ser	Lys	Asp	Met	Val	Pro	His	Ala	Lys	Arg	Ala			
70					75					80					85			
ctc	gcg	gcc	gga	aaa	tcc	gtc	gtc	gtg	gag	aag	ccc	ggc	ggg	gga	aca		403	
Leu	Ala	Ala	Gly	Lys	Ser	Val	Val	Val	Glu	Lys	Pro	Gly	Gly	Gly	Thr			
				90					95					100				
gtg	gcg	gat	ctt	gag	gag	ctc	ctg	gcc	ctc	aaa	gaa	gct	gcc	gat	cct		451	
Val	Ala	Asp	Leu	Glu	Glu	Leu	Leu	Ala	Leu	Lys	Glu	Ala	Ala	Asp	Pro			
			105					110					115					
cag	cga	atc	gtg	cag	gtc	ggg	tac	aac	gtc	cgc	ctg	tct	gaa	tcg	gtt		499	
Gln	Arg	Ile	Val	Gln	Val	Gly	Tyr	Asn	Val	Arg	Leu	Ser	Glu	Ser	Val			
		120					125						130					
cag	aga	tta	aaa	gag	ctt	ctc	gac	gcc	ggc	ctc	atc	ggc	gaa	gtc	gtc		547	
Gln	Arg	Leu	Lys	Glu	Leu	Leu	Asp	Ala	Gly	Leu	Ile	Gly	Glu	Val	Val			
		135					140					145						
agc	gtg	caa	gca	cgc	ggc	gcc	gca	aaa	gta	ggt	gag	cat	atc	acc	gag		595	
Ser	Val	Gln	Ala	Arg	Gly	Ala	Ala	Lys	Val	Gly	Glu	His	Ile	Thr	Glu			
					155					160					165			
cac	ctc	aac	caa	ccc	gca	gac	atg	ggc	ggt	gtg	ttg	tgg	att	ctt	ggc		643	
His	Leu	Asn	Gln	Pro	Ala	Asp	Met	Gly	Gly	Val	Leu	Trp	Ile	Leu	Gly			
				170					175					180				
tgc	cac	atg	ctc	gat	gca	ttg	gtg	gaa	gtc	ttc	gga	gct	cca	gaa	tcc		691	
Cys	His	Met	Leu	Asp	Ala	Leu	Val	Glu	Val	Phe	Gly	Ala	Pro	Glu	Ser			
			185					190						195				
gtg	aac	gcc	cga	gtg	cat	aag	acc	gca	aaa	ctc	tct	gac	gac	acc	agc		739	
Val	Asn	Ala	Arg	Val	His	Lys	Thr	Ala	Lys	Leu	Ser	Asp	Asp	Thr	Ser			
			200				205						210					
cgc	gaa	gac	tca	gcc	tcc	gca	ctg	ctg	tac	tac	cca	gat	ttc	tcc	gtc		787	
Arg	Glu	Asp	Ser	Ala	Ser	Ala	Leu	Leu	Tyr	Tyr	Pro	Asp	Phe	Ser	Val			
			215				220					225						
agc	ttc	agc	ttc	gac	ggc	cac	gat	gat	ctg	gaa	tgg	ttc	gaa	agc	tcc		835	
Ser	Phe	Ser	Phe	Asp	Gly	His	Asp	Asp	Leu	Glu	Trp	Phe	Glu	Ser	Ser			
					235					240					245			
cga	ctc	acg	gtc	tat	gga	acc	aag	ggc	atg	atc	gaa	gcc	gga	atc	ctc		883	
Arg	Leu	Thr	Val	Tyr	Gly	Thr	Lys	Gly	Met	Ile	Glu	Ala	Gly	Ile	Leu			
				250					255					260				
cct	cag	aca	ctg	cgc	gta	tac	ctc	aat	gag	tca	cgc	cag	ggc	tgg	cca		931	
Pro	Gln	Thr	Leu	Arg	Val	Tyr	Leu	Asn	Glu	Ser	Arg	Gln	Gly	Trp	Pro			
			265					270					275					
cag	ggt	tgg	acc	gag	tgg	acc	cag	agc	tac	ttc	acc	cca	ccg	ttt	gct		979	
Gln	Gly	Trp	Thr	Glu	Trp	Thr	Gln	Ser	Tyr	Phe	Thr	Pro	Pro	Phe	Ala			
			280				285						290					
cgc	aca	gaa	tcc	aac	aaa	ttc	tca	gag	ctt	cca	gag	cta	gaa	aac	atc		1027	
Arg	Thr	Glu	Ser	Asn	Lys	Phe	Ser	Glu	Leu	Pro	Glu	Leu	Glu	Asn	Ile			
			295				300					305						
agc	aac	ttc	cgc	aca	gaa	atg	cag	ggg	tgg	gtg	aat	tcc	att	cgc	act		1075	
Ser	Asn	Phe	Arg	Thr	Glu	Met	Gln	Gly	Trp	Val	Asn	Ser	Ile	Arg	Thr			

310	315	320	325	
gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc				1123
Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg				
330	335	340		
att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta				1171
Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val				
345	350	355		
aac atc taagaggagc actccatgaa acc				1200
Asn Ile				

<210> 2348

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 2348

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20 25 30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
35 40 45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
50 55 60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
65 70 75 80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
85 90 95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
100 105 110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
115 120 125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
130 135 140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
145 150 155 160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
165 170 175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
180 185 190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
195 200 205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr

210	215	220
Pro Asp Phe Ser Val	Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu	
225	230	235 240
Trp Phe Glu Ser	Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile	
	245	250 255
Glu Ala Gly Ile Leu Pro Gln Thr	Leu Arg Val Tyr Leu Asn Glu Ser	
	260	265 270
Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe		
	275	280 285
Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro		
	290	295 300
Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val		
	305	310 315 320
Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala		
	325	330 335
Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn		
	340	345 350
Gln Gly Ile Ser Val Asn Ile		
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<210> 2349

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXA01641

<400> 2349

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agacacattt gttgggggac aattttgggg gttgggttatt	ttg gca atc gat aat	115
	Leu Ala Ile Asp Asn	
	1 5	

gcg ctg cgc gtg agc atc cgc ata gat ctc acc gtt ggc gat gcg ccc	163
Ala Leu Arg Val Ser Ile Arg Ile Asp Leu Thr Val Gly Asp Ala Pro	
	10 15 20

gct gct gtg gct gat gtg gcg cta cct gca ggt tcg agt ctg gcg gac	211
Ala Ala Val Ala Asp Val Ala Leu Pro Ala Gly Ser Ser Leu Ala Asp	
	25 30 35

att ttg gat gaa att tta gaa ctc acc gat gca ccc cgg att tcc agg	259
Ile Leu Asp Glu Ile Leu Glu Leu Thr Asp Ala Pro Arg Ile Ser Arg	
	40 45 50

ccg tgg gtg gct cac act gct gcg gga agt ccc att gat tgc ggg att	307
Pro Trp Val Ala His Thr Ala Ala Gly Ser Pro Ile Asp Cys Gly Ile	

55	60	65	
ccg ctt gca gaa aca caa gtg gaa caa ggc agc gtg gtg gtc ctt tca			355
Pro Leu Ala Glu Thr Gln Val Glu Gln Gly Ser Val Val Val Leu Ser			
70	75	80	85
ccc gaa agg gac ttg gaa gcc ccc gtg ttg cgt gat gtc gcc gaa gcg			403
Pro Glu Arg Asp Leu Glu Ala Pro Val Leu Arg Asp Val Ala Glu Ala			
	90	95	100
ttg gtg gag ttt tct tcc acg aac cgc gcc ggg cac ctc gtg gaa ttg			451
Leu Val Glu Phe Ser Ser Thr Asn Arg Ala Gly His Leu Val Glu Leu			
	105	110	115
atg act ttc gcg ggg ctc atc ggg gct gcc gtg tta atg aca agt cct			499
Met Thr Phe Ala Gly Leu Ile Gly Ala Ala Val Leu Met Thr Ser Pro			
	120	125	130
gct gcc tcc gga att att gtg ccc ggc cgc atg gga atc ttc gtc gca			547
Ala Ala Ser Gly Ile Ile Val Pro Gly Arg Met Gly Ile Phe Val Ala			
	135	140	145
atc tgc gct cta ctg ctt ctg tgg ctc cca ccc gcg cac acc ccg atc			595
Ile Cys Ala Leu Leu Leu Leu Trp Leu Pro Pro Ala His Thr Pro Ile			
	150	155	160
ctt cga aac gtc ctg ccg att acc ctg atc ttg ggc gca ggc gga gcg			643
Leu Arg Asn Val Leu Pro Ile Thr Leu Ile Leu Gly Ala Gly Gly Ala			
	170	175	180
gta tca gtg ctg gtt gca ggc act tct ggg act tct ccc ggc gcg ctt			691
Val Ser Val Leu Val Ala Gly Thr Ser Gly Thr Ser Pro Gly Ala Leu			
	185	190	195
acc tgg acg att ttc gct ggc gcg tgc act att ctt gcc agt tcg ctg			739
Thr Trp Thr Ile Phe Ala Gly Ala Cys Thr Ile Leu Ala Ser Ser Leu			
	200	205	210
ctg gtt cat gtg gtg tat cgt cca gca att ctt ctg gtg gca aca ctg			787
Leu Val His Val Val Tyr Arg Pro Ala Ile Leu Leu Val Ala Thr Leu			
	215	220	225
tcc aca ttg ggg ctc ggt ctc tta gtc ctt gca gca acc acc act ctg			835
Ser Thr Leu Gly Leu Gly Leu Leu Val Leu Ala Ala Thr Thr Thr Leu			
	230	235	240
tgg aag ctc aaa gct acc gaa gat ttc agc ggt cca gca gcg atc acg			883
Trp Lys Leu Lys Ala Thr Glu Asp Phe Ser Gly Pro Ala Ala Ile Thr			
	250	255	260
gtc acc gct tcc acc atc acc atg tgc ttc gcc ccg aaa atc gca gca			931
Val Thr Ala Ser Thr Ile Thr Met Cys Phe Ala Pro Lys Ile Ala Ala			
	265	270	275
tcg cta gca ggc ctg cgc gtc cca tcg ctt ccc acc gcc ggc gaa gat			979
Ser Leu Ala Gly Leu Arg Val Pro Ser Leu Pro Thr Ala Gly Glu Asp			
	280	285	290
ctc tcc gtc agc gac ctc acc atg act gat ccc gag aaa aga ata aaa			1027
Leu Ser Val Ser Asp Leu Thr Met Thr Asp Pro Glu Lys Arg Ile Lys			
	295	300	305

aca aca aag acg ctt ttc gac gcc cag atc ctt ggc ctt ggc gtt ttg 1075
 Thr Thr Lys Thr Leu Phe Asp Ala Gln Ile Leu Gly Leu Gly Val Leu
 310 315 320 325
 agc ggg cct ttg gcg ttg ttg tcg gtt acc ccg ggc acc tgg aca acc 1123
 Ser Gly Pro Leu Ala Leu Leu Ser Val Thr Pro Gly Thr Trp Thr Thr
 330 335 340
 acc gtt ttt agt tta tgc atc gcg gtg gct tcg ctg ctt cac gct aat 1171
 Thr Val Phe Ser Leu Cys Ile Ala Val Ala Ser Leu Leu His Ala Asn
 345 350 355
 cgt cat caa gca cca att ccc acg tgg aca ttg atg ggg tta tct gcc 1219
 Arg His Gln Ala Pro Ile Pro Thr Trp Thr Leu Met Gly Leu Ser Ala
 360 365 370
 ctt ggt ttc att tcc atg gcg tta tcc gca agc cga tca ggt tca cta 1267
 Leu Gly Phe Ile Ser Met Ala Leu Ser Ala Ser Arg Ser Gly Ser Leu
 375 380 385
 att gca ctg atc ggt tct gtg gtt atc atc gct gtg ctg gtc agc gtg 1315
 Ile Ala Leu Ile Gly Ser Val Val Ile Ile Ala Val Leu Val Ser Val
 390 395 400 405
 gca ttg tgg atc agt aca gtc ccc acg ctg gaa ccc acc acc att gtg 1363
 Ala Leu Trp Ile Ser Thr Val Pro Thr Leu Glu Pro Thr Thr Ile Val
 410 415 420
 tgg ctt gaa agg ttg gaa tca ctg tgt ctt gca gct agt ctg cca ctc 1411
 Trp Leu Glu Arg Leu Glu Ser Leu Cys Leu Ala Ala Ser Leu Pro Leu
 425 430 435
 gca ctg cat ttg ctg gat gta ttt gga atg ctg cgc ggt ctt gat att 1459
 Ala Leu His Leu Leu Asp Val Phe Gly Met Leu Arg Gly Leu Asp Ile
 440 445 450
 gga ttc ggt gga taagatgcgc agactcatcg cgg 1494
 Gly Phe Gly Gly
 455

<210> 2350

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 2350

Leu Ala Ile Asp Asn Ala Leu Arg Val Ser Ile Arg Ile Asp Leu Thr
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Val Gly Asp Ala Pro Ala Ala Val Ala Asp Val Ala Leu Pro Ala Gly
 20 25 30

Ser Ser Leu Ala Asp Ile Leu Asp Glu Ile Leu Glu Leu Thr Asp Ala
 35 40 45

Pro Arg Ile Ser Arg Pro Trp Val Ala His Thr Ala Ala Gly Ser Pro
 50 55 60

Ile Asp Cys Gly Ile Pro Leu Ala Glu Thr Gln Val Glu Gln Gly Ser

65	70	75	80
Val Val Val Leu Ser 85	Pro Glu Arg Asp Leu Glu Ala Pro Val Leu Arg 90		
Asp Val Ala Glu Ala Leu Val Glu Phe Ser Ser Thr Asn Arg Ala Gly 100	105		110
His Leu Val Glu Leu Met Thr Phe Ala Gly Leu Ile Gly Ala Ala Val 115	120		125
Leu Met Thr Ser Pro Ala Ala Ser Gly Ile Ile Val Pro Gly Arg Met 130	135		140
Gly Ile Phe Val Ala Ile Cys Ala Leu Leu Leu Leu Trp Leu Pro Pro 145	150	155	160
Ala His Thr Pro Ile Leu Arg Asn Val Leu Pro Ile Thr Leu Ile Leu 165	170		175
Gly Ala Gly Gly Ala Val Ser Val Leu Val Ala Gly Thr Ser Gly Thr 180	185		190
Ser Pro Gly Ala Leu Thr Trp Thr Ile Phe Ala Gly Ala Cys Thr Ile 195	200		205
Leu Ala Ser Ser Leu Leu Val His Val Val Tyr Arg Pro Ala Ile Leu 210	215	220	
Leu Val Ala Thr Leu Ser Thr Leu Gly Leu Gly Leu Leu Val Leu Ala 225	230	235	240
Ala Thr Thr Thr Leu Trp Lys Leu Lys Ala Thr Glu Asp Phe Ser Gly 245	250		255
Pro Ala Ala Ile Thr Val Thr Ala Ser Thr Ile Thr Met Cys Phe Ala 260	265		270
Pro Lys Ile Ala Ala Ser Leu Ala Gly Leu Arg Val Pro Ser Leu Pro 275	280		285
Thr Ala Gly Glu Asp Leu Ser Val Ser Asp Leu Thr Met Thr Asp Pro 290	295	300	
Glu Lys Arg Ile Lys Thr Thr Lys Thr Leu Phe Asp Ala Gln Ile Leu 305	310	315	320
Gly Leu Gly Val Leu Ser Gly Pro Leu Ala Leu Leu Ser Val Thr Pro 325	330		335
Gly Thr Trp Thr Thr Thr Val Phe Ser Leu Cys Ile Ala Val Ala Ser 340	345		350
Leu Leu His Ala Asn Arg His Gln Ala Pro Ile Pro Thr Trp Thr Leu 355	360		365
Met Gly Leu Ser Ala Leu Gly Phe Ile Ser Met Ala Leu Ser Ala Ser 370	375	380	
Arg Ser Gly Ser Leu Ile Ala Leu Ile Gly Ser Val Val Ile Ile Ala 385	390	395	400

Val Leu Val Ser Val Ala Leu Trp Ile Ser Thr Val Pro Thr Leu Glu
 405 410 415

Pro Thr Thr Ile Val Trp Leu Glu Arg Leu Glu Ser Leu Cys Leu Ala
 420 425 430

Ala Ser Leu Pro Leu Ala Leu His Leu Leu Asp Val Phe Gly Met Leu
 435 440 445

Arg Gly Leu Asp Ile Gly Phe Gly Gly
 450 455

<210> 2351

<211> 1365

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXA01642

<400> 2351

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ggaatgctgc gcggtcttga tattggattc ggtggataag atg cgc aga ctc atc 115
 Met Arg Arg Leu Ile
 1 5

gcg gtt agc ttg gcc gct ctg ttt atg ttg gct tcc act cca gcg acg 163
 Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala Ser Thr Pro Ala Thr
 10 15 20

agg gca cag gaa gta gaa gct ctc gct tgc ccc gag gta gcg atc gcc 211
 Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro Glu Val Ala Ile Ala
 25 30 35

gat cct tcc tcc gca gtt tta gat gaa cac ctt tcg cag tca tta tcc 259
 Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu Ser Gln Ser Leu Ser
 40 45 50

caa gct cac caa cta gca act ggc gcc ggt gtg atg gtg gca gtc atc 307
 Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val Met Val Ala Val Ile
 55 60 65

gac acc gga gta tcc ctg cat cca cgt ctg ccc cac tta att ccc ggc 355
 Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro His Leu Ile Pro Gly
 70 75 80 85

ggt gat ttc gtg ggc gcc cac caa agc ccc gat gtg cca ggt gaa ctt 403
 Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp Val Pro Gly Glu Leu
 90 95 100

atc gat tgc gac ggc cac ggc acc atc gtc gcc gga atc atc gcc tcc 451
 Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala Gly Ile Ile Ala Ser
 105 110 115

caa gga aac ccc ggc acc ggc tgg cca tat gac ggc agc tcc gat cct 499
 Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp Gly Ser Ser Asp Pro

120	125	130	
tat atc ggt gtc gcc cca gat tcc gga atc atc tcc att aaa caa acc			547
Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile Ser Ile Lys Gln Thr			
135	140	145	
agc tca tat gtg cgt act cgt gaa gat tcc aac gtc gga acg ctg agc			595
Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn Val Gly Thr Leu Ser			
150	155	160	165
acc ctg gcg gaa tcc atc cac cga gct ctc gat tcc ggt gcc cac gtg			643
Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp Ser Gly Ala His Val			
170	175	180	
atc aat att tcc gtg gtg tcc tgt ttg ccc caa tca ccc gac gag gcc			691
Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln Ser Pro Asp Glu Ala			
185	190	195	
gca tcg ttc cag cct ctg acg gat gct ctt aac aga gca gaa ctt caa			739
Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn Arg Ala Glu Leu Gln			
200	205	210	
ggg gtg ata gtg gtg gca gca gca gga aac ctc ggg cag gat tgt cca			787
Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu Gly Gln Asp Cys Pro			
215	220	225	
gtt gga tct acc gtt tat cct gca cat tca gac act gtg ctc tct gtg			835
Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp Thr Val Leu Ser Val			
230	235	240	245
tcg gca cgt ttt gat tct cac acg ctt gca gaa tat tcc atg cct ggc			883
Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu Tyr Ser Met Pro Gly			
250	255	260	
aac caa caa atc ctc tct gca cca agc cac att cag gct ggt cta tca			931
Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile Gln Ala Gly Leu Ser			
265	270	275	
ccg cgt ggc gac ggc ttc gcc agc cac atg atc acc acc gct ggc gaa			979
Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile Thr Thr Ala Gly Glu			
280	285	290	
agc ccc ttc gag ggc acc agt ttt gcc gct cca gtt gtc agc gcc aca			1027
Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro Val Val Ser Ala Thr			
295	300	305	
gct gca ctg ctt cgc cag cat ttt ccc ttt gcc aca ccc tat gaa att			1075
Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala Thr Pro Tyr Glu Ile			
310	315	320	325
cgt gca cga atc ttc aac agc atc gac cct gca aga ggc gct att gat			1123
Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala Arg Gly Ala Ile Asp			
330	335	340	
ccc tac ctg gca ctt act caa gaa atc tat ccc acc act ccc ctg gtt			1171
Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro Thr Thr Pro Leu Val			
345	350	355	
cat gag atc gca cta agt gtt ccc acg ccg ccg gat gat tct cca cgg			1219
His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro Asp Ser Pro Arg			
360	365	370	

gag cgg ggc atc cta gtt acc gca atc att gtt ggg ttg ctc gca gtg 1267
 Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val Gly Leu Leu Ala Val
 375 380 385
 tta gct gtg ctg atg gga cta cgc cga att cat cat cac tcg gcc ttt 1315
 Leu Ala Val Leu Met Gly Leu Arg Arg Ile His His His Ser Ala Phe
 390 395 400 405
 caa aaa gct agc tca agt gtt atc act taatctatga ggcaccgttc 1362
 Gln Lys Ala Ser Ser Val Ile Thr
 410
 aga 1365

<210> 2352

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 2352

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 20 25 30
 Glu Val Ala Ile Ala Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu
 35 40 45
 Ser Gln Ser Leu Ser Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val
 50 55 60
 Met Val Ala Val Ile Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro
 65 70 75 80
 His Leu Ile Pro Gly Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp
 85 90 95
 Val Pro Gly Glu Leu Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala
 100 105 110
 Gly Ile Ile Ala Ser Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp
 115 120 125
 Gly Ser Ser Asp Pro Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile
 130 135 140
 Ser Ile Lys Gln Thr Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn
 145 150 155 160
 Val Gly Thr Leu Ser Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp
 165 170 175
 Ser Gly Ala His Val Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln
 180 185 190
 Ser Pro Asp Glu Ala Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn
 195 200 205

Arg Ala Glu Leu Gln Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu
 210 215 220

Gly Gln Asp Cys Pro Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp
 225 230 235 240

Thr Val Leu Ser Val Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu
 245 250 255

Tyr Ser Met Pro Gly Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile
 260 265 270

Gln Ala Gly Leu Ser Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile
 275 280 285

Thr Thr Ala Gly Glu Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro
 290 295 300

Val Val Ser Ala Thr Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala
 305 310 315 320

Thr Pro Tyr Glu Ile Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala
 325 330 335

Arg Gly Ala Ile Asp Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro
 340 345 350

Thr Thr Pro Leu Val His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro
 355 360 365

Asp Asp Ser Pro Arg Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val
 370 375 380

Gly Leu Leu Ala Val Leu Ala Val Leu Met Gly Leu Arg Arg Ile His
 385 390 395 400

His His Ser Ala Phe Gln Lys Ala Ser Ser Ser Val Ile Thr
 405 410

<210> 2353

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA01643

<400> 2353

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cgatgtctcc ttcccaccg cggagacctg tagttaaccc atg ggc acg atg cga 115
 Met Gly Thr Met Arg
 1 5

gaa atg gtc agt gac cgc att gac cga cta caa gaa gca cac gcg cga 163
 Glu Met Val Ser Asp Arg Ile Asp Arg Leu Gln Glu Ala His Ala Arg
 10 15 20

tca aag cag aag aag ttc ggc ttc tta gtt cgg cca ggc acc ctg atc 211
 Ser Lys Gln Lys Lys Phe Gly Phe Leu Val Arg Pro Gly Thr Leu Ile
 25 30 35

ctt gga tgg ttg gtc acg atc atc ggt ctg atc acc att cca ctt ccc 259
 Leu Gly Trp Leu Val Thr Ile Ile Gly Leu Ile Thr Ile Pro Leu Pro
 40 45 50

ggc caa ggc tgg ctg acc acc ttc att ggt gtg ggc att ttg tct ctg 307
 Gly Gln Gly Trp Leu Thr Thr Phe Ile Gly Val Gly Ile Leu Ser Leu
 55 60 65

gag ctt aaa tgg gcg aag aac ctc ctg gcc tgg gga gtg cat cag tat 355
 Glu Leu Lys Trp Ala Lys Asn Leu Leu Ala Trp Gly Val His Gln Tyr
 70 75 80 85

gat cgc ttc ttc acc tgg tac ggc aag aaa tca ttc cgc ttc cgc atg 403
 Asp Arg Phe Phe Thr Trp Tyr Gly Lys Lys Ser Phe Arg Phe Arg Met
 90 95 100

gcg atg ttg gca ctg atg att ctg ctg att tgg gtg gtg ttc atc gtg 451
 Ala Met Leu Ala Leu Met Ile Leu Leu Ile Trp Val Val Phe Ile Val
 105 110 115

aca ttt tgg ttg atg tgg cac gcc gga act atc ccg tgg gca gat gag 499
 Thr Phe Trp Leu Met Trp His Ala Gly Thr Ile Pro Trp Ala Asp Glu
 120 125 130

ttc ttc acc tgg ctt ggg ttg agc cgc tagcaactat tcgctttgaa 546
 Phe Phe Thr Trp Leu Gly Leu Ser Arg
 135 140

ggc 549

<210> 2354

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 2354

Met Gly Thr Met Arg Glu Met Val Ser Asp Arg Ile Asp Arg Leu Gln
 1 5 10 15

Glu Ala His Ala Arg Ser Lys Gln Lys Lys Phe Gly Phe Leu Val Arg
 20 25 30

Pro Gly Thr Leu Ile Leu Gly Trp Leu Val Thr Ile Ile Gly Leu Ile
 35 40 45

Thr Ile Pro Leu Pro Gly Gln Gly Trp Leu Thr Thr Phe Ile Gly Val
 50 55 60

Gly Ile Leu Ser Leu Glu Leu Lys Trp Ala Lys Asn Leu Leu Ala Trp
 65 70 75 80

Gly Val His Gln Tyr Asp Arg Phe Phe Thr Trp Tyr Gly Lys Lys Ser
 85 90 95

Phe Arg Phe Arg Met Ala Met Leu Ala Leu Met Ile Leu Leu Ile Trp
 100 105 110

Val Val Phe Ile Val Thr Phe Trp Leu Met Trp His Ala Gly Thr Ile
 115 120 125

Pro Trp Ala Asp Glu Phe Phe Thr Trp Leu Gly Leu Ser Arg
 130 135 140

<210> 2355

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXA01645

<400> 2355

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ctgggttctgg tgttcacgcg cattcggcac ccaaaacccc gtg gtg cgc aaa ctc 115
 Val Val Arg Lys Leu
 1 5

tgg ccc agg gat ctg ctg cgc tcg agt ttc tat tgg aag atc atc ggc 163
 Trp Pro Arg Asp Leu Leu Arg Ser Ser Phe Tyr Trp Lys Ile Ile Gly
 10 15 20

tgg gat cga aaa tac tcc atc gct gat cgc ctg gaa gag cgc aaa ggc 211
 Trp Asp Arg Lys Tyr Ser Ile Ala Asp Arg Leu Glu Glu Arg Lys Gly
 25 30 35

cgc ccg gct agg gaa cgg gtg gtc caa gac gtg gaa gtt acg att gat 259
 Arg Pro Ala Arg Glu Arg Val Val Gln Asp Val Glu Val Thr Ile Asp
 40 45 50

aaa ctg cca gaa ttt ttg aaa tgg ttc ttt gaa agc agc gac atc gag 307
 Lys Leu Pro Glu Phe Leu Lys Trp Phe Phe Glu Ser Ser Asp Ile Glu
 55 60 65

ccg ctg tgg ctg tgc ccg atc aag ctt cgg gag gta cca ggt agt tcg 355
 Pro Leu Trp Leu Cys Pro Ile Lys Leu Arg Glu Val Pro Gly Ser Ser
 70 75 80 85

gtt ggt gct gga gaa att ttg agc tcc gct gaa gca atc gac tcc ggt 403
 Val Gly Ala Gly Glu Ile Leu Ser Ser Ala Glu Ala Ile Asp Ser Gly
 90 95 100

gct gct gaa cac cct tgg ccg ctg tat ccc ttg aag aag gac gtg ctg 451
 Ala Ala Glu His Pro Trp Pro Leu Tyr Pro Leu Lys Lys Asp Val Leu
 105 110 115

tgg gtc aac atc gga ttc tgg tcc tca gtg ccg gtt gat ctg atg ggc 499
 Trp Val Asn Ile Gly Phe Trp Ser Ser Val Pro Val Asp Leu Met Gly
 120 125 130

tcc gat gca cca gag gga gca ttt aac aga gaa atc gaa cgc gtc atg 547
 Ser Asp Ala Pro Glu Gly Ala Phe Asn Arg Glu Ile Glu Arg Val Met
 135 140 145

gca gag cta ggc gga cat aaa tcg ctg tac tcc gaa gcg ttc tac acc 595
 Ala Glu Leu Gly Gly His Lys Ser Leu Tyr Ser Glu Ala Phe Tyr Thr
 150 155 160 165
 agg gaa gac ttt gaa aaa ctt tat ggc gga acc atc ccg gcg ctg cta 643
 Arg Glu Asp Phe Glu Lys Leu Tyr Gly Gly Thr Ile Pro Ala Leu Leu
 170 175 180
 aaa aag cag tgg gat ccc cac agc cga ttc ccc ggt ttg tat gaa aag 691
 Lys Lys Gln Trp Asp Pro His Ser Arg Phe Pro Gly Leu Tyr Glu Lys
 185 190 195
 aca gta aaa ggc gcc taggatcgct cactgtaggt aga 729
 Thr Val Lys Gly Ala
 200

<210> 2356

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 2356

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 Glu Glu Arg Lys Gly Arg Pro Ala Arg Glu Arg Val Val Gln Asp Val
 35 40 45
 Glu Val Thr Ile Asp Lys Leu Pro Glu Phe Leu Lys Trp Phe Phe Glu
 50 55 60
 Ser Ser Asp Ile Glu Pro Leu Trp Leu Cys Pro Ile Lys Leu Arg Glu
 65 70 75 80
 Val Pro Gly Ser Ser Val Gly Ala Gly Glu Ile Leu Ser Ser Ala Glu
 85 90 95
 Ala Ile Asp Ser Gly Ala Ala Glu His Pro Trp Pro Leu Tyr Pro Leu
 100 105 110
 Lys Lys Asp Val Leu Trp Val Asn Ile Gly Phe Trp Ser Ser Val Pro
 115 120 125
 Val Asp Leu Met Gly Ser Asp Ala Pro Glu Gly Ala Phe Asn Arg Glu
 130 135 140
 Ile Glu Arg Val Met Ala Glu Leu Gly Gly His Lys Ser Leu Tyr Ser
 145 150 155 160
 Glu Ala Phe Tyr Thr Arg Glu Asp Phe Glu Lys Leu Tyr Gly Gly Thr
 165 170 175
 Ile Pro Ala Leu Leu Lys Lys Gln Trp Asp Pro His Ser Arg Phe Pro
 180 185 190
 Gly Leu Tyr Glu Lys Thr Val Lys Gly Ala
 195 200

<210> 2357

<211> 942

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(919)

<223> RXA01646

<400> 2357

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agcgctcgcg cccacctatt aaggagtatg gtggccttac atg agc gga tta gtt 115
                                         Met Ser Gly Leu Val
                                         1      5

gac ccg gat agt act ttt tta aag acc atc gga aaa ctg agc aac agc 163
Asp Pro Asp Ser Thr Phe Leu Lys Thr Ile Gly Lys Leu Ser Asn Ser
                        10                        15                        20

ttg tcc att ggt cgt gga gta gat caa aaa gag gta atc ccc aaa ggc 211
Leu Ser Ile Gly Arg Gly Val Asp Gln Lys Glu Val Ile Pro Lys Gly
                        25                        30                        35

tgg aac gcc cat tgg gag gca att aca aag ctt aag aga agc ttt gac 259
Trp Asn Ala His Trp Glu Ala Ile Thr Lys Leu Lys Arg Ser Phe Asp
                        40                        45                        50

gcg att cct gct ggg gag cgg gtg cgt tta gct aag aaa acc tcc aac 307
Ala Ile Pro Ala Gly Glu Arg Val Arg Leu Ala Lys Lys Thr Ser Asn
                        55                        60                        65

ctg ttc cgt gga cgc tcc gat gca ggt cac ggc cta gat gtg gca gcg 355
Leu Phe Arg Gly Arg Ser Asp Ala Gly His Gly Leu Asp Val Ala Ala
                        70                        75                        80                        85

ctt ggg gga gtg att gcc att gat ccg gtc aat gcc acc gcc gat gta 403
Leu Gly Gly Val Ile Ala Ile Asp Pro Val Asn Ala Thr Ala Asp Val
                        90                        95                        100

cag ggc atg tgc acg tat gaa gac ctg gta gat gcc act tta agt tat 451
Gln Gly Met Cys Thr Tyr Glu Asp Leu Val Asp Ala Thr Leu Ser Tyr
                        105                        110                        115

ggg ctg atg ccg ttg gtt gtg cct caa ctg aaa acc atc acg ctt ggt 499
Gly Leu Met Pro Leu Val Val Pro Gln Leu Lys Thr Ile Thr Leu Gly
                        120                        125                        130

ggc gca gtg acc gga atg ggc gtg gaa tcc aca tcc ttc cgc aac ggt 547
Gly Ala Val Thr Gly Met Gly Val Glu Ser Thr Ser Phe Arg Asn Gly
                        135                        140                        145

ttg cca cac gaa tca gtg ctg gag atg gat att ttt acc ggc act ggt 595
Leu Pro His Glu Ser Val Leu Glu Met Asp Ile Phe Thr Gly Thr Gly
                        150                        155                        160                        165

gag atc gtg act tgc tcg ccc aca gaa aat gtc gac ctt tac aga ggt 643
Glu Ile Val Thr Cys Ser Pro Thr Glu Asn Val Asp Leu Tyr Arg Gly

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170	175	180	
ttt ccc aac tct tat ggt tgc ctg gga tac gcg gtg cgg cta aaa att			691
Phe Pro Asn Ser Tyr Gly Ser Leu Gly Tyr Ala Val Arg Leu Lys Ile			
185	190	195	
gag ctg gaa cca gtg caa gat tac gtc cag ctg cgc cac gtg cgc ttc			739
Glu Leu Glu Pro Val Gln Asp Tyr Val Gln Leu Arg His Val Arg Phe			
200	205	210	
aac gat tta gag tct ttg acc aaa gcg att gag gaa gtc gcg tct tct			787
Asn Asp Leu Glu Ser Leu Thr Lys Ala Ile Glu Glu Val Ala Ser Ser			
215	220	225	
ctg gag ttt gat aac caa ccc gtc gat tac ctt gac ggc gtg gtg ttt			835
Leu Glu Phe Asp Asn Gln Pro Val Asp Tyr Leu Asp Gly Val Val Phe			
230	235	240	245
tca ccc acg gaa gcc tac tta gtt ctt ggc acg caa acc tca caa cct			883
Ser Pro Thr Glu Ala Tyr Leu Val Leu Gly Thr Gln Thr Ser Gln Pro			
250	255	260	
ggc ccc acc agc gat tac acc agg gat tta agc tac taacgctccc			929
Gly Pro Thr Ser Asp Tyr Thr Arg Asp Leu Ser Tyr			
265	270		
tgcaacacccc aga			942

<210> 2358

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 2358

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Lys Leu Ser Asn Ser Leu Ser Ile Gly Arg Gly Val Asp Gln Lys Glu
20 25 30

Val Ile Pro Lys Gly Trp Asn Ala His Trp Glu Ala Ile Thr Lys Leu
35 40 45

Lys Arg Ser Phe Asp Ala Ile Pro Ala Gly Glu Arg Val Arg Leu Ala
50 55 60

Lys Lys Thr Ser Asn Leu Phe Arg Gly Arg Ser Asp Ala Gly His Gly
65 70 75 80

Leu Asp Val Ala Ala Leu Gly Gly Val Ile Ala Ile Asp Pro Val Asn
85 90 95

Ala Thr Ala Asp Val Gln Gly Met Cys Thr Tyr Glu Asp Leu Val Asp
100 105 110

Ala Thr Leu Ser Tyr Gly Leu Met Pro Leu Val Val Pro Gln Leu Lys
115 120 125

Thr Ile Thr Leu Gly Gly Ala Val Thr Gly Met Gly Val Glu Ser Thr
130 135 140

Ser Phe Arg Asn Gly Leu Pro His Glu Ser Val Leu Glu Met Asp Ile
 145 150 155 160
 Phe Thr Gly Thr Gly Glu Ile Val Thr Cys Ser Pro Thr Glu Asn Val
 165 170 175
 Asp Leu Tyr Arg Gly Phe Pro Asn Ser Tyr Gly Ser Leu Gly Tyr Ala
 180 185 190
 Val Arg Leu Lys Ile Glu Leu Glu Pro Val Gln Asp Tyr Val Gln Leu
 195 200 205
 Arg His Val Arg Phe Asn Asp Leu Glu Ser Leu Thr Lys Ala Ile Glu
 210 215 220
 Glu Val Ala Ser Ser Leu Glu Phe Asp Asn Gln Pro Val Asp Tyr Leu
 225 230 235 240
 Asp Gly Val Val Phe Ser Pro Thr Glu Ala Tyr Leu Val Leu Gly Thr
 245 250 255
 Gln Thr Ser Gln Pro Gly Pro Thr Ser Asp Tyr Thr Arg Asp Leu Ser
 260 265 270
 Tyr

<210> 2359
 <211> 1020
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(997)
 <223> RXA01656

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 Met Thr Glu Thr Gln 5
 gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
 Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met 20
 ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
 Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg 35
 atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
 Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val 50
 ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
 Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala 70 75 80 85	355
aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu 90 95 100	403
ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr 105 110 115	451
acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly 120 125 130	499
gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala 135 140 145	547
atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala 150 155 160 165	595
gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser 170 175 180	643
ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro 185 190 195	691
tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val 200 205 210	739
acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val 215 220 225	787
cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys 230 235 240 245	835
tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr 250 255 260	883
ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly 265 270 275	931
gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg 280 285 290	979
ctc gcc gag cgc ggc tgg tgatcggttg agtttttagct ctc Leu Ala Glu Arg Gly Trp 295	1020

<210> 2360

<211> 299

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2360

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 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
 20 25 30
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
 35 40 45
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
 50 55 60
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65 70 75 80
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
 85 90 95
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
 100 105 110
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
 115 120 125
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
 130 135 140
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
 145 150 155 160
 Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile
 165 170 175
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys
 180 185 190
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly
 195 200 205
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala
 210 215 220
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly
 225 230 235 240
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile
 245 250 255
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val
 260 265 270
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val
 275 280 285

<400> 2361																	60
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gtgcttgagc gaaaaccctg gatgattagc atggtttgtt																	115
Val Lys Ile Asp Glu																	1 5
ttg att gct ctc gcc gcg gag caa ccc act cgc atc tcc agg cgt tcc																	163
Leu Ile Ala Leu Ala Ala Glu Gln Pro Thr Arg Ile Ser Arg Arg Ser																	10 15 20
ggg gtc tcg cgc tcg acc ctg aag cgg gtc ggc gat ggc acc agc gag																	211
Gly Val Ser Arg Ser Thr Leu Lys Arg Val Gly Asp Gly Thr Ser Glu																	25 30 35
ccc acc ctg tcg acg ctg cgt gag gtc gcg ttg gcg ctc ggg ctt gat																	259
Pro Thr Leu Ser Thr Leu Arg Glu Val Ala Leu Ala Leu Gly Leu Asp																	40 45 50
att aag gtc gcc gcg cac cac gcc tgc gat ccc ttt gcg gcc gct gca																	307
Ile Lys Val Ala Ala His His Ala Cys Asp Pro Phe Ala Ala Ala Ala																	55 60 65
gcg cgc acg ctt atc gac gcc tcc gtc ccc gaa aat ccc cac aac cag																	355
Ala Arg Thr Leu Ile Asp Ala Ser Val Pro Glu Asn Pro His Asn Gln																	70 75 80 85
gaa att ctc gct tgg ttg cac cgt ttt gag cgg tgg aat atc aac gat																	403
Glu Ile Leu Ala Trp Leu His Arg Phe Glu Arg Trp Asn Ile Asn Asp																	90 95 100
ccg ctc acc ctt gtc tct gaa gcc gga acg ctt cag ggc atc aca cat																	451
Pro Leu Thr Leu Val Ser Glu Ala Gly Thr Leu Gln Gly Ile Thr His																	105 110 115
cgc cag gat gcg cag ttt gtg aaa ctc aat cca cgc ggc atc gct gag																	499
Arg Gln Asp Ala Gln Phe Val Lys Leu Asn Pro Arg Gly Ile Ala Glu																	120 125 130
cta ccg gag ctt ttc caa cag cac aaa acc aaa tgg gcg ctg tcg ggc																	547
Leu Pro Glu Leu Phe Gln Gln His Lys Thr Lys Trp Ala Leu Ser Gly																	135 140 145
gct gcg gct gcc acg gtg atc atg gga caa att gtg ctg ggg aat tcg																	595
Ala Ala Ala Ala Thr Val Ile Met Gly Gln Ile Val Leu Gly Asn Ser																	150 155 160 165

att gtg tgg cac gaa cct gcc cac gat ctc gat gtc tca gcg ctg ggc 643
 Ile Val Trp His Glu Pro Ala His Asp Leu Asp Val Ser Ala Leu Gly
 170 175 180

acc att gtt gat gtg gca gaa gac gcc gat cta att ctc ctg ccc gca 691
 Thr Ile Val Asp Val Ala Glu Asp Ala Asp Leu Ile Leu Leu Pro Ala
 185 190 195

acg gtc acg gaa ctg gtg gga agt tac acc cag gac agg cta aat ttt 739
 Thr Val Thr Glu Leu Val Gly Ser Tyr Thr Gln Asp Arg Leu Asn Phe
 200 205 210

gtg gca cct gtg caa tta gtt att gat cta cac agc ctc cac atg ttc 787
 Val Ala Pro Val Gln Leu Val Ile Asp Leu His Ser Leu His Met Phe
 215 220 225

gag gaa gcc gat tac ctc acg agc ggt tgg cgc taaaatactt agcgtacgca 840
 Glu Glu Ala Asp Tyr Leu Thr Ser Gly Trp Arg
 230 235 240

ccc 843

<210> 2362
 <211> 240
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2362
 Val Lys Ile Asp Glu Leu Ile Ala Leu Ala Ala Glu Gln Pro Thr Arg
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Ile Ser Arg Arg Ser Gly Val Ser Arg Ser Thr Leu Lys Arg Val Gly
 20 25 30

Asp Gly Thr Ser Glu Pro Thr Leu Ser Thr Leu Arg Glu Val Ala Leu
 35 40 45

Ala Leu Gly Leu Asp Ile Lys Val Ala Ala His His Ala Cys Asp Pro
 50 55 60

Phe Ala Ala Ala Ala Ala Arg Thr Leu Ile Asp Ala Ser Val Pro Glu
 65 70 75 80

Asn Pro His Asn Gln Glu Ile Leu Ala Trp Leu His Arg Phe Glu Arg
 85 90 95

Trp Asn Ile Asn Asp Pro Leu Thr Leu Val Ser Glu Ala Gly Thr Leu
 100 105 110

Gln Gly Ile Thr His Arg Gln Asp Ala Gln Phe Val Lys Leu Asn Pro
 115 120 125

Arg Gly Ile Ala Glu Leu Pro Glu Leu Phe Gln Gln His Lys Thr Lys
 130 135 140

Trp Ala Leu Ser Gly Ala Ala Ala Ala Thr Val Ile Met Gly Gln Ile
 145 150 155 160

Val Leu Gly Asn Ser Ile Val Trp His Glu Pro Ala His Asp Leu Asp
 165 170 175

Val Ser Ala Leu Gly Thr Ile Val Asp Val Ala Glu Asp Ala Asp Leu
 180 185 190
 Ile Leu Leu Pro Ala Thr Val Thr Glu Leu Val Gly Ser Tyr Thr Gln
 195 200 205
 Asp Arg Leu Asn Phe Val Ala Pro Val Gln Leu Val Ile Asp Leu His
 210 215 220
 Ser Leu His Met Phe Glu Glu Ala Asp Tyr Leu Thr Ser Gly Trp Arg
 225 230 235 240

<210> 2363

<211> 738

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(715)

<223> RXA01671

<400> 2363

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tttttgtacc cgaatttgta cccgaattta aggaatcgct atg aat cat gtt gtt 115
 Met Asn His Val Val
 1 5

aat ttt gct tca cat ttg gaa gac gca gcc ctg aag caa gcc gaa gct 163
 Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu Lys Gln Ala Glu Ala
 10 15 20

act gcc acc atg ccg ttt att tac ccg cat gtg gcg ttg atg cct gat 211
 Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val Ala Leu Met Pro Asp
 25 30 35

gct cac ttt ggg ctg ggt tcg tcg gtg gga acg gtg ttc ggc acc aag 259
 Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr Val Phe Gly Thr Lys
 40 45 50

ggt gcg atc att ccg gcg gct gtg ggt gtg gat ata ggt tgc gga atg 307
 Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp Ile Gly Cys Gly Met
 55 60 65

ata gga gtg tgt acc aat tac acg gcc tct gac ctg gag gga cgt gat 355
 Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp Leu Glu Gly Arg Asp
 70 75 80 85

ttg gtg acg ctt ccg gat tac atc gag ccg gtg att ccg ttg tct cct 403
 Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val Ile Pro Leu Ser Pro
 90 95 100

gga aat tac aat tcc acc acc ttg aag gaa acc gcg aag gtg aag gtc 451
 Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr Ala Lys Val Lys Val
 105 110 115

gcg gag ttg gag gaa ctc gcg gag cgc gat ggt gta gat ttg tcg cac 499
 Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly Val Asp Leu Ser His

120	125	130	
tct ccg acg tgg aag cgc cag ttg ggt tgc ctt ggt gga ggt aat cac			547
Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu Gly Gly Gly Asn His			
135	140	145	
ttc att gag ttg tgt ctt gat gag ttg gat cgg gtg tgg atg ttt ttg			595
Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg Val Trp Met Phe Leu			
150	155	160	165
cac tct ggt tcc cgc ggt gtg ggt aac aag att gcc cat aag cac atc			643
His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile Ala His Lys His Ile			
	170	175	180
aag aac gcg cag gcc cag tgt aag aat gag gag ctt ccc gat aag gat			691
Lys Asn Ala Gln Ala Gln Cys Lys Asn Glu Glu Leu Pro Asp Lys Asp			
	185	190	195
ctt gcg tac ctt gac cga ggg gac tgaggagttt gagtcttaca tca			738
Leu Ala Tyr Leu Asp Arg Gly Asp			
200	205		

<210> 2364

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 2364

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Lys Gln Ala Glu Ala Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val	
	20 25 30
Ala Leu Met Pro Asp Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr	
	35 40 45
Val Phe Gly Thr Lys Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp	
	50 55 60
Ile Gly Cys Gly Met Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp	
65	70 75 80
Leu Glu Gly Arg Asp Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val	
	85 90 95
Ile Pro Leu Ser Pro Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr	
	100 105 110
Ala Lys Val Lys Val Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly	
	115 120 125
Val Asp Leu Ser His Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu	
	130 135 140
Gly Gly Gly Asn His Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg	
145	150 155 160
Val Trp Met Phe Leu His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile	
	165 170 175

Ala His Lys His Ile Lys Asn Ala Gln Ala Gln Cys Lys Asn Glu Glu
180 185 190

Leu Pro Asp Lys Asp Leu Ala Tyr Leu Asp Arg Gly Asp
195 200 205

<210> 2365
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> RXA01673

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Met Ser Thr Asn Leu
1 5
ctg gaa tcg acg ccg ccc ttt acc caa ctt cgc acc gga gtc ctc cag 163
Leu Glu Ser Thr Pro Pro Phe Thr Gln Leu Arg Thr Gly Val Leu Gln
10 15 20
aag tac acc ccg ggc ctg ctc tta tgc tcc att gcg gta ctc atc gct 211
Lys Tyr Thr Pro Gly Leu Leu Leu Cys Ser Ile Ala Val Leu Ile Ala
25 30 35
atg atc gtg aat cac ttt ttc tct ggt gtg agt ccg ctt atc gtc gcg 259
Met Ile Val Asn His Phe Phe Ser Gly Val Ser Pro Leu Ile Val Ala
40 45 50
atc att ctt ggc atc atc ctg acc aac ctg att cag ctc cca gca tcg 307
Ile Ile Leu Gly Ile Ile Leu Thr Asn Leu Ile Gln Leu Pro Ala Ser
55 60 65
acc tca ccc ggc atc acg ttg gcg tcg aaa aag ctt ttg cgg ctg gga 355
Thr Ser Pro Gly Ile Thr Leu Ala Ser Lys Lys Leu Leu Arg Leu Gly
70 75 80 85
atc gtc ttc ctt ggt ctg cag tta gtt ttc tca gat att ttg tca ctt 403
Ile Val Phe Leu Gly Leu Gln Leu Val Phe Ser Asp Ile Leu Ser Leu
90 95 100
ggt ttc ccc atg ctg gcg gtg att gtg tgc atc gtt gcc ggt ggt att 451
Gly Phe Pro Met Leu Ala Val Ile Val Cys Ile Val Ala Gly Gly Ile
105 110 115
ttt ggg acc atc ctc atg gga cac ctg ctc aga atg aaa cca acc caa 499
Phe Gly Thr Ile Leu Met Gly His Leu Leu Arg Met Lys Pro Thr Gln
120 125 130
gtt ctg ttg att gct tgt ggc ttt tct att tgt ggc gct gcg gcc gtg 547
Val Leu Leu Ile Ala Cys Gly Phe Ser Ile Cys Gly Ala Ala Ala Val
135 140 145

gca ggt gtt gaa gga gta act gat tcc gaa gaa gaa gag gtc gtt act 595
 Ala Gly Val Glu Gly Val Thr Asp Ser Glu Glu Glu Glu Val Val Thr
 150 155 160 165

gcg gtt gca ctt gtt gtt att ttc gga acg ctg atg att cct ttt atc 643
 Ala Val Ala Leu Val Val Ile Phe Gly Thr Leu Met Ile Pro Phe Ile
 170 175 180

cca ttc gca acc aaa gtc ttg ggg tta tcc cct gaa atc ggt ggg atg 691
 Pro Phe Ala Thr Lys Val Leu Gly Leu Ser Pro Glu Ile Gly Gly Met
 185 190 195

tgg gca ggc gga tcc atc cat gaa atc gcc caa gta gta gca gct gga 739
 Trp Ala Gly Gly Ser Ile His Glu Ile Ala Gln Val Val Ala Ala Gly
 200 205 210

gga gtc att ggt ggt gga gca tta ggt gtt gca gtt gtg gtg aaa ctc 787
 Gly Val Ile Gly Gly Gly Ala Leu Gly Val Ala Val Val Val Lys Leu
 215 220 225

gcc cga gta ctc cta ctt gca ccc att gct gcc att tta agt ttt cgc 835
 Ala Arg Val Leu Leu Leu Ala Pro Ile Ala Ala Ile Leu Ser Phe Arg
 230 235 240 245

cag cgc cgc cag ggt tac acg tcc ccc gat gga aag aga cca ccg gtc 883
 Gln Arg Arg Gln Gly Tyr Thr Ser Pro Asp Gly Lys Arg Pro Pro Val
 250 255 260

gtt ccc cta ttt atc ctt gga ttc ttg gcg atg gta gtt ttg cgc tcc 931
 Val Pro Leu Phe Ile Leu Gly Phe Leu Ala Met Val Val Leu Arg Ser
 265 270 275

act gtt gcg ctc cca gac gag gta att gcg gct gga ggt ttc cta cag 979
 Thr Val Ala Leu Pro Asp Glu Val Ile Ala Ala Gly Gly Phe Leu Gln
 280 285 290

aca gcc ttg ctc tct gca gca atg ttt ggt ctc ggg tgt ggc gta aaa 1027
 Thr Ala Leu Leu Ser Ala Ala Met Phe Gly Leu Gly Cys Gly Val Lys
 295 300 305

atc cag aac ctg atc cat gtt ggg gtc aag cct ttc att ctg gct ttc 1075
 Ile Gln Asn Leu Ile His Val Gly Val Lys Pro Phe Ile Leu Ala Phe
 310 315 320 325

gga tcc acg aca ctt gtc acc agt atc gca ctt gca ggc acc cta ctc 1123
 Gly Ser Thr Thr Leu Val Thr Ser Ile Ala Leu Ala Gly Thr Leu Leu
 330 335 340

acc cac ctc gga tagaaccgaa gacccagttg tac 1158
 Thr His Leu Gly
 345

<210> 2366

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 2366

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Thr Gly Val Leu Gln Lys Tyr Thr Pro Gly Leu Leu Leu Cys Ser Ile
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 Ala Val Leu Ile Ala Met Ile Val Asn His Phe Phe Ser Gly Val Ser
 35 40 45
 Pro Leu Ile Val Ala Ile Ile Leu Gly Ile Ile Leu Thr Asn Leu Ile
 50 55 60
 Gln Leu Pro Ala Ser Thr Ser Pro Gly Ile Thr Leu Ala Ser Lys Lys
 65 70 75 80
 Leu Leu Arg Leu Gly Ile Val Phe Leu Gly Leu Gln Leu Val Phe Ser
 85 90 95
 Asp Ile Leu Ser Leu Gly Phe Pro Met Leu Ala Val Ile Val Cys Ile
 100 105 110
 Val Ala Gly Gly Ile Phe Gly Thr Ile Leu Met Gly His Leu Leu Arg
 115 120 125
 Met Lys Pro Thr Gln Val Leu Leu Ile Ala Cys Gly Phe Ser Ile Cys
 130 135 140
 Gly Ala Ala Ala Val Ala Gly Val Glu Gly Val Thr Asp Ser Glu Glu
 145 150 155 160
 Glu Glu Val Val Thr Ala Val Ala Leu Val Val Ile Phe Gly Thr Leu
 165 170 175
 Met Ile Pro Phe Ile Pro Phe Ala Thr Lys Val Leu Gly Leu Ser Pro
 180 185 190
 Glu Ile Gly Gly Met Trp Ala Gly Gly Ser Ile His Glu Ile Ala Gln
 195 200 205
 Val Val Ala Ala Gly Gly Val Ile Gly Gly Gly Ala Leu Gly Val Ala
 210 215 220
 Val Val Val Lys Leu Ala Arg Val Leu Leu Leu Ala Pro Ile Ala Ala
 225 230 235 240
 Ile Leu Ser Phe Arg Gln Arg Arg Gln Gly Tyr Thr Ser Pro Asp Gly
 245 250 255
 Lys Arg Pro Pro Val Val Pro Leu Phe Ile Leu Gly Phe Leu Ala Met
 260 265 270
 Val Val Leu Arg Ser Thr Val Ala Leu Pro Asp Glu Val Ile Ala Ala
 275 280 285
 Gly Gly Phe Leu Gln Thr Ala Leu Leu Ser Ala Ala Met Phe Gly Leu
 290 295 300
 Gly Cys Gly Val Lys Ile Gln Asn Leu Ile His Val Gly Val Lys Pro
 305 310 315 320
 Phe Ile Leu Ala Phe Gly Ser Thr Thr Leu Val Thr Ser Ile Ala Leu
 325 330 335

Ala Gly Thr Leu Leu Thr His Leu Gly
340 345

<210> 2367

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> RXA01675

<400> 2367

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Met Asn Glu Ile Pro
1 5

gaa tgg ttg act ctt gta tct gtt gaa gca gga aag aga ctt ggg cgg 163
Glu Trp Leu Thr Leu Val Ser Val Glu Ala Gly Lys Arg Leu Gly Arg
10 15 20

cct ggg cca ttg gtg ttt ccg ccg gag ttg gtc act ttg gca gtt gaa 211
Pro Gly Pro Leu Val Phe Pro Pro Glu Leu Val Thr Leu Ala Val Glu
25 30 35

ggg att gag ctt att gaa ctt gag cct tca tgg act tct gat ttg cct 259
Gly Ile Glu Leu Ile Glu Leu Glu Pro Ser Trp Thr Ser Asp Leu Pro
40 45 50

ctg ccg gaa ttc ggg ttc cta gct gcg gat atg gtt gat ttc tat gat 307
Leu Pro Glu Phe Gly Phe Leu Ala Ala Asp Met Val Asp Phe Tyr Asp
55 60 65

gat tat gag ttt agt gaa tgg att ccg ggt gcg tgg cct ctt gct tta 355
Asp Tyr Glu Phe Ser Glu Trp Ile Pro Gly Ala Trp Pro Leu Ala Leu
70 75 80 85

gat ggt gga gga ggt ttc ttt tgc ctt gat ctc cgt gct gcc aac gct 403
Asp Gly Gly Gly Gly Phe Phe Cys Leu Asp Leu Arg Ala Ala Asn Ala
90 95 100

gat gga gag att cct gtt gtg tgg gtg cat gcc agc aac ttg ggt tgg 451
Asp Gly Glu Ile Pro Val Val Trp Val His Ala Ser Asn Leu Gly Trp
105 110 115

ggt gat gat gag gca gta cgc gta gct gcc tcg ttg gca gat ttg ttg 499
Gly Asp Asp Glu Ala Val Arg Val Ala Ala Ser Leu Ala Asp Leu Leu
120 125 130

agt ccg tcg aaa tagaagaatt agcatttacc gga 534
Ser Pro Ser Lys
135

<210> 2368

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 2368

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Met Asn Glu Ile Pro Glu Trp Leu Thr Leu Val Ser Val Glu Ala Gly
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Lys Arg Leu Gly Arg Pro Gly Pro Leu Val Phe Pro Pro Glu Leu Val
          20             25             30

Thr Leu Ala Val Glu Gly Ile Glu Leu Ile Glu Leu Glu Pro Ser Trp
          35             40             45

Thr Ser Asp Leu Pro Leu Pro Glu Phe Gly Phe Leu Ala Ala Asp Met
          50             55             60

Val Asp Phe Tyr Asp Asp Tyr Glu Phe Ser Glu Trp Ile Pro Gly Ala
          65             70             75             80

Trp Pro Leu Ala Leu Asp Gly Gly Gly Gly Phe Phe Cys Leu Asp Leu
          85             90             95

Arg Ala Ala Asn Ala Asp Gly Glu Ile Pro Val Val Trp Val His Ala
          100             105             110

Ser Asn Leu Gly Trp Gly Asp Asp Glu Ala Val Arg Val Ala Ala Ser
          115             120             125

Leu Ala Asp Leu Leu Ser Pro Ser Lys
          130             135

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<210> 2369

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXA01676

<400> 2369

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accagcattt tttgcatact cagtgggtgc tggcccgcgc atg atc ctt cac ggt 115
                               Met Ile Leu His Gly
                               1             5

gtt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt 163
Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
          10             15             20

ggg gcg gga atc ctc ggc gag ctg ttt atc acc caa cgc cag acc atc 211
Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
          25             30             35

atc gtg gtt tca tcg atc gtg ctg att atc cta ggt ttt gtc cag atc 259
Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile
          40             45             50

ttc ggc ggc gga ttc gac ttc gga aaa gca ctc cca gga tta gat cgt 307

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Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg
 55 60 65
 ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta 355
 Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu
 70 75 80 85
 cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc 403
 Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu
 90 95 100
 ggc gcc gtt ctt act ttg gct gcc acc agt gga aac tcc atc acc tca 451
 Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser
 105 110 115
 gca ctc att ttg agt gct tat ggt gcg gga atg gtg ctg ccc ctg atg 499
 Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met
 120 125 130
 gct att gca gcg ctc tgg gcc aaa ctc gga cag cgt gga cag cag atg 547
 Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met
 135 140 145
 ctc cgc ggc cgg gaa ttc acc ttc ttg ggc agg cag tgg cac att gtt 595
 Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val
 150 155 160 165
 tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg 643
 Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp
 170 175 180
 tcc acg aac ggc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc 691
 Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr
 185 190 195
 cag atc tgg cta cag gaa gcc aca ttc tca ctc ggg tca cca ctc ttt 739
 Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe
 200 205 210
 gac atc gca ttg atc att gtc gcc gct ggc ttg ttc ttg tac ttc tgg 787
 Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp
 215 220 225
 aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt 835
 Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser
 230 235 240 245
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 Gly Trp Val Ile Asn Pro Arg
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<210> 2370

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 2370

Met Ile Leu His Gly Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu
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Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu																	
	10 15 20																
atc gca gtt gtt ctg ttg atg tac cga gga aat gcg agt gat acg gcc	211																
Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala																	
	25 30 35																
gag ggc gtt tca gcc gct gcg act tcg gac tcg gct gct gct tcg act	259																
Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser Ala Ala Ala Ser Thr																	
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gct gct tcg ggt tcc gct tct ggt gct gcg gac tcc gat ctg acc agc	307																
Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser																	
	55 60 65																
gtg gaa gca cgc gac cct tcc gac cct gtt gcg gtg gga gac gtt gat	355																
Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala Val Gly Asp Val Asp																	
	70 75 80 85																
gca cct gtt ggg tta gtg gtg ttt tcc gac tac caa tgc ccg ttc tgt	403																
Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr Gln Cys Pro Phe Cys																	
	90 95 100																
gca aag tgg agc gat gaa acc ctg cca cag atg atg aag cat gtg gaa	451																
Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met Met Lys His Val Glu																	
	105 110 115																
gat gga aac ctc cgc att gaa tgg cgt gaa gtg aac atc ttt gga gaa	499																
Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val Asn Ile Phe Gly Glu																	
	120 125 130																
cca tct gag cgt gga gct cgc gcg gca tac gct gcg ggt ttg cag gac	547																
Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala Ala Gly Leu Gln Asp																	
	135 140 145																
gca tac ttg gaa tac cac aac gca ctc ttt gcc aac ggt gaa aaa ccc	595																
Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala Asn Gly Glu Lys Pro																	
	150 155 160 165																
agc gaa gac ctg ctc agc gaa gag gga ctt att aag ctt gct ggt gac	643																
Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp																	
	170 175 180																
ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa	691																
Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu																	
	185 190 195																
act gca gtc gca att gcg caa cat caa cag ctg gga atc gat ctt ggc	739																
Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu Gly Ile Asp Leu Gly																	
	200 205 210																
gcc tac tcc acc cca gct ttc ctc cta ggt ggc cag cca atc atg ggc	787																
Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly Gln Pro Ile Met Gly																	
	215 220 225																
gct cag cct gct tct gta ttt gaa gcc gcc ttc gag caa gca ctg gca	835																
Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe Glu Gln Ala Leu Ala																	
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867

<210> 2372

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 2372

Val Asn Gln Gln Ser Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile
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Ile Ala Val Leu Leu Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn
20 25 30

Ala Ser Asp Thr Ala Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser
35 40 45

Ala Ala Ala Ser Thr Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp
50 55 60

Ser Asp Leu Thr Ser Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala
65 70 75 80

Val Gly Asp Val Asp Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr
85 90 95

Gln Cys Pro Phe Cys Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met
100 105 110

Met Lys His Val Glu Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val
115 120 125

Asn Ile Phe Gly Glu Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala
130 135 140

Ala Gly Leu Gln Asp Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala
145 150 155 160

Asn Gly Glu Lys Pro Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile
165 170 175

Lys Leu Ala Gly Asp Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp
180 185 190

Phe Gln Ser Pro Glu Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu
195 200 205

Gly Ile Asp Leu Gly Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly
210 215 220

Gln Pro Ile Met Gly Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe
225 230 235 240

Glu Gln Ala Leu Ala Ala Lys Glu
245

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cca gtc cct gct ggt tgg tac tcc gag cct tgg tgg gca agc gca ttg    643
Pro Val Pro Ala Gly Trp Tyr Ser Glu Pro Trp Trp Ala Ser Ala Leu
          170                      175                      180

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cgt tcc ggt ctg tgg act gca ggt tcg gtc atg atg ttc tca gca atg 691
 Arg Ser Gly Leu Trp Thr Ala Gly Ser Val Met Met Phe Ser Ala Met
 185 190 195

ttt aac ggc atg gct ggt gtc ggc tac tcc gct gca gac ctt 733
 Phe Asn Gly Met Ala Gly Val Gly Tyr Ser Ala Ala Asp Leu
 200 205 210

tgaaaaaatgg ctatggcgag ggc 756

<210> 2374

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 2374

Val Glu Val Leu Leu Leu Ile Ala Ile Val Val Gly Gly Gly Val Phe
 1 5 10 15

Val Ala Ser Lys Met Gly Ser Asn Asn Asn Lys Lys Gln Glu Glu Ala
 20 25 30

Lys Phe Ala Asp Ala Gln Ala Asp Ala Arg Arg Trp Ile Glu Arg Leu
 35 40 45

Gly Ser Gln Val Leu Thr Ile Ala Gly Thr Asp Ala Ala Ser Thr Gln
 50 55 60

Ala Ile Ala Asp Ala Ser Glu Arg Tyr Thr Ala Ala Ser Ser Gln Ile
 65 70 75 80

Ser Ser Ala Thr Thr Pro Arg Gln Ala Glu Leu Ala Arg Glu Ser Ala
 85 90 95

Leu Glu Gly Leu His Tyr Met Asn Ala Ala Arg Glu Ile Met Gly Met
 100 105 110

Thr Ala Gly Pro Glu Leu Pro Pro Leu Glu Gly Gln Arg Asn Ala Gly
 115 120 125

Arg Val Thr Glu Lys Arg Thr Ile Glu Gln Glu Gly Arg Gln Ile Thr
 130 135 140

Ala Ser Pro Val Ala Thr Asp Glu Thr Pro Asn Tyr Tyr Pro Gly Gly
 145 150 155 160

Asn Val Ala Gly Arg Pro Val Pro Ala Gly Trp Tyr Ser Glu Pro Trp
 165 170 175

Trp Ala Ser Ala Leu Arg Ser Gly Leu Trp Thr Ala Gly Ser Val Met
 180 185 190

Met Phe Ser Ala Met Phe Asn Gly Met Ala Gly Val Gly Tyr Ser Ala
 195 200 205

Ala Asp Leu
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<210> 2375

<211> 702
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(679)
 <223> RXA01685

<400> 2375

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                                         Met Ser Phe Ala Ile
                                         1 5

ggc atc acc gtc cac gca gga cta gga acc acc aca att tca tca ctt 163
Gly Ile Thr Val His Ala Gly Leu Gly Thr Thr Thr Ile Ser Ser Leu
                        10 15 20

ccc gtg gtg tgg act gct gcc agc gga tta tcc ctg ggc tgg acc aca 211
Pro Val Val Trp Thr Ala Ala Ser Gly Leu Ser Leu Gly Trp Thr Thr
                        25 30 35

att tac ttc aat ggc ttc atg att ctg tgc caa ata att gtg ctg cgt 259
Ile Tyr Phe Asn Gly Phe Met Ile Leu Cys Gln Ile Ile Val Leu Arg
                        40 45 50

tcc cag ttc aaa cca caa atg tta gtc caa atc ctg tgg gca ttc ctc 307
Ser Gln Phe Lys Pro Gln Met Leu Val Gln Ile Leu Trp Ala Phe Leu
                        55 60 65

ttt ggg ttt ctt tgt gat tta agc ctg caa cta acc acc tgg gcg caa 355
Phe Gly Phe Leu Cys Asp Leu Ser Leu Gln Leu Thr Thr Trp Ala Gln
                        70 75 80 85

act gac aat tat ttt gtg gcc tgg atc tgg gtt att gtg tcc acc att 403
Thr Asp Asn Tyr Phe Val Ala Trp Ile Trp Val Ile Val Ser Thr Ile
                        90 95 100

ttg atg tcg atc gga gtt ttt att caa gta ctc ccc aac atc act ttc 451
Leu Met Ser Ile Gly Val Phe Ile Gln Val Leu Pro Asn Ile Thr Phe
                        105 110 115

atc gct ggt gaa ggc att gtc tct gcg ctg gtg aag aaa ttt ccc aac 499
Ile Ala Gly Glu Gly Ile Val Ser Ala Leu Val Lys Lys Phe Pro Asn
                        120 125 130

gtg gaa ttt ggc acc atg aaa caa atc gtc gac tgg act ttc gtc tcc 547
Val Glu Phe Gly Thr Met Lys Gln Ile Val Asp Trp Thr Phe Val Ser
                        135 140 145

gtc gct gcc att ttg tcc tgg atc acc atg ggt gga ctt att ggc gtg 595
Val Ala Ala Ile Leu Ser Trp Ile Thr Met Gly Gly Leu Ile Gly Val
                        150 155 160 165

cgc gaa gga aca gtg ttc gcg gcg ttt ttc atc gga ttc ttc gtc cgc 643
Arg Glu Gly Thr Val Phe Ala Ala Phe Phe Ile Gly Phe Phe Val Arg
                        170 175 180

cag tgg cgc aaa ctc tac ctc cgc tcc atc ggt cac taaagagctt 689

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Gln Trp Arg Lys Leu Tyr Leu Arg Ser Ile Gly His
185 190

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702

<210> 2376

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 2376

Met Ser Phe Ala Ile Gly Ile Thr Val His Ala Gly Leu Gly Thr Thr
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Thr Ile Ser Ser Leu Pro Val Val Trp Thr Ala Ala Ser Gly Leu Ser
20 25 30

Leu Gly Trp Thr Thr Ile Tyr Phe Asn Gly Phe Met Ile Leu Cys Gln
35 40 45

Ile Ile Val Leu Arg Ser Gln Phe Lys Pro Gln Met Leu Val Gln Ile
50 55 60

Leu Trp Ala Phe Leu Phe Gly Phe Leu Cys Asp Leu Ser Leu Gln Leu
65 70 75 80

Thr Thr Trp Ala Gln Thr Asp Asn Tyr Phe Val Ala Trp Ile Trp Val
85 90 95

Ile Val Ser Thr Ile Leu Met Ser Ile Gly Val Phe Ile Gln Val Leu
100 105 110

Pro Asn Ile Thr Phe Ile Ala Gly Glu Gly Ile Val Ser Ala Leu Val
115 120 125

Lys Lys Phe Pro Asn Val Glu Phe Gly Thr Met Lys Gln Ile Val Asp
130 135 140

Trp Thr Phe Val Ser Val Ala Ala Ile Leu Ser Trp Ile Thr Met Gly
145 150 155 160

Gly Leu Ile Gly Val Arg Glu Gly Thr Val Phe Ala Ala Phe Phe Ile
165 170 175

Gly Phe Phe Val Arg Gln Trp Arg Lys Leu Tyr Leu Arg Ser Ile Gly
180 185 190

His

<210> 2377

<211> 564

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(541)

<223> RXA01686

<400> 2377

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                                   Met Thr Ser Leu Arg
                                   1 5
gac tta ctt gtt tcc acc aat gcc gac gca gca att gca gat atg tca 163
Asp Leu Leu Val Ser Thr Asn Ala Asp Ala Ala Ile Ala Asp Met Ser
                                   10 15 20
gca ttt atc gaa gaa acc gtg ggc aag caa tcc ggc atc agc ggc atc 211
Ala Phe Ile Glu Glu Thr Val Gly Lys Gln Ser Gly Ile Ser Gly Ile
                                   25 30 35
gca ctc aaa ggc gca atg ggt gct gca acc aag atc gac tcc gac atc 259
Ala Leu Lys Gly Ala Met Gly Ala Ala Thr Lys Ile Asp Ser Asp Ile
                                   40 45 50
gta gcc aaa ggc tcc agg cgc ctc ctc ccg gaa atc gct gac tcc ctc 307
Val Ala Lys Gly Ser Arg Arg Leu Leu Pro Glu Ile Ala Asp Ser Leu
                                   55 60 65
gac gga ctc tgg cag gaa tac caa aat ggt ggc acc gcc gca gat ttc 355
Asp Gly Leu Trp Gln Glu Tyr Gln Asn Gly Gly Thr Ala Ala Asp Phe
                                   70 75 80 85
ggc gcc cac ctc gag gcc aac agc tcc acc gca ctc gac gcg att ctc 403
Gly Ala His Leu Glu Ala Asn Ser Ser Thr Ala Leu Asp Ala Ile Leu
                                   90 95 100
agc gtt gct gac aaa aac gca gag agc atc aac gtt cca gga ctt ggc 451
Ser Val Ala Asp Lys Asn Ala Glu Ser Ile Asn Val Pro Gly Leu Gly
                                   105 110 115
aag gtc tac aag ggc gtg cgc ggc aag gct gcc aaa gta atc gag cag 499
Lys Val Tyr Lys Gly Val Arg Gly Lys Ala Ala Lys Val Ile Glu Gln
                                   120 125 130
gaa ctt cct gca att ggc cag ttg atc gaa aag aac gca caa 541
Glu Leu Pro Ala Ile Gly Gln Leu Ile Glu Lys Asn Ala Gln
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<210> 2378

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 2378

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 20 25 30
Gly Ile Ser Gly Ile Ala Leu Lys Gly Ala Met Gly Ala Ala Thr Lys
 35 40 45

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Ile Asp Ser Asp Ile Val Ala Lys Gly Ser Arg Arg Leu Leu Pro Glu
 50 55 60
 Ile Ala Asp Ser Leu Asp Gly Leu Trp Gln Glu Tyr Gln Asn Gly Gly
 65 70 75 80
 Thr Ala Ala Asp Phe Gly Ala His Leu Glu Ala Asn Ser Ser Thr Ala
 85 90 95
 Leu Asp Ala Ile Leu Ser Val Ala Asp Lys Asn Ala Glu Ser Ile Asn
 100 105 110
 Val Pro Gly Leu Gly Lys Val Tyr Lys Gly Val Arg Gly Lys Ala Ala
 115 120 125
 Lys Val Ile Glu Gln Glu Leu Pro Ala Ile Gly Gln Leu Ile Glu Lys
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 Asn Ala Gln
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<210> 2379
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1522)
 <223> RXA01693

<400> 2379
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 Met Asn Thr Ala Pro
 1 5
 ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc 163
 Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
 10 15 20
 ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat 211
 Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
 25 30 35
 gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca 259
 Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
 40 45 50
 cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca 307
 Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn Pro Glu Pro Leu Thr
 55 60 65
 aaa gca gtt gcg cag gcc tat tcc ggc cac caa ttc gga cag ttt gtg 355
 Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln Phe Gly Gln Phe Val
 70 75 80 85
 gca agc ctt ggt gat ggc cga gcg ctt ctt ctc ggc gaa gcc cgc tca 403

Ala	Ser	Leu	Gly	Asp	Gly	Arg	Ala	Leu	Leu	Leu	Gly	Glu	Ala	Arg	Ser		
				90					95					100			
gct	gac	ggc	gta	ctg	cat	gat	atc	cac	ctc	aaa	gga	tct	gga	cga	acc	451	
Ala	Asp	Gly	Val	Leu	His	Asp	Ile	His	Leu	Lys	Gly	Ser	Gly	Arg	Thr		
			105					110					115				
caa	ttc	tcc	cga	gga	gcc	gat	gga	cgc	gcc	gtc	ctt	ggc	ccc	gtc	tta	499	
Gln	Phe	Ser	Arg	Gly	Ala	Asp	Gly	Arg	Ala	Val	Leu	Gly	Pro	Val	Leu		
			120				125					130					
cgc	gaa	tac	atc	atc	tcc	gaa	gcg	atg	cat	gca	ctt	ggg	gtt	ccc	acc	547	
Arg	Glu	Tyr	Ile	Ile	Ser	Glu	Ala	Met	His	Ala	Leu	Gly	Val	Pro	Thr		
	135					140					145						
acc	agg	tca	ctt	gca	gta	att	agc	acc	ggg	agg	aaa	atc	caa	cga	gga	595	
Thr	Arg	Ser	Leu	Ala	Val	Ile	Ser	Thr	Gly	Arg	Lys	Ile	Gln	Arg	Gly		
150					155					160					165		
agc	gta	gcc	cca	ggc	gca	gtc	ctt	gtt	cga	gta	gca	acc	agc	ctc	att	643	
Ser	Val	Ala	Pro	Gly	Ala	Val	Leu	Val	Arg	Val	Ala	Thr	Ser	Leu	Ile		
				170					175					180			
cga	gtc	gga	tcc	ttc	caa	tac	tcc	aac	atc	tct	ggg	ggc	atc	gaa	cta	691	
Arg	Val	Gly	Ser	Phe	Gln	Tyr	Ser	Asn	Ile	Ser	Gly	Gly	Ile	Glu	Leu		
			185					190					195				
tct	caa	cac	ctg	gcg	aac	tat	acg	atc	acc	agg	cat	ttc	cct	tcg	ttg	739	
Ser	Gln	His	Leu	Ala	Asn	Tyr	Thr	Ile	Thr	Arg	His	Phe	Pro	Ser	Leu		
		200					205					210					
gta	gct	gaa	cta	tcc	gca	cca	acc	ccc	gca	act	tat	gta	tca	ctg	ttt	787	
Val	Ala	Glu	Leu	Ser	Ala	Pro	Thr	Pro	Ala	Thr	Tyr	Val	Ser	Leu	Phe		
		215				220					225						
aaa	gcg	att	ctt	cag	cgc	caa	gca	gac	acc	gtt	gga	aaa	tggt	acc	agg	835	
Lys	Ala	Ile	Leu	Gln	Arg	Gln	Ala	Asp	Thr	Val	Gly	Lys	Trp	Thr	Arg		
230					235					240					245		
ctg	ggg	ttc	gtt	cac	gga	gcc	ctc	aac	aca	gac	aac	acg	ttg	ata	tcc	883	
Leu	Gly	Phe	Val	His	Gly	Ala	Leu	Asn	Thr	Asp	Asn	Thr	Leu	Ile	Ser		
				250					255					260			
gga	gaa	act	gtt	gac	tac	ggc	cca	tgc	gct	ttc	atg	gag	cgc	tac	cgt	931	
Gly	Glu	Thr	Val	Asp	Tyr	Gly	Pro	Cys	Ala	Phe	Met	Glu	Arg	Tyr	Arg		
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ggc	gac	gcg	aaa	ttt	agc	tcc	atc	gac	act	tat	ggg	cgc	tac	aaa	ttt	979	
Gly	Asp	Ala	Lys	Phe	Ser	Ser	Ile	Asp	Thr	Tyr	Gly	Arg	Tyr	Lys	Phe		
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gaa	aac	caa	cct	atg	atc	ctc	gga	tgg	aac	atg	gcc	cgc	ctc	gta	gaa	1027	
Glu	Asn	Gln	Pro	Met	Ile	Leu	Gly	Trp	Asn	Met	Ala	Arg	Leu	Val	Glu		
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Thr	Leu	Leu	Pro	Leu	Leu	Gly	Ala	Thr	Pro	Asp	Glu	Gly	Met	Thr	Ala		
310					315					320					325		
gcc	caa	gaa	gct	ctc	gta	gaa	ttc	gat	gac	ctc	tgc	gaa	caa	gca	atc	1123	
Ala	Gln	Glu	Ala	Leu	Val	Glu	Phe	Asp	Asp	Leu	Cys	Glu	Gln	Ala	Ile		

330	335	340	
cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc			1171
Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly			
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acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc			1219
Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile			
360	365	370	
acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc			1267
Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly			
375	380	385	
ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa			1315
Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu			
390	395	400	405
gca atg cga gca gta aat cca ctt ttc att cca cgc aat cac ctc gtg			1363
Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val			
410	415	420	
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Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His			
425	430	435	
gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc			1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro			
440	445	450	
gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg			1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met			
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Thr Phe Cys Gly Thr			
470			

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<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 2380

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			20					25					30		

Leu	Val	Ile	Leu	Asn	Asp	Asp	Leu	Ala	Tyr	Ser	Leu	Gly	Leu	Asp	Pro
	35						40					45			

Thr	Trp	Leu	Arg	Thr	Pro	Glu	Gly	Val	Gln	Phe	Leu	Leu	Gly	Leu	Asn
	50					55					60				

Pro	Glu	Pro	Leu	Thr	Lys	Ala	Val	Ala	Gln	Ala	Tyr	Ser	Gly	His	Gln
65					70					75					80

Phe	Gly	Gln	Phe	Val	Ala	Ser	Leu	Gly	Asp	Gly	Arg	Ala	Leu	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85							90							95		
Gly	Glu	Ala	Arg 100	Ser	Ala	Asp	Gly	Val 105	Leu	His	Asp	Ile	His 110	Leu	Lys	
Gly	Ser	Gly 115	Arg	Thr	Gln	Phe	Ser 120	Arg	Gly	Ala	Asp	Gly 125	Arg	Ala	Val	
Leu	Gly 130	Pro	Val	Leu	Arg	Glu 135	Tyr	Ile	Ile	Ser	Glu 140	Ala	Met	His	Ala	
Leu 145	Gly	Val	Pro	Thr	Thr 150	Arg	Ser	Leu	Ala	Val 155	Ile	Ser	Thr	Gly	Arg 160	
Lys	Ile	Gln	Arg	Gly 165	Ser	Val	Ala	Pro	Gly 170	Ala	Val	Leu	Val	Arg 175	Val	
Ala	Thr	Ser	Leu 180	Ile	Arg	Val	Gly	Ser 185	Phe	Gln	Tyr	Ser	Asn 190	Ile	Ser	
Gly	Gly	Ile 195	Glu	Leu	Ser	Gln	His 200	Leu	Ala	Asn	Tyr	Thr 205	Ile	Thr	Arg	
His	Phe 210	Pro	Ser	Leu	Val	Ala 215	Glu	Leu	Ser	Ala	Pro 220	Thr	Pro	Ala	Thr	
Tyr 225	Val	Ser	Leu	Phe	Lys 230	Ala	Ile	Leu	Gln	Arg 235	Gln	Ala	Asp	Thr	Val 240	
Gly	Lys	Trp	Thr 245	Arg	Leu	Gly	Phe	Val	His 250	Gly	Ala	Leu	Asn	Thr 255	Asp	
Asn	Thr	Leu	Ile 260	Ser	Gly	Glu	Thr	Val 265	Asp	Tyr	Gly	Pro	Cys 270	Ala	Phe	
Met	Glu	Arg 275	Tyr	Arg	Gly	Asp	Ala 280	Lys	Phe	Ser	Ser	Ile 285	Asp	Thr	Tyr	
Gly	Arg 290	Tyr	Lys	Phe	Glu	Asn 295	Gln	Pro	Met	Ile	Leu 300	Gly	Trp	Asn	Met	
Ala 305	Arg	Leu	Val	Glu	Thr 310	Leu	Leu	Pro	Leu	Leu 315	Gly	Ala	Thr	Pro	Asp 320	
Glu	Gly	Met	Thr 325	Ala	Ala	Gln	Glu	Ala	Leu 330	Val	Glu	Phe	Asp	Asp 335	Leu	
Cys	Glu	Gln	Ala 340	Ile	Arg	Lys	Glu	Phe 345	Ala	Thr	Ala	Leu	Gly 350	Leu	Asp	
Glu	Ser	Asp 355	Thr	Gly	Thr	Val	Glu 360	Gln	Phe	Arg	Glu	Leu 365	Leu	Tyr	Leu	
His	Asn 370	Pro	Asp	Ile	Thr	Thr 375	Leu	Leu	Arg	Ala	Leu 380	Thr	Asp	Asn	Thr	
Ala 385	Pro	Pro	Ser	Gly	Phe 390	Glu	Ala	Phe	Val	His 395	Asp	Trp	Lys	Thr	Gln 400	
Asp	Pro	Asp	Ile 405	Glu	Ala	Met	Arg	Ala	Val 410	Asn	Pro	Leu	Phe	Ile 415	Pro	

Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
 420 425 430

Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
 435 440 445

Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
 450 455 460

Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
 465 470

<210> 2381
 <211> 738
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(715)
 <223> RXA01714

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cctccccaga gttaccccaa taattagtaa attgcagatt gtg atc gat tcc gaa 115
 Val Ile Asp Ser Glu
 1 5

gcg acc tct cag cac aag acc tca gct acc ccg gca gag agc act ccc 163
 Ala Thr Ser Gln His Lys Thr Ser Ala Thr Pro Ala Glu Ser Thr Pro
 10 15 20

gcg gag ttt tcc gaa gcg gtt gag tct atg cac aga gcg cgc ctg cgc 211
 Ala Glu Phe Ser Glu Ala Val Glu Ser Met His Arg Ala Arg Leu Arg
 25 30 35

cca gaa ctt act ttg ggc acg att agg ccg cct cag cgc ctg gcg ccg 259
 Pro Glu Leu Thr Leu Gly Thr Ile Arg Pro Pro Gln Arg Leu Ala Pro
 40 45 50

ttt tcg cac gcc att gga ctc gaa gtc gga aat caa gaa gag tca gac 307
 Phe Ser His Ala Ile Gly Leu Glu Val Gly Asn Gln Glu Glu Ser Asp
 55 60 65

gat gtc tcc acc aac agc gaa ggt gat tcc ttt ggt cgt ttg att ctg 355
 Asp Val Ser Thr Asn Ser Glu Gly Asp Ser Phe Gly Arg Leu Ile Leu
 70 75 80 85

ctc cac gat ccg ggt gcc gaa gaa acc tgg gaa gga gca atg cgc ctt 403
 Leu His Asp Pro Gly Ala Glu Glu Thr Trp Glu Gly Ala Met Arg Leu
 90 95 100

gtc gcc tat att caa gct gac atg gat cac gct gtt gct tcc gac ccg 451
 Val Ala Tyr Ile Gln Ala Asp Met Asp His Ala Val Ala Ser Asp Pro
 105 110 115

cta ttg ccg gaa gta gcg tgg caa tgg ctt aac gaa ggt ttg gaa caa 499
 Leu Leu Pro Glu Val Ala Trp Gln Trp Leu Asn Glu Gly Leu Glu Gln

120	125	130	
gcc ggc gca gga ttt acc aac cta ggc gga acc gta acc tcc aca acc			547
Ala Gly Ala Gly Phe Thr Asn Leu Gly Gly Thr Val Thr Ser Thr Thr			
135	140	145	
tcg gtg cgc ttt ggt gaa atc ggt gga ccg cca agt gcc tac caa gtg			595
Ser Val Arg Phe Gly Glu Ile Gly Gly Pro Pro Ser Ala Tyr Gln Val			
150	155	160	165
gaa atg cgt gcg tcc tgg acc gcg act ggc acc gac ctc acc gcg cat			643
Glu Met Arg Ala Ser Trp Thr Ala Thr Gly Thr Asp Leu Thr Ala His			
170	175	180	
gtt gaa gcg ttc gca gca gtg ctt gcc tct gtt gct gga ctt ccc cca			691
Val Glu Ala Phe Ala Ala Val Leu Ala Ser Val Ala Gly Leu Pro Pro			
185	190	195	
gag ggc gtc acc gaa cta cga agg tagattggac accatgggttt ccg			738
Glu Gly Val Thr Glu Leu Arg Arg			
200	205		

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<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 2382

Val Ile Asp Ser Glu Ala Thr Ser Gln His Lys Thr Ser Ala Thr Pro	
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20	25 30
Arg Ala Arg Leu Arg Pro Glu Leu Thr Leu Gly Thr Ile Arg Pro Pro	
35	40 45
Gln Arg Leu Ala Pro Phe Ser His Ala Ile Gly Leu Glu Val Gly Asn	
50	55 60
Gln Glu Glu Ser Asp Asp Val Ser Thr Asn Ser Glu Gly Asp Ser Phe	
65	70 75 80
Gly Arg Leu Ile Leu Leu His Asp Pro Gly Ala Glu Glu Thr Trp Glu	
85	90 95
Gly Ala Met Arg Leu Val Ala Tyr Ile Gln Ala Asp Met Asp His Ala	
100	105 110
Val Ala Ser Asp Pro Leu Leu Pro Glu Val Ala Trp Gln Trp Leu Asn	
115	120 125
Glu Gly Leu Glu Gln Ala Gly Ala Gly Phe Thr Asn Leu Gly Gly Thr	
130	135 140
Val Thr Ser Thr Thr Ser Val Arg Phe Gly Glu Ile Gly Gly Pro Pro	
145	150 155 160
Ser Ala Tyr Gln Val Glu Met Arg Ala Ser Trp Thr Ala Thr Gly Thr	
165	170 175

cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca 595
 Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro
 150 155 160 165

gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa 643
 Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu
 170 175 180

tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg 691
 Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu
 185 190 195

atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag 739
 Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu
 200 205 210

ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag 787
 Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys
 215 220 225

gtt ctt cct taaaagctgc ttttctaaac gat 819
 Val Leu Pro
 230

<210> 2384

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 2384

Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser
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Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg
 20 25 30

Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
 35 40 45

Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
 50 55 60

Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
 65 70 75 80

Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
 85 90 95

Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
 100 105 110

Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
 115 120 125

Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
 130 135 140

Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
 145 150 155 160

Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
165 170 175

Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
180 185 190

Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
195 200 205

His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
210 215 220

Ala Asp Leu Ile Lys Val Leu Pro
225 230

<210> 2385

<211> 642

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(619)

<223> RXA01729

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taaacttttc tacgaacctt ttactaagaa ggagcccga gtg aag ttg agg aca 115
Val Lys Leu Arg Thr
1 5

atc cca gcc ctg tta gcc gtc gca ctt ctt gca ggc tgt tcg ggt gaa 163
Ile Pro Ala Leu Leu Ala Val Ala Leu Leu Ala Gly Cys Ser Gly Glu
10 15 20

agt gct gat agc caa gcc gtt tcc gct gag gaa acc atg gaa gta acc 211
Ser Ala Asp Ser Gln Ala Val Ser Ala Glu Glu Thr Met Glu Val Thr
25 30 35

act acc tca acc ccg gtg ttc gaa gcc aaa gag gta agc cca atc aca 259
Thr Thr Ser Thr Pro Val Phe Glu Ala Lys Glu Val Ser Pro Ile Thr
40 45 50

gtc cca agc ggc gat atc agg gtt gaa gac cca ggt ctc aat gtt gaa 307
Val Pro Ser Gly Asp Ile Arg Val Glu Asp Pro Gly Leu Asn Val Glu
55 60 65

ttt atc ttc cga ggc acc cgc tac ggc acc aac ggt ggc tca att att 355
Phe Ile Phe Arg Gly Thr Arg Tyr Gly Thr Asn Gly Gly Ser Ile Ile
70 75 80 85

cac atc gcg gtg aaa aac cta aac gac gta gcc ctg cca gcc gac gcc 403
His Ile Ala Val Lys Asn Leu Asn Asp Val Ala Leu Pro Ala Asp Ala
90 95 100

atc gat cca ccc acc ctg gac atc gaa gac tac aac ggc aac aaa acc 451
Ile Asp Pro Pro Thr Leu Asp Ile Glu Asp Tyr Asn Gly Asn Lys Thr
105 110 115

aac atc gaa acc ctc tcc ggc gac gac aac atc cca ctc gac cta cca 499
Asn Ile Glu Thr Leu Ser Gly Asp Asp Asn Ile Pro Leu Asp Leu Pro
120 125 130

ctg ggt gcc ggc gcg aca acg aac ctg caa tac gcg ttc aac acc tca 547
Leu Gly Ala Gly Ala Thr Thr Asn Leu Gln Tyr Ala Phe Asn Thr Ser
135 140 145

aac ggc tca ttg tcg aat gct aaa ttc cag atc gga aac gtc atc tac 595
Asn Gly Ser Leu Ser Asn Ala Lys Phe Gln Ile Gly Asn Val Ile Tyr
150 155 160 165

tca ggc aat ttg aac agc ttg gcg taagttcaaa aaataatttg aat 642
Ser Gly Asn Leu Asn Ser Leu Ala
170

<210> 2386

<211> 173

<212> PRT

<213> Corynebacterium glutamicum

<400> 2386

Val Lys Leu Arg Thr Ile Pro Ala Leu Leu Ala Val Ala Leu Leu Ala
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Gly Cys Ser Gly Glu Ser Ala Asp Ser Gln Ala Val Ser Ala Glu Glu
20 25 30

Thr Met Glu Val Thr Thr Thr Ser Thr Pro Val Phe Glu Ala Lys Glu
35 40 45

Val Ser Pro Ile Thr Val Pro Ser Gly Asp Ile Arg Val Glu Asp Pro
50 55 60

Gly Leu Asn Val Glu Phe Ile Phe Arg Gly Thr Arg Tyr Gly Thr Asn
65 70 75 80

Gly Gly Ser Ile Ile His Ile Ala Val Lys Asn Leu Asn Asp Val Ala
85 90 95

Leu Pro Ala Asp Ala Ile Asp Pro Pro Thr Leu Asp Ile Glu Asp Tyr
100 105 110

Asn Gly Asn Lys Thr Asn Ile Glu Thr Leu Ser Gly Asp Asp Asn Ile
115 120 125

Pro Leu Asp Leu Pro Leu Gly Ala Gly Ala Thr Thr Asn Leu Gln Tyr
130 135 140

Ala Phe Asn Thr Ser Asn Gly Ser Leu Ser Asn Ala Lys Phe Gln Ile
145 150 155 160

Gly Asn Val Ile Tyr Ser Gly Asn Leu Asn Ser Leu Ala
165 170

<210> 2387

<211> 822

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(799)

<223> RXA01731

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cactcaaggt tggacgttgt gttcatgaat aacttttatg atg aac gca tcg tcc 115
                                         Met Asn Ala Ser Ser
                                         1           5

att tct tcc cga ttc aag gat ctt ttt gtg aca ccc agt att gtt ttt 163
Ile Ser Ser Arg Phe Lys Asp Leu Phe Val Thr Pro Ser Ile Val Phe
                10                15                20

gat ttc gat ggc acg ctt gcc att ggc cat ggc cct gtc ctt gcg tat 211
Asp Phe Asp Gly Thr Leu Ala Ile Gly His Gly Pro Val Leu Ala Tyr
                25                30                35

gca ttg tgt gtt gca ccg gag ggt tcc aag gac ttt ctg gag cgt gtg 259
Ala Leu Cys Val Ala Pro Glu Gly Ser Lys Asp Phe Leu Glu Arg Val
                40                45                50

cgc agg gag ctt cgg cgc tat gac gat ggt cag agt att tac cgt gat 307
Arg Arg Glu Leu Arg Arg Tyr Asp Asp Gly Gln Ser Ile Tyr Arg Asp
                55                60                65

ggg tat gac att gtg gct aag ttg gcg tcg gaa ttg ggg att gat gat 355
Gly Tyr Asp Ile Val Ala Lys Leu Ala Ser Glu Leu Gly Ile Asp Asp
                70                75                80                85

ggc acg atg tct gtc gct tat ggc gag agc cgg aag ttg ctt ggt tcg 403
Gly Thr Met Ser Val Ala Tyr Gly Glu Ser Arg Lys Leu Leu Gly Ser
                90                95                100

gat tta gcg cct gtt gag cat gtg cgg ggt att aag gat att ttg tcc 451
Asp Leu Ala Pro Val Glu His Val Arg Gly Ile Lys Asp Ile Leu Ser
                105                110                115

tcg ttg aaa ggt cat gct cgg ttg gtt tta gct acc aat gcc ccg gaa 499
Ser Leu Lys Gly His Ala Arg Leu Val Leu Ala Thr Asn Ala Pro Glu
                120                125                130

aat ggc gtg cat gat ttg ctg cgt cag tgg ggt gtt gct gat ttg ttt 547
Asn Gly Val His Asp Leu Leu Arg Gln Trp Gly Val Ala Asp Leu Phe
                135                140                145

gat cag ttg cat ttt gtg gtg ggt aag cct gca ggg ttg att tcg atc 595
Asp Gln Leu His Phe Val Val Gly Lys Pro Ala Gly Leu Ile Ser Ile
                150                155                160                165

att tct gat ttg cag ctt gat ggt ccg gtg ctt gcg gtg ggc gat att 643
Ile Ser Asp Leu Gln Leu Asp Gly Pro Val Leu Ala Val Gly Asp Ile
                170                175                180

tat gaa ttc gat ctg agt cct gca gcg cag tta ggt gca gat acg gct 691
Tyr Glu Phe Asp Leu Ser Pro Ala Ala Gln Leu Gly Ala Asp Thr Ala
                185                190                195

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Trp Val Cys Ser Arg Val Ser Ser Ser
225 230

<210> 2389

<211> 837

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(814)

<223> RXA01738

<400> 2389

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                                         Met Arg Ile Leu Pro
                                         1 5
atc ggc ccc cac gat gaa atc gcc gtc aac gga tca ata gtc ctt cta 163
Ile Gly Pro His Asp Glu Ile Ala Val Asn Gly Ser Ile Val Leu Leu
                        10 15 20
tcc gag cac gac gga gac atc gta tcg gtc ggc ccc gac ctc ggc acg 211
Ser Glu His Asp Gly Asp Ile Val Ser Val Gly Pro Asp Leu Gly Thr
                        25 30 35
gtg cga gtt acc ctt gaa gag atc gaa agt tta ggt aca ccg acg gca 259
Val Arg Val Thr Leu Glu Glu Ile Glu Ser Leu Gly Thr Pro Thr Ala
                        40 45 50
ccc cgc gat ctg ggt tct cgg gaa gtc gac gca tgc gta tcg ttg ctc 307
Pro Arg Asp Leu Gly Ser Arg Glu Val Asp Ala Cys Val Ser Leu Leu
                        55 60 65
cgc aac cgc gag tta gtg cga ttc gat ccc cac gat ggc agt gaa tta 355
Arg Asn Arg Glu Leu Val Arg Phe Asp Pro His Asp Gly Ser Glu Leu
                        70 75 80 85
acc tat cgg gaa cat agc gtt gct tac ggt gcg agt ggc aag cca ttg 403
Thr Tyr Arg Glu His Ser Val Ala Tyr Gly Ala Ser Gly Lys Pro Leu
                        90 95 100
ttt ccc cga ttg gat cca gcg gtg atc ggc att gtg gag ctg cga ggt 451
Phe Pro Arg Leu Asp Pro Ala Val Ile Gly Ile Val Glu Leu Arg Gly
                        105 110 115
gag gat cgt ttg ctt ctg ggc atg aat gcg cag aaa cgc caa cgc tat 499
Glu Asp Arg Leu Leu Leu Gly Met Asn Ala Gln Lys Arg Gln Arg Tyr
                        120 125 130
tca tta atc gca ggt tat gtt tcg cat ggt gag tcg ctg gaa gac gca 547
Ser Leu Ile Ala Gly Tyr Val Ser His Gly Glu Ser Leu Glu Asp Ala
                        135 140 145
ttc acc aga gaa gtg ttc gag gaa gcg gcg cgc cgg gta tct gag att 595
Phe Thr Arg Glu Val Phe Glu Glu Ala Ala Arg Arg Val Ser Glu Ile
                        150 155 160 165

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tcc tat gtg tcg tct caa cca tgg ccg atc tct ggt tcg ctg atg ctg 643
 Ser Tyr Val Ser Ser Gln Pro Trp Pro Ile Ser Gly Ser Leu Met Leu
 170 175 180

ggt atg aag ggc ttc acg gaa gat gag ttg cct caa ggc gaa act gat 691
 Gly Met Lys Gly Phe Thr Glu Asp Glu Leu Pro Gln Gly Glu Thr Asp
 185 190 195

ggt gaa tta gcg gag aca atc tgg gct tcg cca cta gac att atc gat 739
 Gly Glu Leu Ala Glu Thr Ile Trp Ala Ser Pro Leu Asp Ile Ile Asp
 200 205 210

cgt aag att ccg atc gcc cca ccc gga tcg att gcc tac gac atg atc 787
 Arg Lys Ile Pro Ile Ala Pro Pro Gly Ser Ile Ala Tyr Asp Met Ile
 215 220 225

aac gcc tgg gcg cga gat aaa caa aac taagggagct ttttacagtg 834
 Asn Ala Trp Ala Arg Asp Lys Gln Asn
 230 235

atc 837

<210> 2390

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 2390

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Ser Ile Val Leu Leu Ser Glu His Asp Gly Asp Ile Val Ser Val Gly
 20 25 30

Pro Asp Leu Gly Thr Val Arg Val Thr Leu Glu Glu Ile Glu Ser Leu
 35 40 45

Gly Thr Pro Thr Ala Pro Arg Asp Leu Gly Ser Arg Glu Val Asp Ala
 50 55 60

Cys Val Ser Leu Leu Arg Asn Arg Glu Leu Val Arg Phe Asp Pro His
 65 70 75 80

Asp Gly Ser Glu Leu Thr Tyr Arg Glu His Ser Val Ala Tyr Gly Ala
 85 90 95

Ser Gly Lys Pro Leu Phe Pro Arg Leu Asp Pro Ala Val Ile Gly Ile
 100 105 110

Val Glu Leu Arg Gly Glu Asp Arg Leu Leu Leu Gly Met Asn Ala Gln
 115 120 125

Lys Arg Gln Arg Tyr Ser Leu Ile Ala Gly Tyr Val Ser His Gly Glu
 130 135 140

Ser Leu Glu Asp Ala Phe Thr Arg Glu Val Phe Glu Glu Ala Ala Arg
 145 150 155 160

Arg Val Ser Glu Ile Ser Tyr Val Ser Ser Gln Pro Trp Pro Ile Ser
 165 170 175

Gly Ser Leu Met Leu Gly Met Lys Gly Phe Thr Glu Asp Glu Leu Pro
 180 185 190

Gln Gly Glu Thr Asp Gly Glu Leu Ala Glu Thr Ile Trp Ala Ser Pro
 195 200 205

Leu Asp Ile Ile Asp Arg Lys Ile Pro Ile Ala Pro Pro Gly Ser Ile
 210 215 220

Ala Tyr Asp Met Ile Asn Ala Trp Ala Arg Asp Lys Gln Asn
 225 230 235

<210> 2391
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 <222> (101)..(898)
 <223> RXA01741

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aagtaactgt gtcgattaag ttttggggga aatttttcag atg aca cac atc gct 115
 Met Thr His Ile Ala
 1 5

tta gcc aac tct gcc caa gtt ctg atc cgc ccg gat tct gcg att caa 163
 Leu Ala Asn Ser Ala Gln Val Leu Ile Arg Pro Asp Ser Ala Ile Gln
 10 15 20

ttc ggc atc gac gcc acc cgc gct ggc gtc tta aat atc gat cca tcg 211
 Phe Gly Ile Asp Ala Thr Arg Ala Gly Val Leu Asn Ile Asp Pro Ser
 25 30 35

ctg tcg tcg cga gtc gtc ccg gtg ctg cgg aat ctg cgg acc gcc cga 259
 Leu Ser Ser Arg Val Val Pro Val Leu Arg Asn Leu Arg Thr Ala Arg
 40 45 50

ccg atc gtt gat gtc atc gcc gac ctc acg act gca ggc ctc gca ccc 307
 Pro Ile Val Asp Val Ile Ala Asp Leu Thr Thr Ala Gly Leu Ala Pro
 55 60 65

acc gct gcg agc agt ttg ctc gag gac ctt tta gaa ttc ggt gtg gtc 355
 Thr Ala Ala Ser Ser Leu Leu Glu Asp Leu Leu Glu Phe Gly Val Val
 70 75 80 85

cgc gaa tcg gcg gcg gcg cag gtg ttg ctg ttc ggg gac ggt tcg ctt 403
 Arg Glu Ser Ala Ala Ala Gln Val Leu Leu Phe Gly Asp Gly Ser Leu
 90 95 100

gtc gac gtc acc tcc ttc ctt ttg gaa acc tcc ggc ttt gtt ccc aga 451
 Val Asp Val Thr Ser Phe Leu Leu Glu Thr Ser Gly Phe Val Pro Arg
 105 110 115

ccc cag atc atc gat gag tcg cct cga gag ttt ttc gag ctt ccc tcc 499
 Pro Gln Ile Ile Asp Glu Ser Pro Arg Glu Phe Phe Glu Leu Pro Ser

120	125	130	
agc cac att ttg gtt ctc aac aag ctc gca cat tcc caa cgt cta tcc			547
Ser His Ile Leu Val Leu Asn Lys Leu Ala His Ser Gln Arg Leu Ser			
135	140	145	
ccg ctg ctt cac aaa tat gcg ccg acg tat ctg tgc gcc gcg atc gtc			595
Pro Leu Leu His Lys Tyr Ala Pro Thr Tyr Leu Cys Ala Ala Ile Val			
150	155	160	165
gat aat cgt ggc atc atc ggc ccg ggc ccg aga tca cga tcg ggg ccg			643
Asp Asn Arg Gly Ile Ile Gly Pro Gly Arg Arg Ser Arg Ser Gly Pro			
170	175	180	
tgt ttg atg tgt gtg gat ctg cat cgc tgc gat atc gat ccg cat tgg			691
Cys Leu Met Cys Val Asp Leu His Arg Cys Asp Ile Asp Pro His Trp			
185	190	195	
ctc tct att atc aat cag caa ccc aac ggt ccc acc ttt cct gat ccc			739
Leu Ser Ile Ile Asn Gln Gln Pro Asn Gly Pro Thr Phe Pro Asp Pro			
200	205	210	
gtc acg gag atg gcg acg gct gcc cga ctc gtc gcc tgg gtc act gcc			787
Val Thr Glu Met Ala Thr Ala Ala Arg Leu Val Ala Trp Val Thr Ala			
215	220	225	
gat aca tgg ttg ccc ggc gtt gtg gag gaa gta aac ccc cac gat cga			835
Asp Thr Trp Leu Pro Gly Val Val Glu Glu Val Asn Pro His Asp Arg			
230	235	240	245
aca aac tcg gta cgc acc ctc cct gtg cat cca aaa tgt ccg atg tgt			883
Thr Asn Ser Val Arg Thr Leu Pro Val His Pro Lys Cys Pro Met Cys			
250	255	260	
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265			

<210> 2392

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 2392

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		20						25					30		

Asn	Ile	Asp	Pro	Ser	Leu	Ser	Ser	Arg	Val	Val	Pro	Val	Leu	Arg	Asn
		35					40					45			

Leu	Arg	Thr	Ala	Arg	Pro	Ile	Val	Asp	Val	Ile	Ala	Asp	Leu	Thr	Thr
	50					55					60				

Ala	Gly	Leu	Ala	Pro	Thr	Ala	Ala	Ser	Ser	Leu	Leu	Glu	Asp	Leu	Leu
	65				70					75					80

Glu	Phe	Gly	Val	Val	Arg	Glu	Ser	Ala	Ala	Ala	Gln	Val	Leu	Leu	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85										90					95				
Gly	Asp	Gly	Ser	Leu	Val	Asp	Val	Thr	Ser	Phe	Leu	Leu	Glu	Thr	Ser				
			100					105					110						
Gly	Phe	Val	Pro	Arg	Pro	Gln	Ile	Ile	Asp	Glu	Ser	Pro	Arg	Glu	Phe				
		115					120					125							
Phe	Glu	Leu	Pro	Ser	Ser	His	Ile	Leu	Val	Leu	Asn	Lys	Leu	Ala	His				
		130				135					140								
Ser	Gln	Arg	Leu	Ser	Pro	Leu	Leu	His	Lys	Tyr	Ala	Pro	Thr	Tyr	Leu				
					150					155					160				
Cys	Ala	Ala	Ile	Val	Asp	Asn	Arg	Gly	Ile	Ile	Gly	Pro	Gly	Arg	Arg				
				165					170					175					
Ser	Arg	Ser	Gly	Pro	Cys	Leu	Met	Cys	Val	Asp	Leu	His	Arg	Cys	Asp				
			180					185					190						
Ile	Asp	Pro	His	Trp	Leu	Ser	Ile	Ile	Asn	Gln	Gln	Pro	Asn	Gly	Pro				
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Thr	Phe	Pro	Asp	Pro	Val	Thr	Glu	Met	Ala	Thr	Ala	Ala	Arg	Leu	Val				
		210				215					220								
Ala	Trp	Val	Thr	Ala	Asp	Thr	Trp	Leu	Pro	Gly	Val	Val	Glu	Glu	Val				
		225			230					235				240					
Asn	Pro	His	Asp	Arg	Thr	Asn	Ser	Val	Arg	Thr	Leu	Pro	Val	His	Pro				
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(880)

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				Met	Ala	Asp	Ala	Lys	
				1				5	

aag	cag	gcg	gat	aaa	gcc	gcc	aag	aag	cag	gta	aga	gca	gcc	aag	aag	163
Lys	Gln	Ala	Asp	Lys	Ala	Ala	Lys	Lys	Gln	Val	Arg	Ala	Ala	Lys	Lys	
				10					15					20		

gca	cag	cgc	aag	gag	act	cgc	tca	caa	atg	tgg	cag	gtc	ttc	aac	atg	211
Ala	Gln	Arg	Lys	Glu	Thr	Arg	Ser	Gln	Met	Trp	Gln	Val	Phe	Asn	Met	
				25				30					35			

caa cgc aag cag gat aag gct ctt att ccg ctt ctg ttg ctc gct att	259
Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu Leu Leu Leu Ala Ile	
40 45 50	
ctt ggt atc ccg ctg gtc ctt ttc ctc atc ggt ttg att tgg ggt ggt	307
Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly Leu Ile Trp Gly Gly	
55 60 65	
cag tgg tgg atg ctt ccg atc ggc att gct gca ggt gtt gta gct gca	355
Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala Gly Val Val Ala Ala	
70 75 80 85	
atg ttt att ttc acc cgt cgc gtt gag cgt gac gtg tac aag cgc gcc	403
Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp Val Tyr Lys Arg Ala	
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gaa ggt cag cag ggt gct gct ggt tgg gct gtg gag aac ctc cgc tct	451
Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val Glu Asn Leu Arg Ser	
105 110 115	
ggc gtg ggc atg acc tgg cgc acc aag acc gct gtt gca gtg acc act	499
Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala Val Ala Val Thr Thr	
120 125 130	
cag atg gat gca gtg cac cgc gtc att ggt ctg tgt ggt gtt gtg ctg	547
Gln Met Asp Ala Val His Arg Val Ile Gly Leu Cys Gly Val Val Leu	
135 140 145	
gtc ggc gag ggc tcc cct cac cgc ctg aag cca atg ctt gcg cag caa	595
Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro Met Leu Ala Gln Gln	
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aag aag cgc ctg aac cgc gtg gca cct ggt gtt cca gtg tat gaa atc	643
Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val Pro Val Tyr Glu Ile	
170 175 180	
atc acg ggc aac ggc gaa ggc cag acc cct atc gcg aag ctg cag cgt	691
Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile Ala Lys Leu Gln Arg	
185 190 195	
gaa ctg gtc aag ctg cct cgc aac tac aag aag aac gac gtc gct gcc	739
Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys Asn Asp Val Ala Ala	
200 205 210	
ctg gcc gct cgc att gag gct atg gac aat gtc gga aac gct cct ggc	787
Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val Gly Asn Ala Pro Gly	
215 220 225	
gga tct ttg cct aag ggt cca ttg cca aag ggc gca agc atg tcc ggt	835
Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly Ala Ser Met Ser Gly	
230 235 240 245	
atg aac cgc cgc gct cgc cga cag gct gaa cgc aag ggc gag gct	880
Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg Lys Gly Glu Ala	
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<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 2394

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Gln Val Phe Asn Met Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu
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Leu Leu Leu Ala Ile Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly
50 55 60
Leu Ile Trp Gly Gly Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala
65 70 75 80
Gly Val Val Ala Ala Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp
85 90 95
Val Tyr Lys Arg Ala Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val
100 105 110
Glu Asn Leu Arg Ser Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala
115 120 125
Val Ala Val Thr Thr Gln Met Asp Ala Val His Arg Val Ile Gly Leu
130 135 140
Cys Gly Val Val Leu Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro
145 150 155 160
Met Leu Ala Gln Gln Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val
165 170 175
Pro Val Tyr Glu Ile Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile
180 185 190
Ala Lys Leu Gln Arg Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys
195 200 205
Asn Asp Val Ala Ala Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val
210 215 220
Gly Asn Ala Pro Gly Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly
225 230 235 240
Ala Ser Met Ser Gly Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg
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Lys Gly Glu Ala
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<211> 1740

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1717)

<223> RXA01749

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                               Val Ser Phe Leu Val
                               1                               5

gaa aat caa tta ctc gcg ttg gtt gtc atc atg acg gtc gga cta ttg 163
Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met Thr Val Gly Leu Leu
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ctc ggc cgc atc aaa att ttc ggg ttc cgt ctc ggc gtc gcc gct gta 211
Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu Gly Val Ala Ala Val
                               25                               30                               35

ctg ttt gta ggt cta gcg cta tcc acc att gag ccg gat att tcc gtc 259
Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu Pro Asp Ile Ser Val
                               40                               45                               50

cca tcc ctc att tac gtg gtt gga ctg tcg ctt ttt gtc tac acg atc 307
Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu Phe Val Tyr Thr Ile
                               55                               60                               65

ggg ctg gaa gcc ggc cct gga ttc ttc acc tcc atg aaa acc act ggt 355
Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser Met Lys Thr Thr Gly
70                               75                               80                               85

ctg cgc aac aac gca ctg acc ttg ggc gcc atc atc gcc acc acg gca 403
Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile Ile Ala Thr Thr Ala
                               90                               95                               100

ctc gca tgg gca ctc atc aca gtt ttg aac atc gat gcc gcc tcc ggc 451
Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile Asp Ala Ala Ser Gly
105                               110                               115

gcc ggc atg ctc acc ggc gcg ctc acc aac acc cca gcc atg gcc gca 499
Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr Pro Ala Met Ala Ala
120                               125                               130

gtt gtt gac gca ctt cct tcg ctt atc gac gac acc ggc cag ctt cac 547
Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp Thr Gly Gln Leu His
135                               140                               145

ctc atc gcc gag ctg ccc gtc gtc gca tat tcc ttg gca tac ccc ctc 595
Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser Leu Ala Tyr Pro Leu
150                               155                               160                               165

ggg gtg ctc atc gtt att ctc tcc atc gcc atc ttc agc tct gtg ttc 643
Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile Phe Ser Ser Val Phe
170                               175                               180

aaa gtc gac cac aac aaa gaa gcc gaa gaa gcg ggc gtt gcg gtc cag 691
Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala Gly Val Ala Val Gln
185                               190                               195

gaa ctc aaa ggc cgt cgc atc cgc gtc acc gtc gct gat ctt cca gcc 739

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Leu	Glu	Asn	Ile	Pro	Glu	Leu	Leu	Asn	Leu	His	Val	Ile	Val	Ser	Arg		
		215					220				225						
gtg	gaa	cga	gac	ggg	gag	caa	ttc	atc	ccg	ctt	tat	ggc	gaa	cac	gca		835
Val	Glu	Arg	Asp	Gly	Glu	Gln	Phe	Ile	Pro	Leu	Tyr	Gly	Glu	His	Ala		
						235					240				245		
cgc	atc	ggc	gat	gtc	tta	aca	gtg	gtg	ggg	gcc	gat	gaa	gaa	ctc	aac		883
Arg	Ile	Gly	Asp	Val	Leu	Thr	Val	Val	Gly	Ala	Asp	Glu	Glu	Leu	Asn		
				250					255						260		
cgc	gcg	gaa	aaa	gcc	atc	ggg	gaa	ctc	att	gac	ggc	gac	ccc	tac	agc		931
Arg	Ala	Glu	Lys	Ala	Ile	Gly	Glu	Leu	Ile	Asp	Gly	Asp	Pro	Tyr	Ser		
			265					270					275				
aat	gtg	gaa	ctt	gat	tac	cga	cgc	atc	ttc	gtc	tca	aac	aca	gca	gtc		979
Asn	Val	Glu	Leu	Asp	Tyr	Arg	Arg	Ile	Phe	Val	Ser	Asn	Thr	Ala	Val		
		280					285						290				
gtg	ggc	act	ccc	cta	tcc	aag	ctc	cag	cca	ctg	ttt	aaa	gac	atg	ctg		1027
Val	Gly	Thr	Pro	Leu	Ser	Lys	Leu	Gln	Pro	Leu	Phe	Lys	Asp	Met	Leu		
		295				300					305						
atc	acc	cgc	atc	agg	cgc	ggc	gac	aca	gat	ttg	gtg	gcc	tcc	tcc	gac		1075
Ile	Thr	Arg	Ile	Arg	Arg	Gly	Asp	Thr	Asp	Leu	Val	Ala	Ser	Ser	Asp		
					315					320					325		
atg	act	ttg	cag	ctc	ggg	gac	cgt	gtc	cgc	ggt	gtc	gca	cca	gca	gaa		1123
Met	Thr	Leu	Gln	Leu	Gly	Asp	Arg	Val	Arg	Val	Val	Ala	Pro	Ala	Glu		
				330				335						340			
aaa	ctc	cgc	gaa	gca	acc	caa	ttg	ctc	ggc	gat	tcc	tac	aag	aaa	ctc		1171
Lys	Leu	Arg	Glu	Ala	Thr	Gln	Leu	Leu	Gly	Asp	Ser	Tyr	Lys	Lys	Leu		
			345					350					355				
tcc	gat	ttc	aac	ctg	ctc	cca	ctc	gct	gcc	ggc	ctc	atg	atc	ggg	gtg		1219
Ser	Asp	Phe	Asn	Leu	Leu	Pro	Leu	Ala	Ala	Gly	Leu	Met	Ile	Gly	Val		
		360					365					370					
ctt	gtc	ggc	atg	gtg	gag	ttc	cca	cta	cca	ggg	gga	agc	tcc	ctg	aaa		1267
Leu	Val	Gly	Met	Val	Glu	Phe	Pro	Leu	Pro	Gly	Gly	Ser	Ser	Leu	Lys		
		375				380					385						
ctg	ggg	aac	gca	ggg	gga	ccg	cta	gtt	gtt	gcg	ctg	ctg	ctc	ggc	atg		1315
Leu	Gly	Asn	Ala	Gly	Gly	Pro	Leu	Val	Val	Ala	Leu	Leu	Leu	Gly	Met		
					395					400					405		
atc	aat	cgc	aca	ggc	aag	ttc	gtc	ttg	caa	atc	ccc	tac	gga	gca	aac		1363
Ile	Asn	Arg	Thr	Gly	Lys	Phe	Val	Trp	Gln	Ile	Pro	Tyr	Gly	Ala	Asn		
				410					415					420			
ctt	gcc	ctt	cgc	caa	ctg	ggc	atc	aca	cta	ttt	ttg	gct	gcc	atc	ggg		1411
Leu	Ala	Leu	Arg	Gln	Leu	Gly	Ile	Thr	Leu	Phe	Leu	Ala	Ala	Ile	Gly		
			425					430					435				
acc	tca	gcg	ggc	gca	gga	ttt	cga	tca	gcg	atc	agc	gac	ccc	caa	tca		1459
Thr	Ser	Ala	Gly	Ala	Gly	Phe	Arg	Ser	Ala	Ile	Ser	Asp	Pro	Gln	Ser		

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 Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr Leu Phe Ile Ser Ile
 455 460 465
 acg gtg ctg ttc gtt ggc cac aaa ctg atg aaa atc ccc ttc ggt gaa 1555
 Thr Val Leu Phe Val Gly His Lys Leu Met Lys Ile Pro Phe Gly Glu
 470 475 480 485
 acc gct ggc atc ctc gcc ggt acg caa acc cac cct gct gtg ctg agt 1603
 Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His Pro Ala Val Leu Ser
 490 495 500
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 Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro Ala Met Gly Tyr Thr
 505 510 515
 tct gtg tat ccg ctg gcg atg atc gca aag atc ctg gcc gcc caa acg 1699
 Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile Leu Ala Ala Gln Thr
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 Gly Val Ala Ala Val Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu
 35 40 45
 Pro Asp Ile Ser Val Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu
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 Phe Val Tyr Thr Ile Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser
 65 70 75 80
 Met Lys Thr Thr Gly Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile
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 Ile Ala Thr Thr Ala Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile
 100 105 110
 Asp Ala Ala Ser Gly Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr
 115 120 125
 Pro Ala Met Ala Ala Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp
 130 135 140
 Thr Gly Gln Leu His Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser

145 150 155 160
Leu Ala Tyr Pro Leu Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile
 165 170 175
Phe Ser Ser Val Phe Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala
 180 185 190
Gly Val Ala Val Gln Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val
 195 200 205
Ala Asp Leu Pro Ala Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His
 210 215 220
Val Ile Val Ser Arg Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu
225 230 235 240
Tyr Gly Glu His Ala Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala
 245 250 255
Asp Glu Glu Leu Asn Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp
 260 265 270
Gly Asp Pro Tyr Ser Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val
 275 280 285
Ser Asn Thr Ala Val Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu
290 295 300
Phe Lys Asp Met Leu Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu
305 310 315 320
Val Ala Ser Ser Asp Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val
 325 330 335
Val Ala Pro Ala Glu Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp
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Ser Tyr Lys Lys Leu Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly
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Gly Ser Ser Leu Lys Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala
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 405 410 415
Pro Tyr Gly Ala Asn Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe
 420 425 430
Leu Ala Ala Ile Gly Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile
 435 440 445
Ser Asp Pro Gln Ser Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr
450 455 460
Leu Phe Ile Ser Ile Thr Val Leu Phe Val Gly His Lys Leu Met Lys
465 470 475 480

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135	140	145	
ccc gtt gag cga ctc aat gaa cgt gca cgt gcc ggt gaa ttc ggt aac			595
Pro Val Glu Arg Leu Asn Glu Arg Ala Arg Ala Gly Glu Phe Gly Asn			
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tta gag act gat gaa aat gca gcc atg atg ttc cag gat gct gtg aca			643
Leu Glu Thr Asp Glu Asn Ala Ala Met Met Phe Gln Asp Ala Val Thr			
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gag gcc gaa gag aac gaa atg ttt ctg tgg gag ggt gag aaa gaa aaa			691
Glu Ala Glu Glu Asn Glu Met Phe Leu Trp Glu Gly Glu Lys Glu Lys			
185	190	195	
gac atg ctc acc ttg ttc ttt agt gcc aca gac ggt ctg cca aag tcc			739
Asp Met Leu Thr Leu Phe Phe Ser Ala Thr Asp Gly Leu Pro Lys Ser			
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Ser Val Arg Thr Leu Val Gly Asn Ala Asp Lys Ala Leu Lys Ala Met			
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Gly Gly Ala Glu Lys Met Met Ala Ser Val Tyr Gly Ile Ala Ile Thr			
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gcg atg tcc ttc ttt aca gac ccc aca att tca acg tta acc tca ggc			883
Ala Met Ser Phe Phe Thr Asp Pro Thr Ile Ser Thr Leu Thr Ser Gly			
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aca cta agt cag aac gtt gac ttg gcc gga ttg tcg ttt cca cgg cgc			931
Thr Leu Ser Gln Asn Val Asp Leu Ala Gly Leu Ser Phe Pro Arg Arg			
265	270	275	
atg ggt gtt cgt ttt gcg gcc ccc tat gtg aag cgc tac aac ctg gtt			979
Met Gly Val Arg Phe Ala Ala Pro Tyr Val Lys Arg Tyr Asn Leu Val			
280	285	290	
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Gly Ser Gln Val Lys Trp Asp Ala Tyr Ser Asp Ala Lys Phe Thr Lys			
295	300	305	
ccg ttg ggt aag aat ttt gtt cat gat gac acg ctg tcg gtt gag ggt			1075
Pro Leu Gly Lys Asn Phe Val His Asp Asp Thr Leu Ser Val Glu Gly			
310	315	320	325
tgg gcg cgg ttc tat att aaa gac tcg ttc ccg agt aat act gcg tac			1123
Trp Ala Arg Phe Tyr Ile Lys Asp Ser Phe Pro Ser Asn Thr Ala Tyr			
330	335	340	
ctg cgt ttg cgg att ctc aat ggt act tct ggc acg ttg atc aag act			1171
Leu Arg Leu Arg Ile Leu Asn Gly Thr Ser Gly Thr Leu Ile Lys Thr			
345	350	355	
ctg tac ttc aag ttc acc aag ggc tac caa acg aac ctt aaa ggc cgt			1219
Leu Tyr Phe Lys Phe Thr Lys Gly Tyr Gln Thr Asn Leu Lys Gly Arg			
360	365	370	

gcg ttt att act gat ccg gtg acc gat gag aag atc att aag aat ggt 1267
 Ala Phe Ile Thr Asp Pro Val Thr Asp Glu Lys Ile Ile Lys Asn Gly
 375 380 385
 ctg ctg atc gag ctg gtg aaa aac gat gct ggt gac ttt gtt cca ggt 1315
 Leu Leu Ile Glu Leu Val Lys Asn Asp Ala Gly Asp Phe Val Pro Gly
 390 395 400 405
 cat gtg cag ttt aag acg aag aaa ctg aat ctt gac caa ctc acg cag 1363
 His Val Gln Phe Lys Thr Lys Lys Leu Asn Leu Asp Gln Leu Thr Gln
 410 415 420
 gaa cag atc aat atg ccg ggt cat gac atg atc aag cag gtt gat gcg 1411
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 425 430 435
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 Met Val Asp Ala Val Ser Ala Leu Asn Val Arg Tyr Ser Glu Lys Pro
 440 445 450
 aag gca gtg ttc ttc gta acg cct ccg cat ctt atg aaa tat gcg aag 1507
 Lys Ala Val Phe Phe Val Thr Pro Pro His Leu Met Lys Tyr Ala Lys
 455 460 465
 ttg att ttg att ctc atc aaa cag ctt gtg gat ctg aac ttc gat tcc 1555
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 Ser Tyr Met Thr Arg Glu Asn Gln Lys Pro Asp Tyr Lys Thr Arg Phe
 490 495 500
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 Met Leu Asp Glu Leu Gly Asn Leu Gln Ser Glu Gly His Gly Ile Ala
 505 510 515
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 Gly Phe Glu Thr Met Leu Ser Ile Gly Leu Gly Gln Glu Gln Gln Phe
 520 525 530
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<211> 547

<212> PRT

<213> Corynebacterium glutamicum

<400> 2398

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Asn Leu Lys Thr Asp Ile Tyr Asn Pro Leu Gly Leu Ala Ala Glu Ala

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Ala Glu Val Phe Phe Pro Val Asp Gly Ala Asp Asp Pro Val Trp Pro 65 70 75 80		
Asn Ala Ala Asn Asn Ala Phe Lys Arg Ala Ala Tyr Gly Leu Ile Asp 85 90 95		
Phe Tyr Leu Glu Glu Glu Arg Glu Met Arg Lys Gln Ala Ala Ala Glu 100 105 110		
Asn Trp Asp Ala Lys Val Leu Asp Thr Arg Ile Asp Gln Met Trp Gly 115 120 125		
Lys Val Thr Leu Tyr Asn Cys Tyr Gln Leu Phe Val Gln Leu Ser Ala 130 135 140		
Lys Lys Leu Lys Asn Pro Val Glu Arg Leu Asn Glu Arg Ala Arg Ala 145 150 155 160		
Gly Glu Phe Gly Asn Leu Glu Thr Asp Glu Asn Ala Ala Met Met Phe 165 170 175		
Gln Asp Ala Val Thr Glu Ala Glu Glu Asn Glu Met Phe Leu Trp Glu 180 185 190		
Gly Glu Lys Glu Lys Asp Met Leu Thr Leu Phe Phe Ser Ala Thr Asp 195 200 205		
Gly Leu Pro Lys Ser Ser Val Arg Thr Leu Val Gly Asn Ala Asp Lys 210 215 220		
Ala Leu Lys Ala Met Gly Gly Ala Glu Lys Met Met Ala Ser Val Tyr 225 230 235 240		
Gly Ile Ala Ile Thr Ala Met Ser Phe Phe Thr Asp Pro Thr Ile Ser 245 250 255		
Thr Leu Thr Ser Gly Thr Leu Ser Gln Asn Val Asp Leu Ala Gly Leu 260 265 270		
Ser Phe Pro Arg Arg Met Gly Val Arg Phe Ala Ala Pro Tyr Val Lys 275 280 285		
Arg Tyr Asn Leu Val Gly Ser Gln Val Lys Trp Asp Ala Tyr Ser Asp 290 295 300		
Ala Lys Phe Thr Lys Pro Leu Gly Lys Asn Phe Val His Asp Asp Thr 305 310 315 320		
Leu Ser Val Glu Gly Trp Ala Arg Phe Tyr Ile Lys Asp Ser Phe Pro 325 330 335		
Ser Asn Thr Ala Tyr Leu Arg Leu Arg Ile Leu Asn Gly Thr Ser Gly 340 345 350		
Thr Leu Ile Lys Thr Leu Tyr Phe Lys Phe Thr Lys Gly Tyr Gln Thr 355 360 365		

Asn Leu Lys Gly Arg Ala Phe Ile Thr Asp Pro Val Thr Asp Glu Lys
 370 375 380
 Ile Ile Lys Asn Gly Leu Leu Ile Glu Leu Val Lys Asn Asp Ala Gly
 385 390 395 400
 Asp Phe Val Pro Gly His Val Gln Phe Lys Thr Lys Lys Leu Asn Leu
 405 410 415
 Asp Gln Leu Thr Gln Glu Gln Ile Asn Met Pro Gly His Asp Met Ile
 420 425 430
 Lys Gln Val Asp Ala Met Val Asp Ala Val Ser Ala Leu Asn Val Arg
 435 440 445
 Tyr Ser Glu Lys Pro Lys Ala Val Phe Phe Val Thr Pro Pro His Leu
 450 455 460
 Met Lys Tyr Ala Lys Leu Ile Leu Ile Leu Ile Lys Gln Leu Val Asp
 465 470 475 480
 Leu Asn Phe Asp Ser Ser Tyr Met Thr Arg Glu Asn Gln Lys Pro Asp
 485 490 495
 Tyr Lys Thr Arg Phe Met Leu Asp Glu Leu Gly Asn Leu Gln Ser Glu
 500 505 510
 Gly His Gly Ile Ala Gly Phe Glu Thr Met Leu Ser Ile Gly Leu Gly
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 Gln Glu Gln Gln Phe Ser Ala Thr Ser Cys Val Ala Lys Asn Tyr Ala
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 Leu Ala Ala
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 <222> (101)..(652)
 <223> RXA01752

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 Met Met Glu Gln Asp
 1 5
 ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa 163
 Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys
 10 15 20
 aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg 211
 Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro

25	30	35	
cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc			259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe			
40	45	50	
att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa			307
Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln			
55	60	65	
gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att			355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile			
70	75	80	85
aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa			403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu			
90	95	100	
tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac			451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp			
105	110	115	
aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat ggc gaa cct gag			499
Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu			
120	125	130	
gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag			547
Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys			
135	140	145	
cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg			595
His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr			
150	155	160	165
atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att			643
Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile			
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aag gtg ccg			652
Lys Val Pro			

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<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 2400

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35 40 45

Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
50 55 60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
 65 70 75 80
 Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
 85 90 95
 Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
 100 105 110
 Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
 115 120 125
 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala
 130 135 140
 Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu
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 Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
 165 170 175
 Val Ala Thr Ile Ile Lys Val Pro
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<212> DNA

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<220>

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<223> RXA01753

<400> 2401

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 Met Ser Asn Pro Ser
 1 5

cta gaa cct cta gaa ccg atc gag ctt tct gac ggt act gaa att gaa 163
 Leu Glu Pro Leu Glu Pro Ile Glu Leu Ser Asp Gly Thr Glu Ile Glu
 10 15 20

gtt tca gac gtt gat cca gaa ccg caa gct ggc aat gcg cag atg gaa 211
 Val Ser Asp Val Asp Pro Glu Pro Gln Ala Gly Asn Ala Gln Met Glu
 25 30 35

gta ccc agc tta cgg aca tat gtt ttt cgc gga atc att gcc att gcc 259
 Val Pro Ser Leu Arg Thr Tyr Val Phe Arg Gly Ile Ile Ala Ile Ala
 40 45 50

tgt ttg atc att ggt ttt tat gag agc ttt gtg ctg atg tgg caa aac 307
 Cys Leu Ile Ile Gly Phe Tyr Glu Ser Phe Val Leu Met Trp Gln Asn
 55 60 65

ctc cga atc ggc gtg gcc aac tac tca cta ctt gtg gtg ctc atg gcg 355
 Leu Arg Ile Gly Val Ala Asn Tyr Ser Leu Leu Val Val Leu Met Ala
 70 75 80 85

atc gtg ttg ttt atc gga ctg gac cgc aag cgt gct cgt gca ttg aac	403
Ile Val Leu Phe Ile Gly Leu Asp Arg Lys Arg Ala Arg Ala Leu Asn	
90 95 100	
att cac gac cgc gaa gtc gac tac atc att ggt ggc att gtc gta ctg	451
Ile His Asp Arg Glu Val Asp Tyr Ile Ile Gly Gly Ile Val Val Leu	
105 110 115	
ata gcc atc acg att aag agc cag ctt ctg cca cgt ttt gtg gac tgg	499
Ile Ala Ile Thr Ile Lys Ser Gln Leu Leu Pro Arg Phe Val Asp Trp	
120 125 130	
gaa act ctg ctg cgc ttg gat atg ttc gca ctg tta ttc ttt gcg ttt	547
Glu Thr Leu Leu Arg Leu Asp Met Phe Ala Leu Leu Phe Phe Ala Phe	
135 140 145	
ggt att tcc ggc ctg gtg ttt ggc atg cgc tct acc ttt tct ttt gca	595
Gly Ile Ser Gly Leu Val Phe Gly Met Arg Ser Thr Phe Ser Phe Ala	
150 155 160 165	
ccc ggc tgg att ttg ctg ttt ggc tac aac gcg gtg gca cac ctg atc	643
Pro Gly Trp Ile Leu Leu Phe Gly Tyr Asn Ala Val Ala His Leu Ile	
170 175 180	
atc tcg gtg att ttc ggt ggt ggc ttt tgg ggc ccg gtg atg gca aac	691
Ile Ser Val Ile Phe Gly Gly Gly Phe Trp Gly Pro Val Met Ala Asn	
185 190 195	
atc att gga ctg tct ctt gcg gtg ttg gtg tcc tcc aac agg gac ctg	739
Ile Ile Gly Leu Ser Leu Ala Val Leu Val Ser Ser Asn Arg Asp Leu	
200 205 210	
gtt cag gcc acc tat ttg gca ctg atg acg gtg ttg ttt ggc gtc att	787
Val Gln Ala Thr Tyr Leu Ala Leu Met Thr Val Leu Phe Gly Val Ile	
215 220 225	
att gcc atc atc gtg tgg gcg ctg acc gat ggc agt aag ttc ctc acc	835
Ile Ala Ile Ile Val Trp Ala Leu Thr Asp Gly Ser Lys Phe Leu Thr	
230 235 240 245	
ttg gtc cca gca gtg ctg gca acc atc act gtg gtg ttg gtg tct tcg	883
Leu Val Pro Ala Val Leu Ala Thr Ile Thr Val Val Leu Val Ser Ser	
250 255 260	
cgt tgg agg ctt ggt cag tgg aaa att cgt cgt aga caa ccc acg gtg	931
Arg Trp Arg Leu Gly Gln Trp Lys Ile Arg Arg Arg Gln Pro Thr Val	
265 270 275	
gaa aaa gcc gga ccc gcg ctt atc gcg gtc gtg gtt gcg aca gca ctc	979
Glu Lys Ala Gly Pro Ala Leu Ile Ala Val Val Val Ala Thr Ala Leu	
280 285 290	
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Leu Ala Trp Ile Pro Thr Pro Tyr Val Glu Arg Val Asn Asn Leu Pro	
295 300 305	
ggg ctt caa atg ctg gca aag cct gcc cca ggt gtt atc gca cct att	1075
Gly Leu Gln Met Leu Ala Lys Pro Ala Pro Gly Val Ile Ala Pro Ile	
310 315 320 325	

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 Gly Trp His Ile Asp Asp Val Gln Tyr Tyr Asn Trp Ala Ser Arg Tyr
 330 335 340

ttc ggc ccc ggt tcc tct ctg ctt agg cag acg atg acg gca gat cat 1171
 Phe Gly Pro Gly Ser Ser Leu Leu Arg Gln Thr Met Thr Ala Asp His
 345 350 355

tac aac gag gcg tgg gat cca gat gga ctc gac cga act gtt gtg gtg 1219
 Tyr Asn Glu Ala Trp Asp Pro Asp Gly Leu Asp Arg Thr Val Val Val
 360 365 370

gat acc ctc caa tcg gcg gaa cgg ttc cag cag cgt gcc ttt ggt gac 1267
 Asp Thr Leu Gln Ser Ala Glu Arg Phe Gln Gln Arg Ala Phe Gly Asp
 375 380 385

gag acg ctg tat tcc act ctg aga ggt cga aag tca gat acc gtc cag 1315
 Glu Thr Leu Tyr Ser Thr Leu Arg Gly Arg Lys Ser Asp Thr Val Gln
 390 395 400 405

gtg gat ctg gga tac ggc gtg gac gga cgc gcc tac acg gtg ctc gat 1363
 Val Asp Leu Gly Tyr Gly Val Asp Gly Arg Ala Tyr Thr Val Leu Asp
 410 415 420

gaa act gac ttc ttg acg tac acc aag ctg gtt ttt gaa tgg cag acc 1411
 Glu Thr Asp Phe Leu Thr Tyr Thr Lys Leu Val Phe Glu Trp Gln Thr
 425 430 435

acc aac aac acc gtg gag aag atc tcc gtc atc gcg gtg gat gat cac 1459
 Thr Asn Asn Thr Val Glu Lys Ile Ser Val Ile Ala Val Asp Asp His
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cgc gca gaa gcg aag ttc ccg gag ctt gca cca tcg gtt acc aga atg 1507
 Arg Ala Glu Ala Lys Phe Pro Glu Leu Ala Pro Ser Val Thr Arg Met
 455 460 465

ttt atc cag gtg gct acc att ttg ttc cgt gga aat gac gtg acc atc 1555
 Phe Ile Gln Val Ala Thr Ile Leu Phe Arg Gly Asn Asp Val Thr Ile
 470 475 480 485

gat acc aat acc caa ttg aaa gat ctt gac ctg gtc agc caa gtt ggc 1603
 Asp Thr Asn Thr Gln Leu Lys Asp Leu Asp Leu Val Ser Gln Val Gly
 490 495 500

cgt cag atc gtg gca gaa caa cag gtg ggg agg tca tgatggaaca 1649
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 <212> PRT
 <213> Corynebacterium glutamicum

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Ile	Ile	Ala	Ile	Ala	Cys	Leu	Ile	Ile	Gly	Phe	Tyr	Glu	Ser	Phe	Val															
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Ala	Arg	Ala	Leu	Asn	Ile	His	Asp	Arg	Glu	Val	Asp	Tyr	Ile	Ile	Gly															
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Gly	Ile	Val	Val	Leu	Ile	Ala	Ile	Thr	Ile	Lys	Ser	Gln	Leu	Leu	Pro															
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Arg	Phe	Val	Asp	Trp	Glu	Thr	Leu	Leu	Arg	Leu	Asp	Met	Phe	Ala	Leu															
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Leu	Phe	Phe	Ala	Phe	Gly	Ile	Ser	Gly	Leu	Val	Phe	Gly	Met	Arg	Ser															
145										150										155										
Thr	Phe	Ser	Phe	Ala	Pro	Gly	Trp	Ile	Leu	Leu	Phe	Gly	Tyr	Asn	Ala															
165										170										175										
Val	Ala	His	Leu	Ile	Ile	Ser	Val	Ile	Phe	Gly	Gly	Gly	Phe	Trp	Gly															
180										185										190										
Pro	Val	Met	Ala	Asn	Ile	Ile	Gly	Leu	Ser	Leu	Ala	Val	Leu	Val	Ser															
195										200										205										
Ser	Asn	Arg	Asp	Leu	Val	Gln	Ala	Thr	Tyr	Leu	Ala	Leu	Met	Thr	Val															
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225										230										235										
Ser	Lys	Phe	Leu	Thr	Leu	Val	Pro	Ala	Val	Leu	Ala	Thr	Ile	Thr	Val															
245										250										255										
Val	Leu	Val	Ser	Ser	Arg	Trp	Arg	Leu	Gly	Gln	Trp	Lys	Ile	Arg	Arg															
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Arg	Gln	Pro	Thr	Val	Glu	Lys	Ala	Gly	Pro	Ala	Leu	Ile	Ala	Val	Val															
275										280										285										
Val	Ala	Thr	Ala	Leu	Leu	Ala	Trp	Ile	Pro	Thr	Pro	Tyr	Val	Glu	Arg															
290										295										300										
Val	Asn	Asn	Leu	Pro	Gly	Leu	Gln	Met	Leu	Ala	Lys	Pro	Ala	Pro	Gly															
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325										330										335										
Trp	Ala	Ser	Arg	Tyr	Phe	Gly	Pro	Gly	Ser	Ser	Leu	Leu	Arg	Gln	Thr															
340										345										350										

Met Thr Ala Asp His Tyr Asn Glu Ala Trp Asp Pro Asp Gly Leu Asp
 355 360 365

Arg Thr Val Val Val Asp Thr Leu Gln Ser Ala Glu Arg Phe Gln Gln
 370 375 380

Arg Ala Phe Gly Asp Glu Thr Leu Tyr Ser Thr Leu Arg Gly Arg Lys
 385 390 395 400

Ser Asp Thr Val Gln Val Asp Leu Gly Tyr Gly Val Asp Gly Arg Ala
 405 410 415

Tyr Thr Val Leu Asp Glu Thr Asp Phe Leu Thr Tyr Thr Lys Leu Val
 420 425 430

Phe Glu Trp Gln Thr Thr Asn Asn Thr Val Glu Lys Ile Ser Val Ile
 435 440 445

Ala Val Asp Asp His Arg Ala Glu Ala Lys Phe Pro Glu Leu Ala Pro
 450 455 460

Ser Val Thr Arg Met Phe Ile Gln Val Ala Thr Ile Leu Phe Arg Gly
 465 470 475 480

Asn Asp Val Thr Ile Asp Thr Asn Thr Gln Leu Lys Asp Leu Asp Leu
 485 490 495

Val Ser Gln Val Gly Arg Gln Ile Val Ala Glu Gln Gln Val Gly Arg
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Ser

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<211> 405

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(382)

<223> RXA01760

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 Met Ala Ala Phe Leu
 1 5

gag atc acc ttg aaa atc aat gac gaa ggc cgc cca tca gca gct ggc 163
 Glu Ile Thr Leu Lys Ile Asn Asp Glu Gly Arg Pro Ser Ala Ala Gly
 10 15 20

gtc tac cag gaa tac aag caa cca ttc ctc agc tca att gct ggc gct 211
 Val Tyr Gln Glu Tyr Lys Gln Pro Phe Leu Ser Ser Ile Ala Gly Ala
 25 30 35

aca agc aaa gaa ctc ctc atc cga gaa gaa gac gtg cag gtg ctc cac 259

Thr Ser Lys Glu Leu Leu Ile Arg Glu Glu Asp Val Gln Val Leu His
40 45 50

ggc tgt gac acc gta gct aat gct gaa gat tat ctt gtc agc gaa ctg 307
Gly Cys Asp Thr Val Ala Asn Ala Glu Asp Tyr Leu Val Ser Glu Leu
55 60 65

ttc acg gcc gat gtt gtc ggt ggt cta gct cca cta ttg cag gct gat 355
Phe Thr Ala Asp Val Val Gly Gly Leu Ala Pro Leu Leu Gln Ala Asp
70 75 80 85

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<210> 2404

<211> 94

<212> PRT

<213> Corynebacterium glutamicum

<400> 2404

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Ser Ile Ala Gly Ala Thr Ser Lys Glu Leu Leu Ile Arg Glu Glu Asp
35 40 45

Val Gln Val Leu His Gly Cys Asp Thr Val Ala Asn Ala Glu Asp Tyr
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Leu Leu Gln Ala Asp Pro Glu Ile Arg Ile Tyr Gln Val Ala
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<211> 501

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXA01768

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gcactctccc gtactcattt ctagaaaggt ttttcccgtc atg tct gaa tct act 115
Met Ser Glu Ser Thr
1 5

tct tct gct aac tcc acc acc atc ctc aac gac acc ttc aac ccg aag 163

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Pro	Gly	Val	Pro	Tyr	Ala	Arg	Val	Asp	Asn	Leu	Glu	Phe	Ala	Thr	Arg		
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gac	gaa	ttc	cgc	gct	ttg	gct	acc	gca	gag	atg	gag	gcc	ggt	aac	gtt	259	
Asp	Glu	Phe	Arg	Ala	Trp	Ala	Thr	Ala	Glu	Met	Glu	Ala	Gly	Asn	Val		
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Ile	Ser	Ala	Thr	Ile	Ala	Asn	Ala	Pro	Arg	Glu	Asp	Arg	Ile	Lys	Ser		
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Phe	Val	Met	Asp	Leu	Val	Arg	Asp	Gly	Ile	Asp	Asp	Ala	Ala	Glu	Glu		
		70			75					80					85		
atc	gtc	tca	cgc	att	gat	agc	ggt	gac	ttc	act	atg	aag	gaa	gct	ctc	403	
Ile	Val	Ser	Arg	Ile	Asp	Ser	Gly	Asp	Phe	Thr	Met	Lys	Glu	Ala	Leu		
				90					95					100			
acc	gcg	atc	gcg	gca	tca	atc	aac	gac	ctc	gat	gct	gac	gat	gta	gtc	451	
Thr	Ala	Ile	Ala	Ala	Ser	Ile	Asn	Asp	Leu	Asp	Ala	Asp	Asp	Val	Val		
			105					110					115				
agc	gac	atc	gtt	gaa	aac	cac	ttc	aac	tagtcaacac	accagccctc						498	
Ser	Asp	Ile	Val	Glu	Asn	His	Phe	Asn									
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cac																	501

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 <211> 126
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 <213> Corynebacterium glutamicum

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Thr	Phe	Asn	Pro	Lys	Pro	Gly	Val	Pro	Tyr	Ala	Arg	Val	Asp	Asn	Leu		
			20					25					30				
Glu	Phe	Ala	Thr	Arg	Asp	Glu	Phe	Arg	Ala	Trp	Ala	Thr	Ala	Glu	Met		
		35					40					45					
Glu	Ala	Gly	Asn	Val	Ile	Ser	Ala	Thr	Ile	Ala	Asn	Ala	Pro	Arg	Glu		
		50				55					60						
Asp	Arg	Ile	Lys	Ser	Phe	Val	Met	Asp	Leu	Val	Arg	Asp	Gly	Ile	Asp		
		65			70					75					80		
Asp	Ala	Ala	Glu	Glu	Ile	Val	Ser	Arg	Ile	Asp	Ser	Gly	Asp	Phe	Thr		
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Met	Lys	Glu	Ala	Leu	Thr	Ala	Ile	Ala	Ala	Ser	Ile	Asn	Asp	Leu	Asp		
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(3865)
 <223> RXA01770

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 Met Pro Ile Ile Ile
 1 5
 gat aac ctc aat tct gac gac gac tcc acc atc ggc act gcc acc gaa 163
 Asp Asn Leu Asn Ser Asp Asp Asp Ser Thr Ile Gly Thr Ala Thr Glu
 10 15 20
 tac aac cct gac act gac gcc gat tta ctt gat gct att aac gct gat 211
 Tyr Asn Pro Asp Thr Asp Ala Asp Leu Leu Asp Ala Ile Asn Ala Asp
 25 30 35
 gct gac ctt gat ggc gac gcc acc atc agc act aac gcg aca gaa gaa 259
 Ala Asp Leu Asp Gly Asp Ala Thr Ile Ser Thr Asn Ala Thr Glu Glu
 40 45 50
 ggt gta gac gca gca gct gaa aaa cct aag aaa aag cgt aaa gcc cct 307
 Gly Val Asp Ala Ala Ala Glu Lys Pro Lys Lys Lys Arg Lys Ala Pro
 55 60 65
 gct ctg aag cct aaa gga ctc acg gca aag ttc ttc cac cgt gat ctt 355
 Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe Phe His Arg Asp Leu
 70 75 80 85
 act ggc gta ggt ggt agg acc ggt cgc ctc aac aag aac gta cac ccg 403
 Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn Lys Asn Val His Pro
 90 95 100
 acc aac cca gat ctg tcc tac cag cca gtc tct gat gtc tac acc cca 451
 Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser Asp Val Tyr Thr Pro
 105 110 115
 caa tca gca gat cac aag ggt att aag acc cgc tac atc ctt acc cat 499
 Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg Tyr Ile Leu Thr His
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 cca acc ccc gct gtt gtt ctc agt gag tcc atc agc aac gcg ttt cat 547
 Pro Thr Pro Ala Val Val Leu Ser Glu Ser Ile Ser Asn Ala Phe His
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 gtc tct acc ctg cgt cgc aac aat aat gtc aac aac tct gat tcg gaa 595
 Val Ser Thr Leu Arg Arg Asn Asn Asn Val Asn Asn Ser Asp Ser Glu
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Leu Ala Ala Trp Pro Tyr Leu Tyr Gln Leu Asp Ile Pro Gln Leu Asp	
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Gln Met Ile Asn Val Ala Asp Ile Cys Asp Tyr His Phe His Gly Tyr	
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Asn Leu Trp Val Asp Phe Thr Pro Gln Thr Ile Ala Leu Arg Ser Gly	
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Lys Thr Val Leu Asp Asp Gly Thr Thr Ala Ser Asp Asn Thr Thr His	
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gtc tat tac cgc gtc acc gtt cac gtt att gcc ggt caa gat cat gga	835
Val Tyr Tyr Arg Val Thr Val His Val Ile Ala Gly Gln Asp His Gly	
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Ser Thr Leu Leu Asp Asp Gln Gly Asn Gln Val Leu Asp Arg Asp Asp	
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Asn Pro Ile Ser Thr Pro Ser Ile Lys Arg Ile Gly Ala Val Thr Asp	
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Leu Phe Asp His Asn Pro Phe Gly Phe Ala Ser Val Asn Ser Phe Ala	
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Pro Thr Pro Ile Ala Leu Asp Met Val Val Leu Asn Glu Trp Ser Glu	
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Lys Ser Tyr Gln Leu Cys Glu Arg Val Val Ala Gln Ala Lys Leu Ile	
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Asn Ser Asn Lys Ile Thr Ala His Val Ser Asp Val Ile Lys Gln Asn	
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Ala His Asn Ile Leu Trp Phe Thr Glu Gln Met Asn Pro Gly Thr Thr	
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Asn Leu Ser Glu Val Pro Ile Ser Lys Lys Ser Met Leu Pro Met Ser	
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cgc cag cta cgt att ttg gag cac tac gat gta cca ctg acc gcg tac	1363

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Ser	Ala	Leu	Phe	Trp	Thr	Val	Ser	Ala	Ile	Lys	Asn	Glu	Ser	Met	Val		
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Gln	Tyr	Leu	Val	Arg	Gln	Asn	Met	Gln	Leu	Thr	Leu	Ser	Ser	Asn	Leu		
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Asp	Ala	Leu	Asn	Ser	Ile	Val	Ser	Gln	Leu	Pro	Val	Pro	Asp	Lys	Asp		
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Val	Val	Ala	Ala	Ser	Gly	Tyr	Gln	Ile	Gln	Pro	His	Phe	Ser	Thr	Gln		
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Gln	Arg	Glu	Ala	Ile	Thr	Thr	Asp	Asn	Pro	Leu	Ala	Ile	Ile	Gln	Ala		
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Gly	Ala	Gly	Thr	Gly	Lys	Ser	Thr	Val	Ile	Leu	Glu	Arg	Ile	Glu	Tyr		
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Thr	Ala	Leu	Ser	Ile	Phe	Met	Glu	Ser	His	Ile	Glu	Ala	Phe	Ile	Ser		
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tgc	tac	ctg	ctc	ttg	gat	aag	ctg	atc	gag	cct	cat	gca	tcg	ccg	aag	2083	
Cys	Tyr	Leu	Leu	Leu	Asp	Lys	Leu	Ile	Glu	Pro	His	Ala	Ser	Pro	Lys		

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Glu	Leu	Asp	Met	His	His	Val	Ser	Lys	Gln	Ser	Glu	Phe	Thr	Asp	Ser					
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Val	Arg	Gly	Lys	Arg	Glu	Gln	Met	Glu	Asp	Arg	Val	Ile	Arg	Ser	Met					
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 Lys Arg Lys Ala Pro Ala Leu Lys Pro Lys Gly Leu Thr Ala Lys Phe
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 Phe His Arg Asp Leu Thr Gly Val Gly Gly Arg Thr Gly Arg Leu Asn
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 Lys Asn Val His Pro Thr Asn Pro Asp Leu Ser Tyr Gln Pro Val Ser
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 Asp Val Tyr Thr Pro Gln Ser Ala Asp His Lys Gly Ile Lys Thr Arg

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Val Pro Asp Lys Asp Val Val Ala Ala Ser Gly Tyr Gln Ile Gln Pro
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Tyr Met Ile Gln Leu Arg Asp Leu Leu Tyr Lys Val Met Thr Gln Gly
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Gly Asn Ala Asn Leu Thr Ala Leu Ser Ile Phe Met Glu Ser His Ile
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Leu Glu Ile Ile Ile Cys Tyr Leu Leu Leu Asp Lys Leu Ile Glu Pro
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His Ala Ser Pro Lys Tyr Leu Ile Ile Asp Glu Val Gln Asp Asn Ser
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Val Phe Glu Phe Val Phe Ala Leu Arg Phe Ala Ala Lys His Asn Thr
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Ser Leu Tyr Leu Val Gly Asp Ser Ser Gln Thr Leu Tyr Glu Phe Arg
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Ser Ala Asn Pro Lys Ala Leu Asn Ser Leu Glu Ala Ser Gly Val Phe
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Gly Ile Gln Leu Tyr Ala Asn Ser Phe Asp Ala Pro Thr Ala Asp Ser
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Phe Asp Ala Ala Ile Leu Asn Asn Glu Gln Thr Ile Val Leu Ala His
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Pro Ser Ile Thr Val Arg Asn Leu Gln Ser Asp Lys Gly Phe Asn Asn
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Thr Val Phe Ser Thr Phe Ile Lys Asp Phe Trp Phe Glu Val Thr Ala
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Ala Leu Ala Thr Leu Glu Ala Glu Gln Glu Thr Arg Ala Leu Ala Ala
1060 1065 1070

Ala Glu Ala Gln Ala Gln Ala Leu Leu Leu Glu His Asn Pro Trp Leu
1075 1080 1085

Arg Asp Leu Ser Asp Glu Glu Val Thr Ala Leu Thr Glu Gln Glu Ile

1090	1095	1100
Ile Asn Asn Val Glu Pro Ala Leu Gln Ile Glu Glu Glu Glu Glu Glu		
1105,	1110	1115 1120
Ala Arg Ala Leu Ala Ala Ala Glu Pro Ala Ile Gln Gln Tyr Leu Ser		
	1125	1130 1135
Gln Phe Ala Phe Asp Glu Phe Pro Asp Asp Asp Asn Val Ala Asn Thr		
	1140	1145 1150
Val Val His Val Ala Pro Gln Pro Ile Leu His Gln Ala Val Pro Ala		
	1155	1160 1165
Asp Val Thr Val Gln Ser Ser Thr Ala Pro Val Thr Pro Val Val Ala		
	1170	1175 1180
Asp Leu Glu Val Thr Thr Val Ala Ala Asp Pro Val Glu Pro Thr Ile		
1185	1190	1195 1200
Val Ala Ala Gln Pro Glu Val Asp Asp Asn Leu Val Tyr Ser Thr Ser		
	1205	1210 1215
Thr Pro Asn Ser His Ser Asp Val Ile Ala Val Asn Ser Asp Thr Ser		
	1220	1225 1230
Glu Asn Ala Ala Val Asn Pro Val Leu Ser Asp Ile Glu Ala Leu Arg		
	1235	1240 1245
Ala Ile Phe Asn Asn Gln Asp		
1250	1255	

<210> 2409

<211> 467

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (34)..(444)

<223> RXA01773

<400> 2409

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Met. Ile Thr His Ile Gln Ala

1

5

ggc ctg cat ctt ggt ggc tgc cgc gca gca ggt tta ctg cct ata cca 102
Gly Leu His Leu Gly Gly Cys Arg Ala Ala Gly Leu Leu Pro Ile Pro
10 15 20

gca cat att gat cat att gtg cgc ctg aca gcc gca gat ttc tat gac 150
Ala His Ile Asp His Ile Val Arg Leu Thr Ala Ala Asp Phe Tyr Asp
25 30 35

acc cag tca gca ccg cag ctg ctc agc aac act gtg ctt gat gta ttg 198
Thr Gln Ser Ala Pro Gln Leu Leu Ser Asn Thr Val Leu Asp Val Leu
40 45 50 55

gac acc acc act caa gac ttg aag gca ttg tgg cct gtt gca gaa cat 246

Asp Thr Thr Thr Gln Asp Leu Lys Ala Leu Trp Pro Val Ala Glu His
 60 65 70
 att gct aca acc att cct gaa tct gag aac gtg ctt atc cac tgc cag 294
 Ile Ala Thr Thr Ile Pro Glu Ser Glu Asn Val Leu Ile His Cys Gln
 75 80 85
 atg ggt atc aac cgc tca gct gca ctc atg aca cgg gtg ttg atg ttg 342
 Met Gly Ile Asn Arg Ser Ala Ala Leu Met Thr Arg Val Leu Met Leu
 90 95 100
 cgc aac gat tgc acc gcc gat gaa gca att gca ctg ctg cgt gat cga 390
 Arg Asn Asp Cys Thr Ala Asp Glu Ala Ile Ala Leu Leu Arg Asp Arg
 105 110 115
 cgc tca ccg ttt gta ctg ttc aat gag cat ttt gtg gaa caa ctt cga 438
 Arg Ser Pro Phe Val Leu Phe Asn Glu His Phe Val Glu Gln Leu Arg
 120 125 130 135
 gca ctg taagcgctca aagacccatt acc 467
 Ala Leu

<210> 2410
 <211> 137
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2410
 Met Ile Thr His Ile Gln Ala Gly Leu His Leu Gly Gly Cys Arg Ala
 1 5 10 15
 Ala Gly Leu Leu Pro Ile Pro Ala His Ile Asp His Ile Val Arg Leu
 20 25 30
 Thr Ala Ala Asp Phe Tyr Asp Thr Gln Ser Ala Pro Gln Leu Leu Ser
 35 40 45
 Asn Thr Val Leu Asp Val Leu Asp Thr Thr Thr Gln Asp Leu Lys Ala
 50 55 60
 Leu Trp Pro Val Ala Glu His Ile Ala Thr Thr Ile Pro Glu Ser Glu
 65 70 75 80
 Asn Val Leu Ile His Cys Gln Met Gly Ile Asn Arg Ser Ala Ala Leu
 85 90 95
 Met Thr Arg Val Leu Met Leu Arg Asn Asp Cys Thr Ala Asp Glu Ala
 100 105 110
 Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro Phe Val Leu Phe Asn Glu
 115 120 125
 His Phe Val Glu Gln Leu Arg Ala Leu
 130 135

<210> 2411
 <211> 687
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXA01775

<400> 2411

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ttttattccc cgagaatgtc ctagaaagga actcgacccc atg tcc tat tca ctc 115
                                         Met Ser Tyr Ser Leu
                                         1                               5

att att tct aaa gca cca acc cac tcc atg cct ttt aat gag gct gaa 163
Ile Ile Ser Lys Ala Pro Thr His Ser Met Pro Phe Asn Glu Ala Glu
                        10                        15                        20

ctc cta gag ctt gtc gat gaa ctg cac tcc gac aac acc gtg aaa aag 211
Leu Leu Glu Leu Val Asp Glu Leu His Ser Asp Asn Thr Val Lys Lys
                        25                        30                        35

ccg gtt att gtg cca ctc ccc gat gat ttc tcc tac acc gta gat agc 259
Pro Val Ile Val Pro Leu Pro Asp Asp Phe Ser Tyr Thr Val Asp Ser
                        40                        45                        50

gcc gtg cga cta cat gat ttg ggt gtt gac cag gaa ctg act gac tgg 307
Ala Val Arg Leu His Asp Leu Gly Val Asp Gln Glu Leu Thr Asp Trp
                        55                        60                        65

att act gca caa gtt gct gca gcc tat cca aac cag atc gtc tca gag 355
Ile Thr Ala Gln Val Ala Ala Ala Tyr Pro Asn Gln Ile Val Ser Glu
                        70                        75                        80                        85

att gct gct gcc cct gat ccg caa gcc aag acc tta ttc tcc gcc aat 403
Ile Ala Ala Ala Pro Asp Pro Gln Ala Lys Thr Leu Phe Ser Ala Asn
                        90                        95                        100

gcg tat aac acc agg tct ttt ggt act ttt tgg act gag cac cct att 451
Ala Tyr Asn Thr Arg Ser Phe Gly Thr Phe Trp Thr Glu His Pro Ile
                        105                        110                        115

aca cag ctc caa tac aag cgc tgc tac caa att gtc atc gag aac gtt 499
Thr Gln Leu Gln Tyr Lys Arg Cys Tyr Gln Ile Val Ile Glu Asn Val
                        120                        125                        130

acg ggt gtc tat cat ccg tta cct gtt gat aac tac cgc tac gta ccc 547
Thr Gly Val Tyr His Pro Leu Pro Val Asp Asn Tyr Arg Tyr Val Pro
                        135                        140                        145

cct gtc acg ccc tca ttg cca cag ccg gtc tac cac gaa gct atc gcc 595
Pro Val Thr Pro Ser Leu Pro Gln Pro Val Tyr His Glu Ala Ile Ala
                        150                        155                        160                        165

tta aat gag tct gat gtc gct gat cac ggt act cgt gca gcc aag cac 643
Leu Asn Glu Ser Asp Val Ala Asp His Gly Thr Arg Ala Ala Lys His
                        170                        175                        180

gca atg atc aac cgc aac gta taaccacaca cgccacagat act 687
Ala Met Ile Asn Arg Asn Val
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<210> 2412

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 2412

Met Ser Tyr Ser Leu Ile Ile Ser Lys Ala Pro Thr His Ser Met Pro
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Phe Asn Glu Ala Glu Leu Leu Glu Leu Val Asp Glu Leu His Ser Asp
 20 25 30

Asn Thr Val Lys Lys Pro Val Ile Val Pro Leu Pro Asp Asp Phe Ser
 35 40 45

Tyr Thr Val Asp Ser Ala Val Arg Leu His Asp Leu Gly Val Asp Gln
 50 55 60

Glu Leu Thr Asp Trp Ile Thr Ala Gln Val Ala Ala Ala Tyr Pro Asn
 65 70 75 80

Gln Ile Val Ser Glu Ile Ala Ala Ala Pro Asp Pro Gln Ala Lys Thr
 85 90 95

Leu Phe Ser Ala Asn Ala Tyr Asn Thr Arg Ser Phe Gly Thr Phe Trp
 100 105 110

Thr Glu His Pro Ile Thr Gln Leu Gln Tyr Lys Arg Cys Tyr Gln Ile
 115 120 125

Val Ile Glu Asn Val Thr Gly Val Tyr His Pro Leu Pro Val Asp Asn
 130 135 140

Tyr Arg Tyr Val Pro Pro Val Thr Pro Ser Leu Pro Gln Pro Val Tyr
 145 150 155 160

His Glu Ala Ile Ala Leu Asn Glu Ser Asp Val Ala Asp His Gly Thr
 165 170 175

Arg Ala Ala Lys His Ala Met Ile Asn Arg Asn Val
 180 185

<210> 2413

<211> 1575

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1552)

<223> RXA01776

<400> 2413

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tctcaccocat ccccatcac tattaaagaa aatcaccatc atg acc cac act gat 115
 Met Thr His Thr Asp
 1 5

acc cca gcc cct gca cac ggc gta aca ccg agt gaa ttc gct gtt acc	163
Thr Pro Ala Pro Ala His Gly Val Thr Pro Ser Glu Phe Ala Val Thr	
10 15 20	
tca cac gaa ctc acc acc tca cca aca cct agt ccg aca cag gtc gct	211
Ser His Glu Leu Thr Thr Ser Pro Thr Pro Ser Pro Thr Gln Val Ala	
25 30 35	
att gca gcc cag gaa aaa att cgc cag cgc aag ctc gaa gag ctt aaa	259
Ile Ala Ala Gln Glu Lys Ile Arg Gln Arg Lys Leu Glu Glu Leu Lys	
40 45 50	
gca aaa aag cgc aca gac acg aca gct caa cca ctt cta cct gca cct	307
Ala Lys Lys Arg Thr Asp Thr Thr Ala Gln Pro Leu Leu Pro Ala Pro	
55 60 65	
gtg ctg cat aca cgc cca ctc ccc tca ccg aat cca ccg cga cca tct	355
Val Leu His Thr Arg Pro Leu Pro Ser Pro Asn Pro Pro Arg Pro Ser	
70 75 80 85	
cca ccg gca cct acc act gga cac tgg gaa ctt ctt att gtc agg tca	403
Pro Pro Ala Pro Thr Thr Gly His Trp Glu Leu Leu Ile Val Arg Ser	
90 95 100	
cag cag aag aaa atg acc gca gcc aat ccc ttt ctc aaa ttc ctt cat	451
Gln Gln Lys Lys Met Thr Ala Ala Asn Pro Phe Leu Lys Phe Leu His	
105 110 115	
ctc ggt aaa gcc ttc aac gtg aaa gac cta ggg ctc acc tgc gat cgc	499
Leu Gly Lys Ala Phe Asn Val Lys Asp Leu Gly Leu Thr Cys Asp Arg	
120 125 130	
acc act gat gtt gac ctc tca cgg ctt ggc aag ctc aat ccg ccc agc	547
Thr Thr Asp Val Asp Leu Ser Arg Leu Gly Lys Leu Asn Pro Pro Ser	
135 140 145	
tca ctt atc ctt gaa cta gca acg gca ctt gac ctg cat cca ttc ctc	595
Ser Leu Ile Leu Glu Leu Ala Thr Ala Leu Asp Leu His Pro Phe Leu	
150 155 160 165	
tca gtc gca ctc tct tcg cac agt gcg gtc aac gcc cgt cgc aac caa	643
Ser Val Ala Leu Ser Ser His Ser Ala Val Asn Ala Arg Arg Asn Gln	
170 175 180	
ctt gaa tta acc ctg cac aac cat gac act cag ggc aca gca tta ggt	691
Leu Glu Leu Thr Leu His Asn His Asp Thr Gln Gly Thr Ala Leu Gly	
185 190 195	
cac agc gtt act atg gtc cag cta ccc gag gtc att aat cga gct gct	739
His Ser Val Thr Met Val Gln Leu Pro Glu Val Ile Asn Arg Ala Ala	
200 205 210	
gta gag ccc tat atc aaa ccc aag ggc tcg ggc aat gac ccg ctt gac	787
Val Glu Pro Tyr Ile Lys Pro Lys Gly Ser Gly Asn Asp Pro Leu Asp	
215 220 225	
caa agc ctg aac cac cgc gca ccc acc gta agt gac gtg caa aaa gcc	835
Gln Ser Leu Asn His Arg Ala Pro Thr Val Ser Asp Val Gln Lys Ala	
230 235 240 245	

ctt gtg cag gaa aac aca ggc acg gca aca gac agc aac aac tac ctg	883
Leu Val Gln Glu Asn Thr Gly Thr Ala Thr Asp Ser Asn Asn Tyr Leu	
250 255 260	
ctt cct ttt gat cct gat tct ggt gca cca aaa acc acc gcg ctt aat	931
Leu Pro Phe Asp Pro Asp Ser Gly Ala Pro Lys Thr Thr Ala Leu Asn	
265 270 275	
gcg cct aat aag gat ctc cta cag gcc agg cat gag ctt gcc tat att	979
Ala Pro Asn Lys Asp Leu Leu Gln Ala Arg His Glu Leu Ala Tyr Ile	
280 285 290	
ccc gag atc ccc gcc att gca tgc tgg ctc gat cac ctt gac ccc atc	1027
Pro Glu Ile Pro Ala Ile Ala Ser Trp Leu Asp His Leu Asp Pro Ile	
295 300 305	
atg cgt gtg cac cgt agt ctt gcg ctt tca att ttc cca gtg cag ctt	1075
Met Arg Val His Arg Ser Leu Ala Leu Ser Ile Phe Pro Val Gln Leu	
310 315 320 325	
cta cgt gct gcc gtt gag aat ctc cct cat aac gta acc gat ctg cat	1123
Leu Arg Ala Ala Val Glu Asn Leu Pro His Asn Val Thr Asp Leu His	
330 335 340	
aat cac ctt gat cct gag gat ctg ctc cct gag gaa ctc acc acc tgg	1171
Asn His Leu Asp Pro Glu Asp Leu Leu Pro Glu Glu Leu Thr Thr Trp	
345 350 355	
ctc gat cac ctc ttc gat gca gac tta acc gct ctc gct tca tgc cca	1219
Leu Asp His Leu Phe Asp Ala Asp Leu Thr Ala Leu Ala Ser Cys Pro	
360 365 370	
cag ctt gca cca cct atc gtg cgc agc cac aat cac gcc aaa gcg atc	1267
Gln Leu Ala Pro Pro Ile Val Arg Ser His Asn His Ala Lys Ala Ile	
375 380 385	
gca gct atc acc gtg acc tct gtc atg gac gct ctc atc gcc aaa act	1315
Ala Ala Ile Thr Val Thr Ser Val Met Asp Ala Leu Ile Ala Lys Thr	
390 395 400 405	
ctt gat gcg cat gac gat cca ctg ccc tca cta ccg gag ttt gta gaa	1363
Leu Asp Ala His Asp Asp Pro Leu Pro Ser Leu Pro Glu Phe Val Glu	
410 415 420	
cta ctg cgt gac gct gta gcc cag ctc gca gcg cat ttt aag cag cag	1411
Leu Leu Arg Asp Ala Val Ala Gln Leu Ala Ala His Phe Lys Gln Gln	
425 430 435	
cgc ggc gag gta cta ccg cag ccc aat ggc ttg cga tac gcc acc gac	1459
Arg Gly Glu Val Leu Pro Gln Pro Asn Gly Leu Arg Tyr Ala Thr Asp	
440 445 450	
ttt ggc ctg ctc tct tat att gcc gat ggc tta cat gaa tat gca ctt	1507
Phe Gly Leu Leu Ser Tyr Ile Ala Asp Gly Leu His Glu Tyr Ala Leu	
455 460 465	
gcc atc gac ttc ggg ctg atc tac ccg aat gaa ctc atc acc gag	1552
Ala Ile Asp Phe Gly Leu Ile Tyr Pro Asn Glu Leu Ile Thr Glu	
470 475 480	
taaaccact cctagaaagg tct	1575

<210> 2414

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 2414

Met Thr His Thr Asp Thr Pro Ala Pro Ala His Gly Val Thr Pro Ser
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Glu Phe Ala Val Thr Ser His Glu Leu Thr Thr Ser Pro Thr Pro Ser
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Pro Thr Gln Val Ala Ile Ala Ala Gln Glu Lys Ile Arg Gln Arg Lys
35 40 45

Leu Glu Glu Leu Lys Ala Lys Lys Arg Thr Asp Thr Thr Ala Gln Pro
50 55 60

Leu Leu Pro Ala Pro Val Leu His Thr Arg Pro Leu Pro Ser Pro Asn
65 70 75 80

Pro Pro Arg Pro Ser Pro Pro Ala Pro Thr Thr Gly His Trp Glu Leu
85 90 95

Leu Ile Val Arg Ser Gln Gln Lys Lys Met Thr Ala Ala Asn Pro Phe
100 105 110

Leu Lys Phe Leu His Leu Gly Lys Ala Phe Asn Val Lys Asp Leu Gly
115 120 125

Leu Thr Cys Asp Arg Thr Thr Asp Val Asp Leu Ser Arg Leu Gly Lys
130 135 140

Leu Asn Pro Pro Ser Ser Leu Ile Leu Glu Leu Ala Thr Ala Leu Asp
145 150 155 160

Leu His Pro Phe Leu Ser Val Ala Leu Ser Ser His Ser Ala Val Asn
165 170 175

Ala Arg Arg Asn Gln Leu Glu Leu Thr Leu His Asn His Asp Thr Gln
180 185 190

Gly Thr Ala Leu Gly His Ser Val Thr Met Val Gln Leu Pro Glu Val
195 200 205

Ile Asn Arg Ala Ala Val Glu Pro Tyr Ile Lys Pro Lys Gly Ser Gly
210 215 220

Asn Asp Pro Leu Asp Gln Ser Leu Asn His Arg Ala Pro Thr Val Ser
225 230 235 240

Asp Val Gln Lys Ala Leu Val Gln Glu Asn Thr Gly Thr Ala Thr Asp
245 250 255

Ser Asn Asn Tyr Leu Leu Pro Phe Asp Pro Asp Ser Gly Ala Pro Lys
260 265 270

Thr Thr Ala Leu Asn Ala Pro Asn Lys Asp Leu Leu Gln Ala Arg His
275 280 285

Glu Leu Ala Tyr Ile Pro Glu Ile Pro Ala Ile Ala Ser Trp Leu Asp
 290 295 300
 His Leu Asp Pro Ile Met Arg Val His Arg Ser Leu Ala Leu Ser Ile
 305 310 315 320
 Phe Pro Val Gln Leu Leu Arg Ala Ala Val Glu Asn Leu Pro His Asn
 325 330 335
 Val Thr Asp Leu His Asn His Leu Asp Pro Glu Asp Leu Leu Pro Glu
 340 345 350
 Glu Leu Thr Thr Trp Leu Asp His Leu Phe Asp Ala Asp Leu Thr Ala
 355 360 365
 Leu Ala Ser Cys Pro Gln Leu Ala Pro Pro Ile Val Arg Ser His Asn
 370 375 380
 His Ala Lys Ala Ile Ala Ala Ile Thr Val Thr Ser Val Met Asp Ala
 385 390 395 400
 Leu Ile Ala Lys Thr Leu Asp Ala His Asp Asp Pro Leu Pro Ser Leu
 405 410 415
 Pro Glu Phe Val Glu Leu Leu Arg Asp Ala Val Ala Gln Leu Ala Ala
 420 425 430
 His Phe Lys Gln Gln Arg Gly Glu Val Leu Pro Gln Pro Asn Gly Leu
 435 440 445
 Arg Tyr Ala Thr Asp Phe Gly Leu Leu Ser Tyr Ile Ala Asp Gly Leu
 450 455 460
 His Glu Tyr Ala Leu Ala Ile Asp Phe Gly Leu Ile Tyr Pro Asn Glu
 465 470 475 480
 Leu Ile Thr Glu

<210> 2415

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXA01777

<400> 2415

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tcatacaccga gtaaaccac tctagaaag gtctttaccc atg tct cgt atc atc 115
 Met Ser Arg Ile Ile
 1 5

act gct ccc gtc cac aag cct tat att att gct cgt gaa gtc aag ggg 163
 Thr Ala Pro Val His Lys Pro Tyr Ile Ile Ala Arg Glu Val Lys Gly
 10 15 20

gtc tcc cat gtc cac gac act gtt ggc ggc aag tgg cag gcc acc ttg 211
 Val Ser His Val His Asp Thr Val Gly Gly Lys Trp Gln Ala Thr Leu
 25 30 35

cac aca ctt aaa ccg ggg ccc tcc tgg ccg aaa ccg tca cag ttc act 259
 His Thr Leu Lys Pro Gly Pro Ser Trp Pro Lys Pro Ser Gln Phe Thr
 40 45 50

gcg cct aaa tcc acg tcc atc tgg ttt att gcg gta gca acc cac cca 307
 Ala Pro Lys Ser Thr Ser Ile Trp Phe Ile Ala Val Ala Thr His Pro
 55 60 65

cgt aac cca cgg gca cgc aaa ggt acc cta ctt ggt cgc ggt ggt ctt 355
 Arg Asn Pro Arg Ala Arg Lys Gly Thr Leu Leu Gly Arg Gly Gly Leu
 70 75 80 85

tac gaa ctc aaa gac act gat ctg aac ttt ctc aca gag cga cag gat 403
 Tyr Glu Leu Lys Asp Thr Asp Leu Asn Phe Leu Thr Glu Arg Gln Asp
 90 95 100

ttg ctc gcc aca tct acc tct cgt gac cca gag gat tgc cgt tta cgc 451
 Leu Leu Ala Thr Ser Thr Ser Arg Asp Pro Glu Asp Cys Arg Leu Arg
 105 110 115

ttt aat tcg cgt cac gat gca gca gca ttt tta cat gct aac gcc cgc 499
 Phe Asn Ser Arg His Asp Ala Ala Ala Phe Leu His Ala Asn Ala Arg
 120 125 130

cac atc aac aag ctt ttt cat cca gca cta ggt cat gct cgc tac gat 547
 His Ile Asn Lys Leu Phe His Pro Ala Leu Gly His Ala Arg Tyr Asp
 135 140 145

ctc ata gat gtg taagcacaac gcttagctta tga 582
 Leu Ile Asp Val
 150

<210> 2416

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 2416

Met Ser Arg Ile Ile Thr Ala Pro Val His Lys Pro Tyr Ile Ile Ala
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Arg Glu Val Lys Gly Val Ser His Val His Asp Thr Val Gly Gly Lys
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Trp Gln Ala Thr Leu His Thr Leu Lys Pro Gly Pro Ser Trp Pro Lys
 35 40 45

Pro Ser Gln Phe Thr Ala Pro Lys Ser Thr Ser Ile Trp Phe Ile Ala
 50 55 60

Val Ala Thr His Pro Arg Asn Pro Arg Ala Arg Lys Gly Thr Leu Leu
 65 70 75 80

Gly Arg Gly Gly Leu Tyr Glu Leu Lys Asp Thr Asp Leu Asn Phe Leu
 85 90 95

Thr Glu Arg Gln Asp Leu Leu Ala Thr Ser Thr Ser Arg Asp Pro Glu
 100 105 110

Asp Cys Arg Leu Arg Phe Asn Ser Arg His Asp Ala Ala Ala Phe Leu
 115 120 125

His Ala Asn Ala Arg His Ile Asn Lys Leu Phe His Pro Ala Leu Gly
 130 135 140

His Ala Arg Tyr Asp Leu Ile Asp Val
 145 150

<210> 2417

<211> 1260

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1237)

<223> RXA01778

<400> 2417

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 Met Leu Tyr Gln His
 1 5

acc aca cgc ggg ctg atc att agt gac gcg atc atc gcg aaa atc agc 163
 Thr Thr Arg Gly Leu Ile Ile Ser Asp Ala Ile Ile Ala Lys Ile Ser
 10 15 20

caa gtc aac caa ctg ctg cta cta aga ccc acg ctg ttg caa gac aaa 211
 Gln Val Asn Gln Leu Leu Leu Leu Arg Pro Thr Leu Leu Gln Asp Lys
 25 30 35

gat atg cac cat gcg aca ttg agt agc gac acc cca tca att cgc agt 259
 Asp Met His His Ala Thr Leu Ser Ser Asp Thr Pro Ser Ile Arg Ser
 40 45 50

cgc cgt cgc tcc tat cgc gag aat aaa gcc gcc tat gcg acc acg agc 307
 Arg Arg Arg Ser Tyr Arg Glu Asn Lys Ala Ala Tyr Ala Thr Thr Ser
 55 60 65

acc atc aga aac cgt gag acc ttt ttc agc aca tct gat att gat ttc 355
 Thr Ile Arg Asn Arg Glu Thr Phe Phe Ser Thr Ser Asp Ile Asp Phe
 70 75 80 85

gcc ata ctc atg att cag gac gta caa gaa tct ctc gta tct ttt gac 403
 Ala Ile Leu Met Ile Gln Asp Val Gln Glu Ser Leu Val Ser Phe Asp
 90 95 100

ccc acc ttg gct caa gat atg aag cca aga acc aac gca gtc att tct 451
 Pro Thr Leu Ala Gln Asp Met Lys Pro Arg Thr Asn Ala Val Ile Ser
 105 110 115

gca ctc aat gag cta cgc gag cca ctg gat acc ttc tac cgt gcc cat 499
 Ala Leu Asn Glu Leu Arg Glu Pro Leu Asp Thr Phe Tyr Arg Ala His

120	125	130	
gaa tac ggt gac atc atc agc gat ggt gct tat gag ttc gat cat gct			547
Glu Tyr Gly Asp Ile Ile Ser Asp Gly Ala Tyr Glu Phe Asp His Ala			
135	140	145	
gcc att gat gca caa cac agc ctt agt gaa ctc gtt gcc ggt ctg cat			595
Ala Ile Asp Ala Gln His Ser Leu Ser Glu Leu Val Ala Gly Leu His			
150	155	160	165
aat tat gac aac ctc atg ttt ccc cag gaa acc gct ccg ttg atg agt			643
Asn Tyr Asp Asn Leu Met Phe Pro Gln Glu Thr Ala Pro Leu Met Ser			
	170	175	180
gaa tcc aat ggc att cag ctg gct cag tac tat aag tcc acc aaa ctc			691
Glu Ser Asn Gly Ile Gln Leu Ala Gln Tyr Tyr Lys Ser Thr Lys Leu			
	185	190	195
gat gag tca caa ttg acg gtg gaa cct aat gag cct ggt atc agc att			739
Asp Glu Ser Gln Leu Thr Val Glu Pro Asn Glu Pro Gly Ile Ser Ile			
	200	205	210
atg tgg cac gcc cat gat ttc acc tgg tct tgc cta gtg cgc tat gac			787
Met Trp His Ala His Asp Phe Thr Trp Ser Cys Leu Val Arg Tyr Asp			
	215	220	225
gac atg aac cgt tac cct gag cat ttc agc att tct ttt aaa gac atg			835
Asp Met Asn Arg Tyr Pro Glu His Phe Ser Ile Ser Phe Lys Asp Met			
230	235	240	245
ctg atc cct gaa cag atc tat act ttc cac ttc acc cca cgt gag gca			883
Leu Ile Pro Glu Gln Ile Tyr Thr Phe His Phe Thr Pro Arg Glu Ala			
	250	255	260
atg caa ctg cgc aag gga ctt ttt aat gcc atc gct gcc tac aag tct			931
Met Gln Leu Arg Lys Gly Leu Phe Asn Ala Ile Ala Ala Tyr Lys Ser			
	265	270	275
cag aca tgg ggt gat gag aac act gat ctc acc aag gct gaa ctc gaa			979
Gln Thr Trp Gly Asp Glu Asn Thr Asp Leu Thr Lys Ala Glu Leu Glu			
	280	285	290
ttt ggt ggc acc tcc atg acc ttc cgc gcc ggc ctc tca cag ctt agc			1027
Phe Gly Gly Thr Ser Met Thr Phe Arg Ala Gly Leu Ser Gln Leu Ser			
295	300	305	
gtc acc gga cct cct gat cac cgc cag gtg ttc tgc ttg tcg tct tct			1075
Val Thr Gly Pro Pro Asp His Arg Gln Val Phe Cys Leu Ser Ser Ser			
310	315	320	325
ggt cgt gag gat cac aac acc ccg cca aac atg cga gac gga cat gtc			1123
Gly Arg Glu Asp His Asn Thr Pro Pro Asn Met Arg Asp Gly His Val			
	330	335	340
att gat att gcg gtt act caa ttg tcc acc ctg cgt aac ctc att cgg			1171
Ile Asp Ile Ala Val Thr Gln Leu Ser Thr Leu Arg Asn Leu Ile Arg			
	345	350	355
gta ctg tgc acc act cac ccg gat cat tca cca gca ctg cta cct tat			1219
Val Leu Cys Thr Thr His Pro Asp His Ser Pro Ala Leu Leu Pro Tyr			
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1260

<210> 2418

<211> 379

<212> PRT

<213> Corynebacterium glutamicum

<400> 2418

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Leu Leu Gln Asp Lys Asp Met His His Ala Thr Leu Ser Ser Asp Thr
 35 40 45

Pro Ser Ile Arg Ser Arg Arg Arg Ser Tyr Arg Glu Asn Lys Ala Ala
 50 55 60

Tyr Ala Thr Thr Ser Thr Ile Arg Asn Arg Glu Thr Phe Phe Ser Thr
 65 70 75 80

Ser Asp Ile Asp Phe Ala Ile Leu Met Ile Gln Asp Val Gln Glu Ser
 85 90 95

Leu Val Ser Phe Asp Pro Thr Leu Ala Gln Asp Met Lys Pro Arg Thr
 100 105 110

Asn Ala Val Ile Ser Ala Leu Asn Glu Leu Arg Glu Pro Leu Asp Thr
 115 120 125

Phe Tyr Arg Ala His Glu Tyr Gly Asp Ile Ile Ser Asp Gly Ala Tyr
 130 135 140

Glu Phe Asp His Ala Ala Ile Asp Ala Gln His Ser Leu Ser Glu Leu
 145 150 155 160

Val Ala Gly Leu His Asn Tyr Asp Asn Leu Met Phe Pro Gln Glu Thr
 165 170 175

Ala Pro Leu Met Ser Glu Ser Asn Gly Ile Gln Leu Ala Gln Tyr Tyr
 180 185 190

Lys Ser Thr Lys Leu Asp Glu Ser Gln Leu Thr Val Glu Pro Asn Glu
 195 200 205

Pro Gly Ile Ser Ile Met Trp His Ala His Asp Phe Thr Trp Ser Cys
 210 215 220

Leu Val Arg Tyr Asp Asp Met Asn Arg Tyr Pro Glu His Phe Ser Ile
 225 230 235 240

Ser Phe Lys Asp Met Leu Ile Pro Glu Gln Ile Tyr Thr Phe His Phe
 245 250 255

Thr Pro Arg Glu Ala Met Gln Leu Arg Lys Gly Leu Phe Asn Ala Ile

260	265	270
Ala Ala Tyr Lys Ser Gln Thr Trp Gly Asp Glu Asn Thr Asp Leu Thr		
275	280	285
Lys Ala Glu Leu Glu Phe Gly Gly Thr Ser Met Thr Phe Arg Ala Gly		
290	295	300
Leu Ser Gln Leu Ser Val Thr Gly Pro Pro Asp His Arg Gln Val Phe		
305	310	315
Cys Leu Ser Ser Ser Gly Arg Glu Asp His Asn Thr Pro Pro Asn Met		
325	330	335
Arg Asp Gly His Val Ile Asp Ile Ala Val Thr Gln Leu Ser Thr Leu		
340	345	350
Arg Asn Leu Ile Arg Val Leu Cys Thr Thr His Pro Asp His Ser Pro		
355	360	365
Ala Leu Leu Pro Tyr Gly Gln Gln Tyr Thr Ile		
370	375	

<210> 2419

<211> 1542

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1519)

<223> RXA01779

<400> 2419

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Arg Thr His Arg Ala Leu Gly Leu Ala Ala Leu Thr Ala Thr Ala Leu
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cta ctg agc tca tgc tcg acc acc gct gac ctt ctc ggc gcc gat tct 211
Leu Leu Ser Ser Cys Ser Thr Thr Ala Asp Leu Leu Gly Ala Asp Ser
          25          30          35
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Val Ala Gln Ala Val Thr Asp Gly Gly Ser Ala Leu Asp Pro Thr Ala
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gct cat gtg ctc acc atc acc aat gcc act gca atg act ctt gct gag 307
Ala His Val Leu Thr Ile Thr Asn Ala Thr Ala Met Thr Leu Ala Glu
          55          60          65
cta cca gaa aac acc gac cct gac gca gcc aat aac acg gag cca aca 355
Leu Pro Glu Asn Thr Asp Pro Asp Ala Ala Asn Asn Thr Glu Pro Thr
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Gly Ser Glu Gln Pro Thr Val Ala Ala Met Ala Asp Pro Glu Asn Asn	
120 125 130	
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Ala Glu Leu Thr Thr Ala His Ile Leu Glu Ile Asp Pro Ala Thr Gly	
135 140 145	
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Thr Ala Thr Pro Arg Gln Asp Ile Ala Leu Thr Glu Asp Phe Gln Thr	
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Met Ala Ser Ser Phe Ser Gln Ile Arg Asn Gly Trp Gly Thr Thr Gln	
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Leu Ile Gly Gln His Pro Asp Asp Pro Lys Gln Pro Ile Arg Ser Ala	
185 190 195	
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Asp Thr Trp Thr Val Thr Gly Ser Thr Gln Ile Thr Gly Phe Asn Thr	
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Asn Thr Pro Thr Gly Thr Glu Asp Ala Ala Tyr Thr Met Pro Ala Thr	
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Glu Pro Ala Val Gly Leu Cys Ala Leu Glu Ser Gly Ser Asp Ala Pro	
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Leu Asp Glu His Arg Glu Leu Ser Thr Ser Ala Leu Arg Thr Ala Ser	
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Val Leu Ser Ser Ser Gly Ser Ala Thr Leu Lys Leu His Asp Pro Met	
265 270 275	
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Val Met Ser Ala Thr Gly Ile Val Gln Ala Arg Ala Tyr Val Asp Gly	
280 285 290	
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Ile Thr Ile Glu Glu Ser Glu Ala Ala Gln Ala Glu Ser Asp Ala Gln	
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Ala Ala Thr Asp His Pro Leu Ala Ala Leu Gly Leu Ser Asn Pro Thr
 330 335 340

agc tca gcg ttg gtt cca ggt ctt gct gag ctt gat tgt ctc agt gct 1171
 Ser Ser Ala Leu Val Pro Gly Leu Ala Glu Leu Asp Cys Leu Ser Ala
 345 350 355

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 Asp Gln Ala Ala Thr Trp His Asn Arg Asp Thr Ser Ile Gly Thr Gly
 360 365 370

aag ccc agc gtg ctt gct gtc atc aac gcg gaa atg gcc gat gac ttt 1267
 Lys Pro Ser Val Leu Ala Val Ile Asn Ala Glu Met Ala Asp Asp Phe
 375 380 385

acc ctg cag ctg ttg agc tca ggt gcc acc act gcc gaa acg cag ctt 1315
 Thr Leu Gln Leu Leu Ser Ser Gly Ala Thr Thr Ala Glu Thr Gln Leu
 390 395 400 405

gcc cag ctg ccg gat gaa acc gcg ttc gtg ctc att gac cca tca tct 1363
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ccg gca cca aca acc cag att aat tct att gct gtt gat gag cgc gac 1459
 Pro Ala Pro Thr Thr Gln Ile Asn Ser Ile Ala Val Asp Glu Arg Asp
 440 445 450

ccc aac atc atc tac gcc act ttt agc ggc gat gac cac ctg tac caa 1507
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<210> 2420

<211> 473

<212> PRT

<213> Corynebacterium glutamicum

<400> 2420

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 20 25 30

Leu Gly Ala Asp Ser Val Ala Gln Ala Val Thr Asp Gly Gly Ser Ala
 35 40 45

Leu Asp Pro Thr Ala Ala His Val Leu Thr Ile Thr Asn Ala Thr Ala
 50 55 60

Met Thr Leu Ala Glu Leu Pro Glu Asn Thr Asp Pro Asp Ala Ala Asn
 65 70 75 80

Asn Thr Glu Pro Thr Met Ala Gln Ser Ala Leu Lys Arg Ile Tyr Gly
 85 90 95
 Leu Glu Ile Ala Ala Asp Gly Thr Leu Ile Ala Val Ala Ala Pro Leu
 100 105 110
 Thr Ser Arg Asn Ser Gly Ser Glu Gln Pro Thr Val Ala Ala Met Ala
 115 120 125
 Asp Pro Glu Asn Asn Ala Glu Leu Thr Thr Ala His Ile Leu Glu Ile
 130 135 140
 Asp Pro Ala Thr Gly Thr Ala Thr Pro Arg Gln Asp Ile Ala Leu Thr
 145 150 155 160
 Glu Asp Phe Gln Thr Met Ala Ser Ser Phe Ser Gln Ile Arg Asn Gly
 165 170 175
 Trp Gly Thr Thr Gln Leu Ile Gly Gln His Pro Asp Asp Pro Lys Gln
 180 185 190
 Pro Ile Arg Ser Ala Asp Thr Trp Thr Val Thr Gly Ser Thr Gln Ile
 195 200 205
 Thr Gly Phe Asn Thr Asn Thr Pro Thr Gly Thr Glu Asp Ala Ala Tyr
 210 215 220
 Thr Met Pro Ala Thr Glu Pro Ala Val Gly Leu Cys Ala Leu Glu Ser
 225 230 235 240
 Gly Ser Asp Ala Pro Leu Asp Glu His Arg Glu Leu Ser Thr Ser Ala
 245 250 255
 Leu Arg Thr Ala Ser Val Leu Ser Ser Ser Gly Ser Ala Thr Leu Lys
 260 265 270
 Leu His Asp Pro Met Val Met Ser Ala Thr Gly Ile Val Gln Ala Arg
 275 280 285
 Ala Tyr Val Asp Gly Glu Val Ile Asn Gln His Glu Ile Gly Asp Leu
 290 295 300
 Arg Glu Gln Leu Gly Ile Thr Ile Glu Glu Ser Glu Ala Ala Gln Ala
 305 310 315 320
 Glu Ser Asp Ala Gln Ala Ala Thr Asp His Pro Leu Ala Ala Leu Gly
 325 330 335
 Leu Ser Asn Pro Thr Ser Ser Ala Leu Val Pro Gly Leu Ala Glu Leu
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 Asp Cys Leu Ser Ala Asp Gln Ala Ala Thr Trp His Asn Arg Asp Thr
 355 360 365
 Ser Ile Gly Thr Gly Lys Pro Ser Val Leu Ala Val Ile Asn Ala Glu
 370 375 380
 Met Ala Asp Asp Phe Thr Leu Gln Leu Leu Ser Ser Gly Ala Thr Thr
 385 390 395 400
 Ala Glu Thr Gln Leu Ala Gln Leu Pro Asp Glu Thr Ala Phe Val Leu

	405		410		415
Ile Asp Pro Ser Ser Gly Ala Val Thr Asp Leu Phe Phe Ile Gln Ser					
	420		425		430
Leu Asn Thr Asp Leu Pro Ala Pro Thr Thr Gln Ile Asn Ser Ile Ala					
	435		440		445
Val Asp Glu Arg Asp Pro Asn Ile Ile Tyr Ala Thr Phe Ser Gly Asp					
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(475)

<223> RXA01780

<400> 2421

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Pro Lys Ala Ala Phe Tyr Pro Leu Thr Met Asp His Leu Thr Asp Leu
                                     10 15 20
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Gly Leu Asp Pro Glu Gln Leu Ile Asn Glu Leu Pro Thr Ile Thr Tyr
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Asp Val Gln Pro His Asn Val Phe Val Leu Gln Phe Ser Thr Ala Asp
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cgc agc acc gtg ttc ctc aaa gac aaa agt gtt gtc act cac gat cac 451
Arg Ser Thr Val Phe Leu Lys Asp Lys Ser Val Val Thr His Asp His
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ggg acc aat tgc tgt gat tcc gca taatcctgat gaagccagcg cca 498

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<210> 2422

<211> 125

<212> PRT

<213> Corynebacterium glutamicum

<400> 2422

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Pro Thr Ile Thr Tyr Asp Val Gln Pro His Asn Val Phe Val Leu Gln
35 40 45

Phe Ser Thr Ala Asp Val Arg Val Tyr Gln Glu Gly Asn Thr Leu Phe
50 55 60

Ile Arg Ser Ala Glu Leu Ile Asn Pro Glu Leu Arg Gln Arg Gln Arg
65 70 75 80

Thr Gln Leu Asn Asp Asp Leu Asn Asn Pro Ala Ser Leu Arg Val Cys
85 90 95

Asp Glu Ile Ser Gly Arg Ser Thr Val Phe Leu Lys Asp Lys Ser Val
100 105 110

Val Thr His Asp His Gly Thr Asn Cys Cys Asp Ser Ala
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<212> DNA

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<220>

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<222> (101)..(361)

<223> RXA01781

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Val Leu Ser Leu Thr
1 5

atc acg gga cca att gct gtg att ccg cat aat cct gat gaa gcc agc 163
Ile Thr Gly Pro Ile Ala Val Ile Pro His Asn Pro Asp Glu Ala Ser
10 15 20

gcc aag gct gtc gct acc aaa cat aag cac acc ttg tcc ggc gct acc 211
Ala Lys Ala Val Ala Thr Lys His Lys His Thr Leu Ser Gly Ala Thr
25 30 35

tct gat cac cct tat gcc ggc atg acg ctt aaa gac atg att gaa cag 259

Ser Asp His Pro Tyr Ala Gly Met Thr Leu Lys Asp Met Ile Glu Gln
 40 45 50

ggc ttt acg ctc aca ccg ctg gaa ttc ccg ctc tgt gct gtc gat gat 307
 Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Leu Cys Ala Val Asp Asp
 55 60 65

cca aca gat tct gat cgc acc atg cac gtg atc aat gtt cgc gag cac 355
 Pro Thr Asp Ser Asp Arg Thr Met His Val Ile Asn Val Arg Glu His
 70 75 80 85

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 Ser Met

<210> 2424

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 2424

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 20 25 30

Leu Ser Gly Ala Thr Ser Asp His Pro Tyr Ala Gly Met Thr Leu Lys
 35 40 45

Asp Met Ile Glu Gln Gly Phe Thr Leu Thr Pro Leu Glu Phe Pro Leu
 50 55 60

Cys Ala Val Asp Asp Pro Thr Asp Ser Asp Arg Thr Met His Val Ile
 65 70 75 80

Asn Val Arg Glu His Ser Met
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<210> 2425

<211> 519

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(496)

<223> RXA01782

<400> 2425

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cccacacaat tccacccttt aagaaaagga cttagccatc atg acc acc ttc gcc 115
 Met Thr Thr Phe Ala
 1 5

ctt att gct agc ccc aac aat gtt gat ccc act gct gag tcc cca ctc 163
 Leu Ile Ala Ser Pro Asn Asn Val Asp Pro Thr Ala Glu Ser Pro Leu
 10 15 20

gcc att gaa atc cat acc gat gag gac agc agc tat cca cta ggg ctt 211
 Ala Ile Glu Ile His Thr Asp Glu Asp Ser Ser Tyr Pro Leu Gly Leu
 25 30 35

att gac tca gac cac ctg gtt cct gct gtg att tac ggc gat atg gtg 259
 Ile Asp Ser Asp His Leu Val Pro Ala Val Ile Tyr Gly Asp Met Val
 40 45 50

atc tac acc aaa aca ctg ctc gca cag acc cca cca gat gat gtg tcc 307
 Ile Tyr Thr Lys Thr Leu Leu Ala Gln Thr Pro Pro Asp Asp Val Ser
 55 60 65

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 Thr Ala Ser Ala Phe Phe Asp Lys Leu Thr Ala Leu Asp Ala Gln Gly
 70 75 80 85

cgc acc cgt gat ctg gtc tac agc gcc acc tac agc caa ctt gtt att 403
 Arg Thr Arg Asp Leu Val Tyr Ser Ala Thr Tyr Ser Gln Leu Val Ile
 90 95 100

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 Ala Gly His Asn Arg Thr Val Leu Thr Asp Asp Ser Glu Phe Tyr Asp
 105 110 115

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<210> 2426

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 2426

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 20 25 30

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 35 40 45

Tyr Gly Asp Met Val Ile Tyr Thr Lys Thr Leu Leu Ala Gln Thr Pro
 50 55 60

Pro Asp Asp Val Ser Thr Ala Ser Ala Phe Phe Asp Lys Leu Thr Ala
 65 70 75 80

Leu Asp Ala Gln Gly Arg Thr Arg Asp Leu Val Tyr Ser Ala Thr Tyr
 85 90 95

Ser Gln Leu Val Ile Ala Gly His Asn Arg Thr Val Leu Thr Asp Asp
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Ser Glu Phe Tyr Asp Glu Phe Tyr Gln Val Ile Glu Ala Ala Pro Gly
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Val Ile Leu Lys
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<220>
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<222> (101)..(337)
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Met Ile Asn Leu Phe
1 5
gct gca gcc ctg ccc gca ttc gag cct ttg agt att acc tcc ata ctc 163
Ala Ala Ala Leu Pro Ala Phe Glu Pro Leu Ser Ile Thr Ser Ile Leu
10 15 20
gtg ctc ggt gct gtg gca ttg atc tgt ggc ctc cct gtt ttt ctc gca 211
Val Leu Gly Ala Val Ala Leu Ile Cys Gly Leu Pro Val Phe Leu Ala
25 30 35
ctg gaa aaa agc gct gag ctc gat gat ctc ttc gca gca ctc atc atc 259
Leu Glu Lys Ser Ala Glu Leu Asp Asp Leu Phe Ala Ala Leu Ile Ile
40 45 50
gct gta ctt tta ggt ttt gct gct tat acg ttt gtg ctc ccc aag ctc 307
Ala Val Leu Leu Gly Phe Ala Ala Tyr Thr Phe Val Leu Pro Lys Leu
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Val Glu Leu Gly Cys Thr Ile Cys Gln Leu
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<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 2428
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Pro Val Phe Leu Ala Leu Glu Lys Ser Ala Glu Leu Asp Asp Leu Phe
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Val Asp Gln Phe Val 5																
gag ttc ggc ggt gga caa gca aac att aac cct gat gga tca gcg acc 163																
Glu Phe Gly Gly Gly Gln Ala Asn Ile Asn Pro Asp Gly Ser Ala Thr 20																
ggt gat tgg gag ggt tct ttc agc atc aac ttc tac gat ggt ttg gtg 211																
Val Asp Trp Glu Gly Ser Phe Ser Ile Asn Phe Tyr Asp Gly Leu Val 35																
ccg ttt acc atc acg aat ccg cac ctc gag gtt tct gta gct ggt act 259																
Pro Phe Thr Ile Thr Asn Pro His Leu Glu Val Ser Val Ala Gly Thr 40 45 50																
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Gly Val Leu Thr Gly Asp Leu Thr Ser Tyr Ala Val Glu Met Ser Asn 55 60 65																
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Pro Asn Glu Lys Thr Pro Leu Thr Asp Leu Tyr Glu Asp Val Thr Ile 70 75 80 85																
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Thr Thr Phe Gly Gly Val Asn Leu Asp Pro Glu Gly Val Val Thr Ser 90 95 100																
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Asn Pro Asp Tyr Asp Gly Val Ile Val Asp Val Pro Leu Asp Ala Thr 105 110 115																
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Ser Gln Val Thr Ser Gly Ala Gly Trp Gly Ala Trp Pro Gln Gly Phe 120 125 130																
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Phe Thr Asn Gly Pro Gly Leu Val Asn Ser Gln Leu Leu His Arg Gln
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gct 699

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<212> PRT
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Tyr Asp Gly Leu Val Pro Phe Thr Ile Thr Asn Pro His Leu Glu Val
 35 40 45

Ser Val Ala Gly Thr Gly Val Leu Thr Gly Asp Leu Thr Ser Tyr Ala
50 55 60

Val Glu Met Ser Asn Pro Asn Glu Lys Thr Pro Leu Thr Asp Leu Tyr
65 70 75 80

Glu Asp Val Thr Ile Thr Thr Phe Gly Gly Val Asn Leu Asp Pro Glu
 85 90 95

Gly Val Val Thr Ser Asn Pro Asp Tyr Asp Gly Val Ile Val Asp Val
100 105 110

Pro Leu Asp Ala Thr Ser Gln Val Thr Ser Gly Ala Gly Trp Gly Ala
115 120 125

Trp Pro Gln Gly Phe Leu Asp Phe His Phe Asp Thr Asn Leu Pro Ser
130 135 140

Tyr Trp Tyr Ser Ser Asp Gly Ala Gly Asp Pro Lys Lys Ala Pro Met
145 150 155 160

Ser Phe Asn Val Asp Phe Thr Asn Gly Pro Gly Leu Val Asn Ser Gln
 165 170 175

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<212> DNA
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<220>

<221> CDS

<222> (101)..(541)

<223> RXA01788

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                                         1                               5

ccc atc tac atc att tct ttt gcc cca gcg gat gat ctc cac ggc gtt 163
Pro Ile Tyr Ile Ile Ser Phe Ala Pro Ala Asp Asp Leu His Gly Val
                        10                        15                        20

gga gga ttc gag tgg gtt cca gca tca aca cca gaa aac aaa gct gcc 211
Gly Gly Phe Glu Trp Val Pro Ala Ser Thr Pro Glu Asn Lys Ala Ala
                        25                        30                        35

gcc ttc acg acc ttt gat cgt caa ttc gat gat tct cgt aac aat ggt 259
Ala Phe Thr Thr Phe Asp Arg Gln Phe Asp Asp Ser Arg Asn Asn Gly
                        40                        45                        50

ggc tcg cat att gtg cgt cta ctc aat atc tct gat ccc aat atc aca 307
Gly Ser His Ile Val Arg Leu Leu Asn Ile Ser Asp Pro Asn Ile Thr
                        55                        60                        65

gcg gat atg acc caa gac gat att acc gcg tac ctc gac tca aac atc 355
Ala Asp Met Thr Gln Asp Asp Ile Thr Ala Tyr Leu Asp Ser Asn Ile
                        70                        75                        80                        85

gac cgc tgg gaa tcc acg gaa cat gcg ctc aag cag ttt gtc cca ctt 403
Asp Arg Trp Glu Ser Thr Glu His Ala Leu Lys Gln Phe Val Pro Leu
                        90                        95                        100

aac gcg ggt gct gat cgc gta cct acc ggt ggt gcc gac gag cac att 451
Asn Ala Gly Ala Asp Arg Val Pro Thr Gly Gly Ala Asp Glu His Ile
                        105                        110                        115

acc cac gcc tgc cgc ata ata act gtg cag cgt agc tgc aca cgg att 499
Thr His Ala Cys Arg Ile Ile Thr Val Gln Arg Ser Cys Thr Arg Ile
                        120                        125                        130

cac ctg cgc tgt gga tgc atc cca aca cca caa cac cgc ccc 541
His Leu Arg Cys Gly Cys Ile Pro Thr Pro Gln His Arg Pro
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<210> 2432

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 2432

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Asp Leu His Gly Val Gly Gly Phe Glu Trp Val Pro Ala Ser Thr Pro

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20	25	30
Glu Asn Lys Ala Ala Ala Phe Thr Thr Phe Asp Arg Gln Phe Asp Asp		
35	40	45
Ser Arg Asn Asn Gly Gly Ser His Ile Val Arg Leu Leu Asn Ile Ser		
50	55	60
Asp Pro Asn Ile Thr Ala Asp Met Thr Gln Asp Asp Ile Thr Ala Tyr		
65	70	75
Leu Asp Ser Asn Ile Asp Arg Trp Glu Ser Thr Glu His Ala Leu Lys		
85	90	95
Gln Phe Val Pro Leu Asn Ala Gly Ala Asp Arg Val Pro Thr Gly Gly		
100	105	110
Ala Asp Glu His Ile Thr His Ala Cys Arg Ile Ile Thr Val Gln Arg		
115	120	125
Ser Cys Thr Arg Ile His Leu Arg Cys Gly Cys Ile Pro Thr Pro Gln		
130	135	140
His Arg Pro		
145		

<210> 2433

<211> 765

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(742)

<223> RXA01789

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Met Pro His Asn Pro	5
1	
atc gaa ctt cac act aat gat gta ctc gat gct ctc gac att gac gcc	163
Ile Glu Leu His Thr Asn Asp Val Leu Asp Ala Leu Asp Ile Asp Ala	
10	15
20	
atc tgc gac gat gtg ttt ctc tac acc gac ttc gag cac acc cca ggt	211
Ile Cys Asp Asp Val Phe Leu Tyr Thr Asp Phe Glu His Thr Pro Gly	
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35	
cag ctt gat cgc ttc gag caa ctc gcc ttc aca aaa atc tac gac atg	259
Gln Leu Asp Arg Phe Glu Gln Leu Ala Phe Thr Lys Ile Tyr Asp Met	
40	45
50	
ctg gaa aca gct gct gaa aaa ttc cca gat gta gca att aat gac act	307
Leu Glu Thr Ala Ala Glu Lys Phe Pro Asp Val Ala Ile Asn Asp Thr	
55	60
65	
tta agc act ggc aac cac gct gct gaa cag tac ttt ctt gcc aat ccc	355

Leu Ser Thr Gly Asn His Ala Ala Glu Gln Tyr Phe Leu Ala Asn Pro
 70 75 80 85
 ggc aac atc atc gtg ctg acc agc ttc gcg ctc aat cag acc gat ctc 403
 Gly Asn Ile Ile Val Leu Thr Ser Phe Ala Leu Asn Gln Thr Asp Leu
 90 95 100
 cgc gac ctc ata atc tca ccg tgc att aag tac aca gca cat gca cga 451
 Arg Asp Leu Ile Ile Ser Pro Cys Ile Lys Tyr Thr Ala His Ala Arg
 105 110 115
 gca ctc atg cgt gcg gtg aca cga aca ttg tgc act gca aac aac cct 499
 Ala Leu Met Arg Ala Val Thr Arg Thr Leu Cys Thr Ala Asn Asn Pro
 120 125 130
 gta gaa cgc gcg act atc ttc cct gtg tct gtc gct aat gcc tta agc 547
 Val Glu Arg Ala Thr Ile Phe Pro Val Ser Val Ala Asn Ala Leu Ser
 135 140 145
 atc gaa gcg ctg tgt tcc gaa tat cat gcg ttc cgc acc aag cag gtg 595
 Ile Glu Ala Leu Cys Ser Glu Tyr His Ala Phe Arg Thr Lys Gln Val
 150 155 160 165
 ctc aac act gct gca ctc atc aat cct gat aac act ctt ata ccc atg 643
 Leu Asn Thr Ala Ala Leu Ile Asn Pro Asp Asn Thr Leu Ile Pro Met
 170 175 180
 ttg ttg agc aaa gcg tat gag gca tac gcc tgg cac aag ggt gtc gaa 691
 Leu Leu Ser Lys Ala Tyr Glu Ala Tyr Ala Trp His Lys Gly Val Glu
 185 190 195
 tcc gcg caa cga ggt agc aac cta gct cgt gag tac tac gca gga ctt 739
 Ser Ala Gln Arg Gly Ser Asn Leu Ala Arg Glu Tyr Tyr Ala Gly Leu
 200 205 210
 atc tgaaaattca ctactcaact ctg 765
 Ile

<210> 2434

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 2434

Met Pro His Asn Pro Ile Glu Leu His Thr Asn Asp Val Leu Asp Ala
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 Leu Asp Ile Asp Ala Ile Cys Asp Asp Val Phe Leu Tyr Thr Asp Phe
 20 25 30
 Glu His Thr Pro Gly Gln Leu Asp Arg Phe Glu Gln Leu Ala Phe Thr
 35 40 45
 Lys Ile Tyr Asp Met Leu Glu Thr Ala Ala Glu Lys Phe Pro Asp Val
 50 55 60
 Ala Ile Asn Asp Thr Leu Ser Thr Gly Asn His Ala Ala Glu Gln Tyr
 65 70 75 80

His Pro Asp Leu
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<210> 2437
<211> 486
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(463)
<223> RXA01791

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caacactatc cgggtccaaat ctagaaaaga gacaaccccc atg acc tcc ccc acc 115
Met Thr Ser Pro Thr
1 5
acg tta aag ccc tgg tct att cgc gga ccc atc gac ggt gaa tac acc 163
Thr Leu Lys Pro Trp Ser Ile Arg Gly Pro Ile Asp Gly Glu Tyr Thr
10 15 20
atg ctt gag gca tat ccg ttt cag tat gta gca aat act cgc ccg gcc 211
Met Leu Glu Ala Tyr Pro Phe Gln Tyr Val Ala Asn Thr Arg Pro Ala
25 30 35
atc atg ctc tac gca ctc gat gaa aac ggt gta ccg gaa caa tat gcc 259
Ile Met Leu Tyr Ala Leu Asp Glu Asn Gly Val Pro Glu Gln Tyr Ala
40 45 50
gac ctc acc atc aac ctt gcc gat gtg gag ctc aag caa ctt aac cac 307
Asp Leu Thr Ile Asn Leu Ala Asp Val Glu Leu Lys Gln Leu Asn His
55 60 65
gtc atc att aac cca gat ctg cac gct gat gtt acc gaa ctg tgc att 355
Val Ile Ile Asn Pro Asp Leu His Ala Asp Val Thr Glu Leu Cys Ile
70 75 80 85
agc gcc ggc ctg ctg cga cct ggt gtt ctg ggc cag cac caa gtc ggt 403
Ser Ala Gly Leu Leu Arg Pro Gly Val Leu Gly Gln His Gln Val Gly
90 95 100
agc acc acc gcc aag gtc tac cga ctc act gag cgt gct gat ggc tgg 451
Ser Thr Thr Ala Lys Val Tyr Arg Leu Thr Glu Arg Ala Asp Gly Trp
105 110 115
cta cag ctg ttt tagcagctac ctgcgcctaa tcc 486
Leu Gln Leu Phe
120

<210> 2438
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 2438
Met Thr Ser Pro Thr Thr Leu Lys Pro Trp Ser Ile Arg Gly Pro Ile

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Asn Thr Arg Pro Ala Ile Met Leu Tyr Ala Leu Asp Glu Asn Gly Val	35	40	45
Pro Glu Gln Tyr Ala Asp Leu Thr Ile Asn Leu Ala Asp Val Glu Leu	50	55	60
Lys Gln Leu Asn His Val Ile Ile Asn Pro Asp Leu His Ala Asp Val	65	70	75
Thr Glu Leu Cys Ile Ser Ala Gly Leu Leu Arg Pro Gly Val Leu Gly	85	90	95
Gln His Gln Val Gly Ser Thr Thr Ala Lys Val Tyr Arg Leu Thr Glu	100	105	110
Arg Ala Asp Gly Trp Leu Gln Leu Phe	115	120	

<210> 2439

<211> 396

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(373)

<223> RXA01792

<400> 2439

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ccccaccca tactcactcc aaaacaagaa agtagtcate atg cct cag tac acc 115
 Met Pro Gln Tyr Thr
 1 5

atc aca atc acc gac gag cag aaa gct gtt cta cac agc ctc acc aac 163
 Ile Thr Ile Thr Asp Glu Gln Lys Ala Val Leu His Ser Leu Thr Asn
 10 15 20

ccc cat atc gcc act gct gaa cac ggc gct atc acc gca atc gag att 211
 Pro His Ile Ala Thr Ala Glu His Gly Ala Ile Thr Ala Ile Glu Ile
 25 30 35

cat gac gac cac gat gtt gtt gtc tat cac gtt caa cca gac ggc aca 259
 His Asp Asp His Asp Val Val Val Tyr His Val Gln Pro Asp Gly Thr
 40 45 50

cta act tac gag cgc ctt gtt gaa ggc ttc cat tac ggc tgg aca cgt 307
 Leu Thr Tyr Glu Arg Leu Val Glu Gly Phe His Tyr Gly Trp Thr Arg
 55 60 65

ttt gac agc gaa ggt ttt gag atc gac tcc gac aat aac cgc gtt gta 355
 Phe Asp Ser Glu Gly Phe Glu Ile Asp Ser Asp Asn Asn Arg Val Val
 70 75 80 85

gac gga ctc cgc gac gaa tagttaacaa caacgaccgc aca
 Asp Gly Leu Arg Asp Glu
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396

<210> 2440
 <211> 91
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2440
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 His Ser Leu Thr Asn Pro His Ile Ala Thr Ala Glu His Gly Ala Ile
 20 25 30
 Thr Ala Ile Glu Ile His Asp Asp His Asp Val Val Val Tyr His Val
 35 40 45
 Gln Pro Asp Gly Thr Leu Thr Tyr Glu Arg Leu Val Glu Gly Phe His
 50 55 60
 Tyr Gly Trp Thr Arg Phe Asp Ser Glu Gly Phe Glu Ile Asp Ser Asp
 65 70 75 80
 Asn Asn Arg Val Val Asp Gly Leu Arg Asp Glu
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<210> 2441
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 <212> DNA
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<220>
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 <223> RXA01793

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 Met Ala Gln Tyr Arg
 1 5
 gtc agt ttt atc gcg ctc gcc gag tca acc atc gag gtc gaa gca gac 163
 Val Ser Phe Ile Ala Leu Ala Glu Ser Thr Ile Glu Val Glu Ala Asp
 10 15 20
 agt cct gaa gaa gca ctc gac cta gcc aat gca gaa ttt gac tac ccg 211
 Ser Pro Glu Glu Ala Leu Asp Leu Ala Asn Ala Glu Phe Asp Tyr Pro
 25 30 35
 gtc acc ttg gcc ggc gat ccc tat gag ctg cac gac tgg gaa gca cgc 259
 Val Thr Leu Ala Gly Asp Pro Tyr Glu Leu His Asp Trp Glu Ala Arg
 40 45 50
 gct gaa att gaa tgg ctc gat acc agc tcg acc ccg cag caa cgc ctt 307
 Ala Glu Ile Glu Trp Leu Asp Thr Ser Ser Thr Pro Gln Gln Arg Leu

55 60 65

gga gaa cat gtc gtc aag atc gaa gat taaactcgat cattaacac 354
 Gly Glu His Val Val Lys Ile Glu Asp
 70 75

act 357

<210> 2442
 <211> 78
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2442
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 Glu Val Glu Ala Asp Ser Pro Glu Glu Ala Leu Asp Leu Ala Asn Ala
 20 25 30
 Glu Phe Asp Tyr Pro Val Thr Leu Ala Gly Asp Pro Tyr Glu Leu His
 35 40 45
 Asp Trp Glu Ala Arg Ala Glu Ile Glu Trp Leu Asp Thr Ser Ser Thr
 50 55 60
 Pro Gln Gln Arg Leu Gly Glu His Val Val Lys Ile Glu Asp
 65 70 75

<210> 2443
 <211> 357
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
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 <223> RXA01794

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 Met Ala Thr His Arg
 1 5
 gtt cat ttt gtc gca acc gca tcc gcc tac atc gac gtt gag gca gat 163
 Val His Phe Val Ala Thr Ala Ser Ala Tyr Ile Asp Val Glu Ala Asp
 10 15 20
 tcc ccc gaa gat gct ata gaa aaa gcg tat gat ctc gcc ggt gat ctg 211
 Ser Pro Glu Asp Ala Ile Glu Lys Ala Tyr Asp Leu Ala Gly Asp Leu
 25 30 35
 ccc ggc ctc atc gcc gac aac gaa ttt gat ctc ggt gaa tgg gag gta 259
 Pro Gly Leu Ile Ala Asp Asn Glu Phe Asp Leu Gly Glu Trp Glu Val
 40 45 50
 cag gcc gat gtc cag tgg cct gat aac tct gta cct cgc gag caa cgc 307

Gln Ala Asp Val Gln Trp Pro Asp Asn Ser Val Pro Arg Glu Gln Arg
 55 60 65

ctt gaa gag ggc gtt gac ctg ctc gat taaacagaat taactcaaac 354
 Leu Glu Glu Gly Val Asp Leu Leu Asp
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ccc 357

<210> 2444

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 2444

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Leu Ala Gly Asp Leu Pro Gly Leu Ile Ala Asp Asn Glu Phe Asp Leu
 35 40 45

Gly Glu Trp Glu Val Gln Ala Asp Val Gln Trp Pro Asp Asn Ser Val
 50 55 60

Pro Arg Glu Gln Arg Leu Glu Glu Gly Val Asp Leu Leu Asp
 65 70 75

<210> 2445

<211> 1317

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1294)

<223> RXA01799

<400> 2445

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aaaatcccca tagtttcccc cggtgcatat ccttaaaggt atg gaa att ccg ctg 115
 Met Glu Ile Pro Leu
 1 5

ccc aca tcc ctt atc gat gtc atc act gat ggt gcc ctc ggc caa acc 163
 Pro Thr Ser Leu Ile Asp Val Ile Thr Asp Gly Ala Leu Gly Gln Thr
 10 15 20

tgc att gat cag gca ttt gct gcc caa ttg ggg cga gtt act gga gtc 211
 Cys Ile Asp Gln Ala Phe Ala Ala Gln Leu Gly Arg Val Thr Gly Val
 25 30 35

gaa ttc aac ctt tct gac gat aaa acc gcg gct gaa gtg agg atc aat 259
 Glu Phe Asn Leu Ser Asp Asp Lys Thr Ala Ala Glu Val Arg Ile Asn
 40 45 50

aag gcg tcg ggg agt cct ttt gat acc acc ggt gaa gtc att gcg tgg	307
Lys Ala Ser Gly Ser Pro Phe Asp Thr Thr Gly Glu Val Ile Ala Trp	
55 60 65	
att aat aat cag gaa ttt gag tgg gtc agc acg cgc ggt gag gat ttg	355
Ile Asn Asn Gln Glu Phe Glu Trp Val Ser Thr Arg Gly Glu Asp Leu	
70 75 80 85	
gga ctg cct gaa ttg cag ggc att cag ccg ctc gac gat gat ctg atc	403
Gly Leu Pro Glu Leu Gln Gly Ile Gln Pro Leu Asp Asp Asp Leu Ile	
90 95 100	
acc gcc gca cgc acg ctg tat agc aat gcg ccg gcg ttc atc gcc ccg	451
Thr Ala Ala Arg Thr Leu Tyr Ser Asn Ala Pro Ala Phe Ile Ala Pro	
105 110 115	
ttg cgc gat ggt cgc agg gcg ttg gtt gcg atc aat cac acg cca aaa	499
Leu Arg Asp Gly Arg Arg Ala Leu Val Ala Ile Asn His Thr Pro Lys	
120 125 130	
ctg gtt ggt atc cgt cgc acg ctc atc gaa ggc ctg cag gcg ctg aag	547
Leu Val Gly Ile Arg Arg Thr Leu Ile Glu Gly Leu Gln Ala Leu Lys	
135 140 145	
cct gga act gac ctc aaa cgg gca ttg act tca ttt gct gca ttc tgc	595
Pro Gly Thr Asp Leu Lys Arg Ala Leu Thr Ser Phe Ala Ala Phe Cys	
150 155 160 165	
gaa ctg ggc atc cga ttc gat gac aac cgc atc tcc ttc agc gat ggc	643
Glu Leu Gly Ile Arg Phe Asp Asp Asn Arg Ile Ser Phe Ser Asp Gly	
170 175 180	
acc tcg ctg ttg ctt cgt ggc ggc aaa gtc atc gaa atc gca ggc ggg	691
Thr Ser Leu Leu Leu Arg Gly Gly Lys Val Ile Glu Ile Ala Gly Gly	
185 190 195	
ctg agc ttg cgc gac gta cgc gcg gat gcg gcg ttc atg tcc gct gag	739
Leu Ser Leu Arg Asp Val Arg Ala Asp Ala Ala Phe Met Ser Ala Glu	
200 205 210	
cat caa ttg ctt ttc gac gcc atc tcc tcg tct cac aac gtc acc ttt	787
His Gln Leu Leu Phe Asp Ala Ile Ser Ser Ser His Asn Val Thr Phe	
215 220 225	
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Asp Pro His Thr Asn Val Ala Thr Val Ala Asn Glu His Gln Val His	
230 235 240 245	
gcc atc ccc ctt gct gtt atc gac ggc acg cgt tgg gta tgg aca tgg	883
Ala Ile Pro Leu Ala Val Ile Asp Gly Thr Arg Trp Val Trp Thr Trp	
250 255 260	
tct tta aaa gaa ctc aat ggt caa gca act gaa ggc ctt gcc cgc ttt	931
Ser Leu Lys Glu Leu Asn Gly Gln Ala Thr Glu Gly Leu Ala Arg Phe	
265 270 275	
ggt ttc gat aac ggc cta cta ctg ctc acc aat gca gag atc ctt gct	979
Gly Phe Asp Asn Gly Leu Leu Leu Leu Thr Asn Ala Glu Ile Leu Ala	
280 285 290	
gag gaa gcc acc gca ttc aac ctg att gat gtg gct aaa cag gtg ctc	1027

Glu Glu Ala Thr Ala Phe Asn Leu Ile Asp Val Ala Lys Gln Val Leu
 295 300 305
 aac act tgg acg cac acc atc gtg cag caa cct gat ggc acc gga att 1075
 Asn Thr Trp Thr His Thr Ile Val Gln Gln Pro Asp Gly Thr Gly Ile
 310 315 320 325
 gtc ctg ctg ctg gat cat cct cgg ctg cag ctt ccg cca gca tca cat 1123
 Val Leu Leu Leu Asp His Pro Arg Leu Gln Leu Pro Pro Ala Ser His
 330 335 340
 gca gct gtt gag gcc acg ctg tat cac cag cta cca ggc gat att gat 1171
 Ala Ala Val Glu Ala Thr Leu Tyr His Gln Leu Pro Gly Asp Ile Asp
 345 350 355
 gcc cgc cgc gcg gtg gcg tcc tat gca gct cac cga cag ctt cct ttt 1219
 Ala Arg Arg Ala Val Ala Ser Tyr Ala Ala His Arg Gln Leu Pro Phe
 360 365 370
 gat ggc tac gca ctc acc gtt gag ggc caa caa gtc ggc gtg act ttt 1267
 Asp Gly Tyr Ala Leu Thr Val Glu Gly Gln Gln Val Gly Val Thr Phe
 375 380 385
 gac ggc gag cat tta aca aag gtg ggc tagtttttcta gcaaaaccca 1314
 Asp Gly Glu His Leu Thr Lys Val Gly
 390 395
 acc 1317

<210> 2446

<211> 398

<212> PRT

<213> Corynebacterium glutamicum

<400> 2446

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 Arg Val Thr Gly Val Glu Phe Asn Leu Ser Asp Asp Lys Thr Ala Ala
 35 40 45
 Glu Val Arg Ile Asn Lys Ala Ser Gly Ser Pro Phe Asp Thr Thr Gly
 50 55 60
 Glu Val Ile Ala Trp Ile Asn Asn Gln Glu Phe Glu Trp Val Ser Thr
 65 70 75 80
 Arg Gly Glu Asp Leu Gly Leu Pro Glu Leu Gln Gly Ile Gln Pro Leu
 85 90 95
 Asp Asp Asp Leu Ile Thr Ala Ala Arg Thr Leu Tyr Ser Asn Ala Pro
 100 105 110
 Ala Phe Ile Ala Pro Leu Arg Asp Gly Arg Arg Ala Leu Val Ala Ile
 115 120 125
 Asn His Thr Pro Lys Leu Val Gly Ile Arg Arg Thr Leu Ile Glu Gly

130	135	140
Leu Gln Ala Leu Lys Pro Gly Thr Asp Leu Lys Arg Ala Leu Thr Ser 145 150 155 160		
Phe Ala Ala Phe Cys Glu Leu Gly Ile Arg Phe Asp Asp Asn Arg Ile 165 170 175		
Ser Phe Ser Asp Gly Thr Ser Leu Leu Arg Gly Gly Lys Val Ile 180 185 190		
Glu Ile Ala Gly Gly Leu Ser Leu Arg Asp Val Arg Ala Asp Ala Ala 195 200 205		
Phe Met Ser Ala Glu His Gln Leu Leu Phe Asp Ala Ile Ser Ser Ser 210 215 220		
His Asn Val Thr Phe Asp Pro His Thr Asn Val Ala Thr Val Ala Asn 225 230 235 240		
Glu His Gln Val His Ala Ile Pro Leu Ala Val Ile Asp Gly Thr Arg 245 250 255		
Trp Val Trp Thr Trp Ser Leu Lys Glu Leu Asn Gly Gln Ala Thr Glu 260 265 270		
Gly Leu Ala Arg Phe Gly Phe Asp Asn Gly Leu Leu Leu Leu Thr Asn 275 280 285		
Ala Glu Ile Leu Ala Glu Glu Ala Thr Ala Phe Asn Leu Ile Asp Val 290 295 300		
Ala Lys Gln Val Leu Asn Thr Trp Thr His Thr Ile Val Gln Gln Pro 305 310 315 320		
Asp Gly Thr Gly Ile Val Leu Leu Leu Asp His Pro Arg Leu Gln Leu 325 330 335		
Pro Pro Ala Ser His Ala Ala Val Glu Ala Thr Leu Tyr His Gln Leu 340 345 350		
Pro Gly Asp Ile Asp Ala Arg Arg Ala Val Ala Ser Tyr Ala Ala His 355 360 365		
Arg Gln Leu Pro Phe Asp Gly Tyr Ala Leu Thr Val Glu Gly Gln Gln 370 375 380		
Val Gly Val Thr Phe Asp Gly Glu His Leu Thr Lys Val Gly 385 390 395		

<210> 2447

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXA01800

<400> 2447

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                                   Val Lys Pro Leu Gly
                                   1 5

aag atc gcc gtt cct tgg act tgg tac ctg gga att gtt ggg gtc atc 163
Lys Ile Ala Val Pro Trp Thr Trp Tyr Leu Gly Ile Val Gly Val Ile
                                   10 15 20

ata ttt gat gtg gtg gca gca ata acg atg ctc acc ctc gtg ccc aac 211
Ile Phe Asp Val Val Ala Ala Ile Thr Met Leu Thr Leu Val Pro Asn
                                   25 30 35

aaa atg ccc gaa aga gtc aac agt ggg ctt gtc gcg ctg ggt gga tcg 259
Lys Met Pro Glu Arg Val Asn Ser Gly Leu Val Ala Leu Gly Gly Ser
                                   40 45 50

tat gca ccc ccg atg agc cgg gaa aca ctc att gcc aga gtc att gcc 307
Tyr Ala Pro Pro Met Ser Arg Glu Thr Leu Ile Ala Arg Val Ile Ala
                                   55 60 65

ggg gca gtg ctg gtt ctg gtg att tct tta ggt att tcg ctg ctg att 355
Gly Ala Val Leu Val Leu Val Ile Ser Leu Gly Ile Ser Leu Leu Ile
                                   70 75 80 85

tcc gcg cag tcc aag aac ctc gcg tcc gat cac ccg gat gca tct gcc 403
Ser Ala Gln Ser Lys Asn Leu Ala Ser Asp His Pro Asp Ala Ser Ala
                                   90 95 100

att cag att gct cgg cgt tgg gcg ttt ttg aac aat att caa agc tgt 451
Ile Gln Ile Ala Arg Arg Trp Ala Phe Leu Asn Asn Ile Gln Ser Cys
                                   105 110 115

atc ggc tgg ttt agt ttc ttc ctc gca gcg att ttg agc atc tca tcg 499
Ile Gly Trp Phe Ser Phe Phe Leu Ala Ala Ile Leu Ser Ile Ser Ser
                                   120 125 130

cta aga ctc aac ggc cca ggt gcc acc acg cat ctt gag atg gcc gtt 547
Leu Arg Leu Asn Gly Pro Gly Ala Thr Thr His Leu Glu Met Ala Val
                                   135 140 145

tac atc atc gct gtg tcg gtg ttg gct tgg gcg ttg atg att tcc ttg 595
Tyr Ile Ile Ala Val Ser Val Leu Ala Trp Ala Leu Met Ile Ser Leu
                                   150 155 160 165

cga cgc ggc cag gtg gcg att gat cgt gcc att cca att cgg gaa gat 643
Arg Arg Gly Gln Val Ala Ile Asp Arg Ala Ile Pro Ile Arg Glu Asp
                                   170 175 180

gat tcc gaa ctg aaa tgg ggc atg atc tac cac gat gct tca gac aaa 691
Asp Ser Glu Leu Lys Trp Gly Met Ile Tyr His Asp Ala Ser Asp Lys
                                   185 190 195

cga gtt ttc gtg gaa ctc gat gat ggc cac acg acc gtc atc aac atg 739
Arg Val Phe Val Glu Leu Asp Asp Gly His Thr Thr Val Ile Asn Met
                                   200 205 210

gcg cgc ggg gga gcg tgg ctg ctc atc gca gtg atg gtg ctg cct gcg 787
Ala Arg Gly Gly Ala Trp Leu Leu Ile Ala Val Met Val Leu Pro Ala

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215 220 225
 ctg gcc atc gtc ggt tgg gtt ttg cta gaa aac tagcccacct ttgttaaag 840
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ctc

843

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 <213> Corynebacterium glutamicum

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 35 40 45
 Ala Leu Gly Gly Ser Tyr Ala Pro Pro Met Ser Arg Glu Thr Leu Ile
 50 55 60
 Ala Arg Val Ile Ala Gly Ala Val Leu Val Leu Val Ile Ser Leu Gly
 65 70 75 80
 Ile Ser Leu Leu Ile Ser Ala Gln Ser Lys Asn Leu Ala Ser Asp His
 85 90 95
 Pro Asp Ala Ser Ala Ile Gln Ile Ala Arg Arg Trp Ala Phe Leu Asn
 100 105 110
 Asn Ile Gln Ser Cys Ile Gly Trp Phe Ser Phe Phe Leu Ala Ala Ile
 115 120 125
 Leu Ser Ile Ser Ser Leu Arg Leu Asn Gly Pro Gly Ala Thr Thr His
 130 135 140
 Leu Glu Met Ala Val Tyr Ile Ile Ala Val Ser Val Leu Ala Trp Ala
 145 150 155 160
 Leu Met Ile Ser Leu Arg Arg Gly Gln Val Ala Ile Asp Arg Ala Ile
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 Pro Ile Arg Glu Asp Asp Ser Glu Leu Lys Trp Gly Met Ile Tyr His
 180 185 190
 Asp Ala Ser Asp Lys Arg Val Phe Val Glu Leu Asp Asp Gly His Thr
 195 200 205
 Thr Val Ile Asn Met Ala Arg Gly Gly Ala Trp Leu Leu Ile Ala Val
 210 215 220
 Met Val Leu Pro Ala Leu Ala Ile Val Gly Trp Val Leu Leu Glu Asn
 225 230 235 240

Glu Gly Cys Leu Tyr Phe Asp Trp Phe Arg Asn Thr Asp Tyr Pro Gly
35 40 45

Glu Tyr Leu Val Ile Gly Val Trp Thr Asp Glu Gly Ala Thr Glu His
50 55 60

Lys Lys Ser Glu His Phe Leu Arg Ala Gln Glu Thr Leu Pro Pro Leu
65 70 75 80

Leu Gln Gln Thr Pro Met Ile Ile Gln Ser Glu Phe Ser Lys Lys Lys
85 90 95

Gly Trp Glu Arg Phe Ser Asp Phe Thr Val Tyr
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<210> 2451

<211> 453

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(430)

<223> RXA01805

<400> 2451

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Val Val Val Val Ile
1 5

ttg att aat gtg aaa ttc aag cca ttg cca gaa tat gta gac acc ttc 163
Leu Ile Asn Val Lys Phe Lys Pro Leu Pro Glu Tyr Val Asp Thr Phe
10 15 20

cgc gag cag gta gcg gag ttt aca gaa aag acc cgt gcg gaa gaa gga 211
Arg Glu Gln Val Ala Glu Phe Thr Glu Lys Thr Arg Ala Glu Glu Gly
25 30 35

aac atc ttc ttc gat tgg tca att aac acc gac aac cca aac gag ttc 259
Asn Ile Phe Phe Asp Trp Ser Ile Asn Thr Asp Asn Pro Asn Glu Phe
40 45 50

atc ctc atc gaa gca ttc cag gac gac gct gcc gaa gct cac gtc aac 307
Ile Leu Ile Glu Ala Phe Gln Asp Asp Ala Ala Glu Ala His Val Asn
55 60 65

agc gac cac ttc aag gcg gcc tgt gag ctg ttc cca acc atc ctg tct 355
Ser Asp His Phe Lys Ala Ala Cys Glu Leu Phe Pro Thr Ile Leu Ser
70 75 80 85

gag acc cca gag atc atc aac acc ctt atc gag ggc aag act gag tgg 403
Glu Thr Pro Glu Ile Ile Asn Thr Leu Ile Glu Gly Lys Thr Glu Trp
90 95 100

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Asp Arg Met Ala Glu Phe Ala Val Asn
105 110

ttg 453

<210> 2452

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 2452

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Tyr Val Asp Thr Phe Arg Glu Gln Val Ala Glu Phe Thr Glu Lys Thr
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Arg Ala Glu Glu Gly Asn Ile Phe Phe Asp Trp Ser Ile Asn Thr Asp
 35 40 45

Asn Pro Asn Glu Phe Ile Leu Ile Glu Ala Phe Gln Asp Asp Ala Ala
 50 55 60

Glu Ala His Val Asn Ser Asp His Phe Lys Ala Ala Cys Glu Leu Phe
 65 70 75 80

Pro Thr Ile Leu Ser Glu Thr Pro Glu Ile Ile Asn Thr Leu Ile Glu
 85 90 95

Gly Lys Thr Glu Trp Asp Arg Met Ala Glu Phe Ala Val Asn
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<210> 2453

<211> 603

<212> DNA

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<220>

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accagtgacc ccgcacacat ttcattgaagg gagttaaac atg agt tcg ctc gac 115
 Met Ser Ser Leu Asp
 1 5

aat gcc ccg ctg ctg gaa ttg gat gtt cag gaa tgg gta aac cac gaa 163
 Asn Ala Pro Leu Leu Glu Leu Asp Val Gln Glu Trp Val Asn His Glu
 10 15 20

ggc ttg agc aat gag gac ctg cgc ggc aag gtt gtg gtg gtg gag gtg 211
 Gly Leu Ser Asn Glu Asp Leu Arg Gly Lys Val Val Val Val Glu Val
 25 30 35

ttt cag atg cta tgc cct gga tgc gtg aat cac ggt gtc cct cag gct 259
 Phe Gln Met Leu Cys Pro Gly Cys Val Asn His Gly Val Pro Gln Ala
 40 45 50

caa aaa atc cac cgc atg att gat gaa tcc caa gtg caa gtc atc ggg 307
 Gln Lys Ile His Arg Met Ile Asp Glu Ser Gln Val Gln Val Ile Gly
 55 60 65

ctg cac agc gtg ttt gag cac cat gat gtg atg aca cct gag gct ttg 355
 Leu His Ser Val Phe Glu His His Asp Val Met Thr Pro Glu Ala Leu 85
 70 75 80
 aaa gtg ttc atc gat gag ttt ggg atc aag ttc ccc gtg gca gtg gat 403
 Lys Val Phe Ile Asp Glu Phe Gly Ile Lys Phe Pro Val Ala Val Asp 100
 90 95
 atg ccg agg gaa ggc cag cgg att cct tgc acg atg aaa aag tat cgt 451
 Met Pro Arg Glu Gly Gln Arg Ile Pro Ser Thr Met Lys Lys Tyr Arg 115
 105 110
 ttg gaa gga acg ccc agc atc att ttg gct gat cga aaa gga cgg att 499
 Leu Glu Gly Thr Pro Ser Ile Ile Leu Ala Asp Arg Lys Gly Arg Ile 130
 120 125
 cgt cag gtg cag ttc ggg cag gtt gat gat ttc gtg ctg gga ttg ctg 547
 Arg Gln Val Gln Phe Gly Gln Val Asp Asp Phe Val Leu Gly Leu Leu 145
 135 140
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<210> 2454

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 2454

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 20 25 30
 Val Val Val Glu Val Phe Gln Met Leu Cys Pro Gly Cys Val Asn His
 35 40 45
 Gly Val Pro Gln Ala Gln Lys Ile His Arg Met Ile Asp Glu Ser Gln
 50 55 60
 Val Gln Val Ile Gly Leu His Ser Val Phe Glu His His Asp Val Met
 65 70 75 80
 Thr Pro Glu Ala Leu Lys Val Phe Ile Asp Glu Phe Gly Ile Lys Phe
 85 90 95
 Pro Val Ala Val Asp Met Pro Arg Glu Gly Gln Arg Ile Pro Ser Thr
 100 105 110
 Met Lys Lys Tyr Arg Leu Glu Gly Thr Pro Ser Ile Ile Leu Ala Asp
 115 120 125
 Arg Lys Gly Arg Ile Arg Gln Val Gln Phe Gly Gln Val Asp Asp Phe
 130 135 140
 Val Leu Gly Leu Leu Leu Gly Ser Leu Leu Ser Glu Thr Asp Glu Thr

145

150

155

160

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<212> DNA

<213> Corynebacterium glutamicum

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gtagagtcc ttcttcccct gccagaaagg cacctcacag gtg caa tta tta cac 115
 Val Gln Leu Leu His
 1 5

acc ccc gca gcc ata tcc att tcc ttc gac gac ccc aac ctc atc tct 163
 Thr Pro Ala Ala Ile Ser Ile Ser Phe Asp Asp Pro Asn Leu Ile Ser
 10 15 20

acc gca ggg ctg gtc ccg acc atg gcc ctg gcc gag gac cgg tta aca 211
 Thr Ala Gly Leu Val Pro Thr Met Ala Leu Ala Glu Asp Arg Leu Thr
 25 30 35

gta cca acc gac aaa ggt gct aac cca ggt gcc aaa atc acg acc ctc 259
 Val Pro Thr Asp Lys Gly Ala Asn Pro Gly Ala Lys Ile Thr Thr Leu
 40 45 50

att gcg ggg atg gtc gcc ggt gcc gac tcc atc gac gat atc gat gca 307
 Ile Ala Gly Met Val Ala Gly Ala Asp Ser Ile Asp Asp Ile Asp Ala
 55 60 65

ctc cgc cac ggc ggt atg cac cga ctc ttt gac tgg atc tac gcc ccc 355
 Leu Arg His Gly Gly Met His Arg Leu Phe Asp Trp Ile Tyr Ala Pro
 70 75 80 85

tcc acg ttg ggg tcg ttc ctc cgg gcc ttt acc ttc ggg cat gtc cgc 403
 Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr Phe Gly His Val Arg
 90 95 100

caa ctc gac gct gtg gcc tcc cgg ttc ctg gtg ggt ctg gca aca cag 451
 Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val Gly Leu Ala Thr Gln
 105 110 115

gcc ccg gcc ctg gtc ccg gtt gat gct tct acc agt gat tac gtc ttc 499
 Ala Pro Ala Leu Val Pro Val Asp Ala Ser Thr Ser Asp Tyr Val Phe
 120 125 130

atc gat gtt gat gac acc atc att aag gtc cac gga cat cag aaa caa 547
 Ile Asp Val Asp Asp Thr Ile Ile Lys Val His Gly His Gln Lys Gln
 135 140 145

ggc gct ggt ttt ggt tac tcc ggt atc cgt gga ctc aac gcc ctg ctg 595
 Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly Leu Asn Ala Leu Leu
 150 155 160 165

gcc aca gtg acc aca cca gag tca gca cca gtg gtc gtg gcc caa cga 643

Ala Thr Val Thr Thr Pro Glu Ser Ala Pro Val Val Val Ala Gln Arg
 170 175 180

tta cgg aaa gga tgc tgc ggt tcc ccg cgg ggt gca ggc cgg ttg att 691
 Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly Ala Gly Arg Leu Ile
 185 190 195

gct gat gcg gtg gct acc acc ccg cgt ttg ccg ggg atg gag gat gag 739
 Ala Asp Ala Val Ala Thr Thr Arg Arg Leu Pro Gly Met Glu Asp Glu
 200 205 210

aag atc ctt tta cgc gcg gat tct gcc ttt tat ggc cat ccc agt atc 787
 Lys Ile Leu Leu Arg Ala Asp Ser Ala Phe Tyr Gly His Pro Ser Ile
 215 220 225

agt gct gcg atc aag gca ggg gcg gat gtg tct tca ccg tgc gga 832
 Ser Ala Ala Ile Lys Ala Gly Ala Asp Val Ser Ser Arg Cys Gly
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<210> 2456

<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 2456

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Pro Asn Leu Ile Ser Thr Ala Gly Leu Val Pro Thr Met Ala Leu Ala
 20 25 30

Glu Asp Arg Leu Thr Val Pro Thr Asp Lys Gly Ala Asn Pro Gly Ala
 35 40 45

Lys Ile Thr Thr Leu Ile Ala Gly Met Val Ala Gly Ala Asp Ser Ile
 50 55 60

Asp Asp Ile Asp Ala Leu Arg His Gly Gly Met His Arg Leu Phe Asp
 65 70 75 80

Trp Ile Tyr Ala Pro Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr
 85 90 95

Phe Gly His Val Arg Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val
 100 105 110

Gly Leu Ala Thr Gln Ala Pro Ala Leu Val Pro Val Asp Ala Ser Thr
 115 120 125

Ser Asp Tyr Val Phe Ile Asp Val Asp Asp Thr Ile Ile Lys Val His
 130 135 140

Gly His Gln Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly Ile Arg Gly
 145 150 155 160

Leu Asn Ala Leu Leu Ala Thr Val Thr Thr Pro Glu Ser Ala Pro Val
 165 170 175

Val Val Ala Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser Pro Arg Gly
 180 185 190

Ala Gly Arg Leu Ile Ala Asp Ala Val Ala Thr Thr Arg Arg Leu Pro
 195 200 205

Gly Met Glu Asp Glu Lys Ile Leu Leu Arg Ala Asp Ser Ala Phe Tyr
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Gly His Pro Ser Ile Ser Ala Ala Ile Lys Ala Gly Ala Asp Val Ser
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Ser Arg Cys Gly

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 Met Thr Pro Asn Val
 1 5

aag aaa gcg atc gcc cag gtt cct gat gat gcg tgg cag aca att aag 163
 Lys Lys Ala Ile Ala Gln Val Pro Asp Asp Ala Trp Gln Thr Ile Lys
 10 15 20

tac acc aac gcg atc ttc gac gag gac acc ggg cgc tgg atc tcg gtg 211
 Tyr Thr Asn Ala Ile Phe Asp Glu Asp Thr Gly Arg Trp Ile Ser Val
 25 30 35

gcc gag gtc gcc gag ata ccg ttc acc gca ttt acc tcc cgg aag aaa 259
 Ala Glu Val Ala Glu Ile Pro Phe Thr Ala Phe Thr Ser Arg Lys Lys
 40 45 50

acc gac cac atc ccc gga ctg ctg gtg gta cgc cgg ata ccg gag ctg 307
 Thr Asp His Ile Pro Gly Leu Leu Val Val Arg Arg Ile Pro Glu Leu
 55 60 65

aat aac aag gat gtg gat cag ccg ggg ttg ttt gat cta cac cgc ttc 355
 Asn Asn Lys Asp Val Asp Gln Pro Gly Leu Phe Asp Leu His Arg Phe
 70 75 80 85

cat gcg gtg ttc acc acc gcc gac cca ggc atc ctc gat act gtt gct 403
 His Ala Val Phe Thr Thr Ala Asp Pro Gly Ile Leu Asp Thr Val Ala
 90 95 100

gcg gat aaa acc cac cgt caa cac gca atc atc gaa caa gtc aac gcg 451
 Ala Asp Lys Thr His Arg Gln His Ala Ile Ile Glu Gln Val Asn Ala
 105 110 115

gac gta aag gcc agt gcg ttg gcg cat atg cca tca ggt gta ttc acc 499
 Asp Val Lys Ala Ser Ala Leu Ala His Met Pro Ser Gly Val Phe Thr
 120 125 130

gcc aac agc gcc tgg ttg gtg tgt gcg gtc atg gcg ttc aac ctc acc 547
 Ala Asn Ser Ala Trp Leu Val Cys Ala Val Met Ala Phe Asn Leu Thr
 135 140 145

cgc aca gcc ggt gtg atc gct gca ggc gcg atg gcc agg gcc acc acc 595
 Arg Thr Ala Gly Val Ile Ala Ala Gly Ala Met Ala Arg Ala Thr Thr
 150 155 160 165

gca acg atc cgg cgg aaa ctt gtg gcc gtt ccg gcc agg att gca cgc 643
 Ala Thr Ile Arg Arg Lys Leu Val Ala Val Pro Ala Arg Ile Ala Arg
 170 175 180

agc gcc cgg aga ttg att ctt cac ttg cca cgg aac tgg cgg tgg gaa 691
 Ser Ala Arg Arg Leu Ile Leu His Leu Pro Arg Asn Trp Arg Trp Glu
 185 190 195

acc cag tgg tca aga ttg tgt gat cac ggc cgt tta cca ccg 733
 Thr Gln Trp Ser Arg Leu Cys Asp His Gly Arg Leu Pro Pro
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<210> 2458

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 2458

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 20 25 30

Arg Trp Ile Ser Val Ala Glu Val Ala Glu Ile Pro Phe Thr Ala Phe
 35 40 45

Thr Ser Arg Lys Lys Thr Asp His Ile Pro Gly Leu Leu Val Val Arg
 50 55 60

Arg Ile Pro Glu Leu Asn Asn Lys Asp Val Asp Gln Pro Gly Leu Phe
 65 70 75 80

Asp Leu His Arg Phe His Ala Val Phe Thr Thr Ala Asp Pro Gly Ile
 85 90 95

Leu Asp Thr Val Ala Ala Asp Lys Thr His Arg Gln His Ala Ile Ile
 100 105 110

Glu Gln Val Asn Ala Asp Val Lys Ala Ser Ala Leu Ala His Met Pro
 115 120 125

Ser Gly Val Phe Thr Ala Asn Ser Ala Trp Leu Val Cys Ala Val Met
 130 135 140

Ala Phe Asn Leu Thr Arg Thr Ala Gly Val Ile Ala Ala Gly Ala Met

145		150		155		160
Ala Arg Ala Thr Thr	Ala Thr Ile Arg Arg	Lys Leu Val Ala Val Pro				
	165	170			175	
Ala Arg Ile Ala Arg Ser Ala Arg	Arg Leu Ile Leu His Leu Pro Arg					
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Leu Pro Pro						
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<212> DNA

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<223> RXA01820

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                                         Met Ser Ala Ser Phe
                                         1                               5

gat gac ccc aac ctc atc tcg ctt gct gga ctg gtt cca acc atg cac 163
Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu Val Pro Thr Met His
                               10                               15                               20

tta gcc gat gct gcc agc ctg tcc acc ttg gcc cag gac cgg ttg agc 211
Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala Gln Asp Arg Leu Ser
                               25                               30                               35

atc acc ggt gat aaa ggt gcc aat gct ggt gcg aag atc gcc tcc cta 259
Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala Lys Ile Ala Ser Leu
                               40                               45                               50

gtc gcg ggc atg gtc gcc ggt gct gat tcc atc gat gac atg gat gta 307
Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile Asp Asp Met Asp Val
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ctc cgc cac gga ggt atg cgc cga ctt ttc gac cgg atc tac gcc cca 355
Leu Arg His Gly Gly Met Arg Arg Leu Phe Asp Arg Ile Tyr Ala Pro
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tcc aca ttg ggg tct ttt ctg cgg gcc ttc act ttc ggc cac gta cgc 403
Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr Phe Gly His Val Arg
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caa ctc gat gct gtg gcc tcc cga ttc ctg gtc aac ctg gcc agg cag 451
Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val Asn Leu Ala Arg Gln
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gca cca cac ctg gtg cca cca cca ccg gca ggc agt ggc ggt aac ggg 499

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Ala	Pro	His	Leu	Val	Pro	Pro	Pro	Pro	Ala	Gly	Ser	Gly	Gly	Asn	Gly		
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Tyr	Val	Phe	Val	Asp	Val	Asp	Asp	Thr	Ile	Ile	Glu	Val	His	Gly	His		
	135					140					145						
acc	aaa	caa	ggc	gcc	ggc	ttt	ggc	tac	tcc	ggc	atc	cgt	gga	ctc	aac	595	
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Arg	Leu	Ile	Ala	Asp	Ala	Met	Thr	Thr	Thr	Arg	Arg	Leu	Pro	Gly	Met		
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gag	gat	aag	aaa	atc	ctc	gtc	cgg	gca	gat	tcg	gcg	tat	tat	ggc	cat	787	
Glu	Asp	Lys	Lys	Ile	Leu	Val	Arg	Ala	Asp	Ser	Ala	Tyr	Tyr	Gly	His		
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ccc	agt	gtc	agt	gtg	gcc	cta	agg	tcc	ggc	gcg	gat	gtg	tcc	gtc	acg	835	
Pro	Ser	Val	Ser	Val	Ala	Leu	Arg	Ser	Gly	Ala	Asp	Val	Ser	Val	Thr		
230					235				240					245			
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gat	gcg	tgg	cag	acg	att	cag	tac	acc	gat	gcg	atc	ttc	gat	gag	gca	931	
Asp	Ala	Trp	Gln	Thr	Ile	Gln	Tyr	Thr	Asp	Ala	Ile	Phe	Asp	Glu	Ala		
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Ala	Phe	Thr	Ser	Arg	Lys	Lys	Ala	Asp	His	Val	Pro	Gly	Arg	Leu	Val		
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gta	cgc	cgc	att	cct	gag	ctg	aat	aag	aag	gat	gtg	tat	cag	cgc	ggc	1075	
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Gly	Val	Leu	Asp	Thr	Val	Ala	Ala	Asp	Lys	Thr	His	Arg	Gln	His	Ala		
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Ile	Ile	Glu	Gln	Val	Asn	Ala	Asp	Leu	Lys	Ala	Ser	Ala	Leu	Ala	His		

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Leu Pro Ser Gly Thr Phe Thr Ala Asn Ser Ala Trp Leu Val Cys Ala			
375	380	385	
gtc atg gcg ttt aat ctc acc cgt gcc acc ggg gtt atc gct gca ggc			1315
Val Met Ala Phe Asn Leu Thr Arg Ala Thr Gly Val Ile Ala Ala Gly			
390	395	400	405
ggg atg gcc aag gcc acc acc gcg acg atc cgg cgg aca ctg atg gcc			1363
Gly Met Ala Lys Ala Thr Thr Ala Thr Ile Arg Arg Thr Leu Met Ala			
410	415	420	
gtt cca gcc cgg gtc gcc cgc agg tcc cgc cga ctg gtg ctc cac ctt			1411
Val Pro Ala Arg Val Ala Arg Arg Ser Arg Arg Leu Val Leu His Leu			
425	430	435	
ccc gag ggg tgg acg tgg caa cca cag tgg cag aaa ctg ttt gat cac			1459
Pro Glu Gly Trp Thr Trp Gln Pro Gln Trp Gln Lys Leu Phe Asp His			
440	445	450	
ggc cat tca cca ccg taaccggtag ctccctgacc acc			1497
Gly His Ser Pro Pro			
455			

<210> 2460

<211> 458

<212> PRT

<213> Corynebacterium glutamicum

<400> 2460

Met Ser Ala Ser Phe Asp Asp Pro Asn Leu Ile Ser Leu Ala Gly Leu			
1	5	10	15
Val Pro Thr Met His Leu Ala Asp Ala Ala Ser Leu Ser Thr Leu Ala			
20	25	30	
Gln Asp Arg Leu Ser Ile Thr Gly Asp Lys Gly Ala Asn Ala Gly Ala			
35	40	45	
Lys Ile Ala Ser Leu Val Ala Gly Met Val Ala Gly Ala Asp Ser Ile			
50	55	60	
Asp Asp Met Asp Val Leu Arg His Gly Gly Met Arg Arg Leu Phe Asp			
65	70	75	80
Arg Ile Tyr Ala Pro Ser Thr Leu Gly Ser Phe Leu Arg Ala Phe Thr			
85	90	95	
Phe Gly His Val Arg Gln Leu Asp Ala Val Ala Ser Arg Phe Leu Val			
100	105	110	
Asn Leu Ala Arg Gln Ala Pro His Leu Val Pro Pro Pro Pro Ala Gly			
115	120	125	
Ser Gly Gly Asn Gly Tyr Val Phe Val Asp Val Asp Asp Thr Ile Ile			
130	135	140	
Glu Val His Gly His Thr Lys Gln Gly Ala Gly Phe Gly Tyr Ser Gly			

145 150 155 160
 Ile Arg Gly Leu Asn Ala Leu Leu Ala Thr Val Thr Thr Ala Gln Ser
 165 170 175
 Ala Pro Ile Ile Val Gly Gln Arg Leu Arg Lys Gly Ser Cys Gly Ser
 180 185 190
 Pro Arg Gly Ala His Arg Leu Ile Ala Asp Ala Met Thr Thr Thr Arg
 195 200 205
 Arg Leu Pro Gly Met Glu Asp Lys Lys Ile Leu Val Arg Ala Asp Ser
 210 215 220
 Ala Tyr Tyr Gly His Pro Ser Val Ser Val Ala Leu Arg Ser Gly Ala
 225 230 235 240
 Asp Val Ser Val Thr Val Arg Met Thr Pro Asn Val Lys Lys Ala Ile
 245 250 255
 Val Ala Ile Pro Glu Asp Ala Trp Gln Thr Ile Gln Tyr Thr Asp Ala
 260 265 270
 Ile Phe Asp Glu Ala Ser Gln Ser Trp Ile Ser Leu Ala Gln Val Ala
 275 280 285
 Glu Val Pro Phe Thr Ala Phe Thr Ser Arg Lys Lys Ala Asp His Val
 290 295 300
 Pro Gly Arg Leu Val Val Arg Arg Ile Pro Glu Leu Asn Lys Lys Asp
 305 310 315 320
 Val Tyr Gln Pro Gly Leu Phe Asp Leu His Arg Phe His Ala Val Phe
 325 330 335
 Thr Thr Ala Asp Pro Gly Val Leu Asp Thr Val Ala Ala Asp Lys Thr
 340 345 350
 His Arg Gln His Ala Ile Ile Glu Gln Val Asn Ala Asp Leu Lys Ala
 355 360 365
 Ser Ala Leu Ala His Leu Pro Ser Gly Thr Phe Thr Ala Asn Ser Ala
 370 375 380
 Trp Leu Val Cys Ala Val Met Ala Phe Asn Leu Thr Arg Ala Thr Gly
 385 390 395 400
 Val Ile Ala Ala Gly Gly Met Ala Lys Ala Thr Thr Ala Thr Ile Arg
 405 410 415
 Arg Thr Leu Met Ala Val Pro Ala Arg Val Ala Arg Arg Ser Arg Arg
 420 425 430
 Leu Val Leu His Leu Pro Glu Gly Trp Thr Trp Gln Pro Gln Trp Gln
 435 440 445
 Lys Leu Phe Asp His Gly His Ser Pro Pro
 450 455

Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly Asp Ala Val Ala Glu
 185 190 195
 cag gtg cgt gcg ctg ctc cct gac ggt gtg gac gta gtc ttc gac cta 739
 Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp Val Val Phe Asp Leu
 200 205 210
 gtc ggc ggg gag gcg ttg cgg gtg gtt gct ccc tta gcg aag aat ccg 787
 Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro Leu Ala Lys Asn Pro
 215 220 225
 gcg cac gtg atc tcg gcg gct gat gct gcc acc gtg gga gaa ctc ggt 835
 Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr Val Gly Glu Leu Gly
 230 235 240 245
 gga cag gtg ctg cgc cgc acc ccg gaa atg gtc gga cag atc acc ggg 883
 Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val Gly Gln Ile Thr Gly
 250 255 260
 gtg gtc cag tac ggg ctg gtc gac ccg aag gtc gat acg acc tac ccg 931
 Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val Asp Thr Thr Tyr Pro
 265 270 275
 ctg gaa cag gcc ggt aag gcc ctg gcc cac gtt gag cag ggc cac gcc 979
 Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val Glu Gln Gly His Ala
 280 285 290
 cgc ggc aag atc gtc ctc gag ctc atc acc tcc cag gac taaccagaca 1028
 Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser Gln Asp
 295 300 305
 acgcggtgac ctc 1041

<210> 2462

<211> 306

<212> PRT

<213> Corynebacterium glutamicum

<400> 2462

Met Ser Lys Val Tyr Val Ser Asn Glu Tyr Gly Gly Pro Glu Asn Gln
 1 5 10 15
 Glu Leu Ile Thr Arg Asn Thr Pro Gln Pro Gly Pro Gly Glu Leu Gly
 20 25 30
 Val Lys Val His Ala Ala Gly Val Asn Pro Leu Asp Trp Lys Val Arg
 35 40 45
 Ser Gly Val Ala Gly Thr Pro Arg Glu Leu Pro Ala Pro Leu Gly Glu
 50 55 60
 Glu Ala Ser Gly Ile Val Thr Ala Val Gly Asp Gly Val Glu Gly Phe
 65 70 75 80
 Ala Val Gly Asp Pro Val Leu Gly Leu Val Ala Pro Gly Val Gly Gly
 85 90 95
 Tyr Ala Glu Asp Thr Leu Leu Val Ala Glu Ser Thr Val Leu Lys Pro
 100 105 110

Glu Glu Ile Ser Phe Thr Asp Ala Ala Ala Ile Pro Val Ala Gly Ala
 115 120 125
 Ser Ala Tyr Ala Gly Thr His Gln Val Glu Leu Glu Pro Gly Gln Ser
 130 135 140
 Leu Leu Ile Asn Gly Ala Gly Gly Gly Val Gly Leu Met Ala Ala Gln
 145 150 155 160
 Ile Gly Arg Val His Lys Phe Gln Val Val Gly Val Asp His Glu Asp
 165 170 175
 Lys Arg Glu Leu Ile Glu Ser Thr Gly Ala Ile Phe Val Ala Thr Gly
 180 185 190
 Asp Ala Val Ala Glu Gln Val Arg Ala Leu Leu Pro Asp Gly Val Asp
 195 200 205
 Val Val Phe Asp Leu Val Gly Gly Glu Ala Leu Arg Val Val Ala Pro
 210 215 220
 Leu Ala Lys Asn Pro Ala His Val Ile Ser Ala Ala Asp Ala Ala Thr
 225 230 235 240
 Val Gly Glu Leu Gly Gly Gln Val Leu Arg Arg Thr Pro Glu Met Val
 245 250 255
 Gly Gln Ile Thr Gly Val Val Gln Tyr Gly Leu Val Asp Pro Lys Val
 260 265 270
 Asp Thr Thr Tyr Pro Leu Glu Gln Ala Gly Lys Ala Leu Ala His Val
 275 280 285
 Glu Gln Gly His Ala Arg Gly Lys Ile Val Leu Glu Leu Ile Thr Ser
 290 295 300
 Gln Asp
 305

<210> 2463

<211> 303

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(280)

<223> RXA01844

<400> 2463

gaccaattgg tctgctgca tccgcatgat cgccaacgcc agttgcgggt aggcgtccac 60

gacctcggcc agggcctcga cgggcaggta gagcgcgcag gtg gtc tca atc gcc 115
 Val Val Ser Ile Ala
 1 5

cag gag ttg gag atc att gag gac ggc acg ggt gcg gtg ctc gtc tcg 163
 Gln Glu Leu Glu Ile Ile Glu Asp Gly Thr Gly Ala Val Leu Val Ser
 10 15 20

gag cag gca acc acc ttc gac aac ggg ttc atc ggc tac tcc tac ttc 211
Glu Gln Ala Thr Thr Phe Asp Asn Gly Phe Ile Gly Tyr Ser Tyr Phe
25 30 35

acc acc ggt acg gac gga gcc acc tgc atc acc gac ctt cgc ctc agg 259
Thr Thr Gly Thr Asp Gly Ala Thr Cys Ile Thr Asp Leu Arg Leu Arg
40 45 50

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gcc tcc cca ctg ccg cag gtt taaccggtac tagccggttt ttc          303
Ala Ser Pro Leu Pro Gln Val
.      55                      60
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<210> 2464

<211> 60

<212> PRT

<213> Corynebacterium glutamicum

<400> 2464

Val Val Ser Ile Ala Gln Glu Leu Glu Ile Ile Glu Asp Gly Thr Gly
1 5 10 15

Ala Val Leu Val Ser Glu Gln Ala Thr Thr Phe Asp Asn Gly Phe Ile
20 25 30

Gly Tyr Ser Tyr Phe Thr Thr Gly Thr Asp Gly Ala Thr Cys Ile Thr
35 40 45

Asp Leu Arg Leu Arg Ala Ser Pro Leu Pro Gln Val
50 55 60

<210> 2465

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) . . (508)

<223> RXA01845

<400> 2465

ggctccgtcc gtaccggtgg tgaagtagga gtagccgatg aacccgttgt cgaagggtggt 60

tgccctgctcc gagacgagca ccgcacccgt gccgtcctca atg atc tcc aac tcc 115
Met Ile Ser Asn Ser
1 5

tg	gc	at	ga	ac	ac	tg	gc	ct	ta	ct	cc	gt	ga	gc	ct	163
Trp	Ala	Ile	Glu	Thr	Thr	Cys	Ala	Leu	Tyr	Leu	Pro	Val	Glu	Ala	Leu	
				10					15					20		

gcc gag gtc gtg gac gcc tac ccg caa ctg gcg ttg gcg atc atg cgg 211
Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala Leu Ala Ile Met Arg
25 30 35

atg cag cag gac caa ttg gtc cgg tcc cgg gaa cgc gag acc gca cag 259
Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu Arg Glu Thr Ala Gln
40 45 50

acc acc tcg act gtc gag cag cgc gtg gcc gcc gcc ctc caa cac ctg 307
 Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala Ala Leu Gln His Leu
 55 60 65

gac gcc aag ctc ggg caa atc cga caa gac gga tcc agc ctg ctg cag 355
 Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly Ser Ser Leu Leu Gln
 70 75 80 85

gtc cgc ctg cgc cgc gac gac gtg gcc ggc acc acc gtc gag tcc gcc 403
 Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr Thr Val Glu Ser Ala
 90 95 100

tcc cgg gca atg gcg cgg atg aag aaa acc ggt gtc atc gac tcc ggc 451
 Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly Val Ile Asp Ser Gly
 105 110 115

cgc gaa tgg atc gcc att acc aac cac cag gcc ctg gcc gac ctg gtc 499
 Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala Leu Ala Asp Leu Val
 120 125 130

gcc ggc ctc taaacgcca catccctctc tct 531
 Ala Gly Leu
 135

<210> 2466

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 2466

Met Ile Ser Asn Ser Trp Ala Ile Glu Thr Thr Cys Ala Leu Tyr Leu
 1 5 10 15

Pro Val Glu Ala Leu Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala
 20 25 30

Leu Ala Ile Met Arg Met Gln Gln Asp Gln Leu Val Arg Ser Arg Glu
 35 40 45

Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala
 50 55 60

Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly
 65 70 75 80

Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr
 85 90 95

Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly
 100 105 110

Val Ile Asp Ser Gly Arg Glu Trp Ile Ala Ile Thr Asn His Gln Ala
 115 120 125

Leu Ala Asp Leu Val Ala Gly Leu
 130 135

<210> 2467

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXA01856

<400> 2467

cactctccag cggtcgcgcc agatatgcag ccaactcttg atcgtggtgt ggaagcgctg 60

gttgtagctg cttctgcgtg gctagtaaaa taattggcta atg aat cct ttt ctt 115
 Met Asn Pro Phe Leu
 1 5

tcg gac acg ttg att gtc cag cag acc tct tcc ttc ctg tct aac aac 163
 Ser Asp Thr Leu Ile Val Gln Gln Thr Ser Ser Phe Leu Ser Asn Asn
 10 15 20

ttt gag atc tac aat cca gac ggc gaa gtt gtt atc aga atc aaa act 211
 Phe Glu Ile Tyr Asn Pro Asp Gly Glu Val Val Ile Arg Ile Lys Thr
 25 30 35

gaa ggg tcg ttg ggc tct cgg ctg gtc aag ggc gac cgc aga ttc aca 259
 Glu Gly Ser Leu Gly Ser Arg Leu Val Lys Gly Asp Arg Arg Phe Thr
 40 45 50

ctg gaa gac gcc ttc ggc acc cca ttg atg cag gtg cgc gat ccc atg 307
 Leu Glu Asp Ala Phe Gly Thr Pro Leu Met Gln Val Arg Asp Pro Met
 55 60 65

aac ttt gtt cgc gac acc tat gaa att gat gat cca aat ggc aat ccc 355
 Asn Phe Val Arg Asp Thr Tyr Glu Ile Asp Asp Pro Asn Gly Asn Pro
 70 75 80 85

att gct cat gtg cgg aag cgt ttc acc ttc ttc aac aag cgg atg gac 403
 Ile Ala His Val Arg Lys Arg Phe Thr Phe Phe Asn Lys Arg Met Asp
 90 95 100

atc gaa cta cca ggt gac cgc gtt att gaa atg cac ggt aac ttc ctt 451
 Ile Glu Leu Pro Gly Asp Arg Val Ile Glu Met His Gly Asn Phe Leu
 105 110 115

gga ttt gaa ttt gag ttc cgc atg ggc gat cgg att cct gcg aaa gta 499
 Gly Phe Glu Phe Glu Phe Arg Met Gly Asp Arg Ile Pro Ala Lys Val
 120 125 130

acc cga aaa tgg tcc ggc gct ggc aac gga tac cta ggc cga agc acc 547
 Thr Arg Lys Trp Ser Gly Ala Gly Asn Gly Tyr Leu Gly Arg Ser Thr
 135 140 145

tac gcc ctt att ttc gat gaa gaa gcc cct gat gaa atc aga aaa gtc 595
 Tyr Ala Leu Ile Phe Asp Glu Glu Ala Pro Asp Glu Ile Arg Lys Val
 150 155 160 165

atc att gga ggc atg gtc gcg cta gat ctg atc cgg gag aag gaa cgt 643
 Ile Ile Gly Gly Met Val Ala Leu Asp Leu Ile Arg Glu Lys Glu Arg
 170 175 180

aat taagccaccc ccgtttcatg tct 669
 Asn

<210> 2468

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 2468

Met Asn Pro Phe Leu Ser Asp Thr Leu Ile Val Gln Gln Thr Ser Ser
1 5 10 15

Phe Leu Ser Asn Asn Phe Glu Ile Tyr Asn Pro Asp Gly Glu Val Val
20 25 30

Ile Arg Ile Lys Thr Glu Gly Ser Leu Gly Ser Arg Leu Val Lys Gly
35 40 45

Asp Arg Arg Phe Thr Leu Glu Asp Ala Phe Gly Thr Pro Leu Met Gln
50 55 60

Val Arg Asp Pro Met Asn Phe Val Arg Asp Thr Tyr Glu Ile Asp Asp
65 70 75 80

Pro Asn Gly Asn Pro Ile Ala His Val Arg Lys Arg Phe Thr Phe Phe
85 90 95

Asn Lys Arg Met Asp Ile Glu Leu Pro Gly Asp Arg Val Ile Glu Met
100 105 110

His Gly Asn Phe Leu Gly Phe Glu Phe Glu Phe Arg Met Gly Asp Arg
115 120 125

Ile Pro Ala Lys Val Thr Arg Lys Trp Ser Gly Ala Gly Asn Gly Tyr
130 135 140

Leu Gly Arg Ser Thr Tyr Ala Leu Ile Phe Asp Glu Glu Ala Pro Asp
145 150 155 160

Glu Ile Arg Lys Val Ile Ile Gly Gly Met Val Ala Leu Asp Leu Ile
165 170 175

Arg Glu Lys Glu Arg Asn
180

<210> 2469

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01857

<400> 2469

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tcgtactaat ctaacttaat ctctccctag gagttctccc atg gct tca cgc cgt 115
Met Ala Ser Arg Arg

	1	5	
ttc cgt atg atg ctc acc gca agc atc acc gca gct tcc ctt ggt ttt			163
Phe Arg Met Met Leu Thr Ala Ser Ile Thr Ala Ala Ser Leu Gly Phe			
	10	20	
tcc ctc acc cca gca atc gcc gat gaa gct gta acc gtt gct acg gca			211
Ser Leu Thr Pro Ala Ile Ala Asp Glu Ala Val Thr Val Ala Thr Ala			
	25	35	
ccc tcc gtc gga ttc gat tcc ggc gtc gaa cgc gat gca cca ttc acc			259
Pro Ser Val Gly Phe Asp Ser Gly Val Glu Arg Asp Ala Pro Phe Thr			
	40	50	
gca gtt cca cac gac gta gtt ctc ggc gtt gga gcg acc cag tcc gag			307
Ala Val Pro His Asp Val Val Leu Gly Val Gly Ala Thr Gln Ser Glu			
	55	65	
ctc att ttc aac tgg atc acc gcg cag ggc cta acc ggc cag gtt gca			355
Leu Ile Phe Asn Trp Ile Thr Ala Gln Gly Leu Thr Gly Gln Val Ala			
	70	80	85
cag atc tcc ctg gac gat acc ttc gca tcc cca atc acc gtt gat gca			403
Gln Ile Ser Leu Asp Asp Thr Phe Ala Ser Pro Ile Thr Val Asp Ala			
	90	95	100
gtt tct gaa aac gtc agc atc gtg aac acc gaa ggc gat tcc cgc gac			451
Val Ser Glu Asn Val Ser Ile Val Asn Thr Glu Gly Asp Ser Arg Asp			
	105	110	115
cga gct gaa ggt gaa tac gtt gaa tac cgc gat ggc gca gtc aac cgc			499
Arg Ala Glu Gly Glu Tyr Val Glu Tyr Arg Asp Gly Ala Val Asn Arg			
	120	125	130
gca acc gta gat agc ctc gca gaa aac acc acc tac tcc tac cgc gtc			547
Ala Thr Val Asp Ser Leu Ala Glu Asn Thr Thr Tyr Ser Tyr Arg Val			
	135	140	145
ggc tcc gaa gct gac ggc tgg tcc gaa gtg caa acc ttc aac acc ggc			595
Gly Ser Glu Ala Asp Gly Trp Ser Glu Val Gln Thr Phe Asn Thr Gly			
	150	155	160
acc tac ggt gac aac tgg aac ttc ctc ttc ttc ggc gac acc cag ctg			643
Thr Tyr Gly Asp Asn Trp Asn Phe Leu Phe Phe Gly Asp Thr Gln Leu			
	170	175	180
tac aac acc cac tcc aac cgt gca gaa gaa gtc cag aac tgg gca aac			691
Tyr Asn Thr His Ser Asn Arg Ala Glu Glu Val Gln Asn Trp Ala Asn			
	185	190	195
aac ctg gaa cgg cgg ccc acc aat cga aaa ccc agg aac ctc ctt cat			739
Asn Leu Glu Arg Arg Pro Thr Asn Arg Lys Pro Arg Asn Leu Leu His			
	200	205	210
cct ctc cgc ggg tgatcaggca aaccactcca gct			774
Pro Leu Arg Gly			
	215		

<210> 2470

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 2470

Met Ala Ser Arg Arg Phe Arg Met Met Leu Thr Ala Ser Ile Thr Ala
1 5 10 15
Ala Ser Leu Gly Phe Ser Leu Thr Pro Ala Ile Ala Asp Glu Ala Val
20 25 30
Thr Val Ala Thr Ala Pro Ser Val Gly Phe Asp Ser Gly Val Glu Arg
35 40 45
Asp Ala Pro Phe Thr Ala Val Pro His Asp Val Val Leu Gly Val Gly
50 55 60
Ala Thr Gln Ser Glu Leu Ile Phe Asn Trp Ile Thr Ala Gln Gly Leu
65 70 75 80
Thr Gly Gln Val Ala Gln Ile Ser Leu Asp Asp Thr Phe Ala Ser Pro
85 90 95
Ile Thr Val Asp Ala Val Ser Glu Asn Val Ser Ile Val Asn Thr Glu
100 105 110
Gly Asp Ser Arg Asp Arg Ala Glu Gly Glu Tyr Val Glu Tyr Arg Asp
115 120 125
Gly Ala Val Asn Arg Ala Thr Val Asp Ser Leu Ala Glu Asn Thr Thr
130 135 140
Tyr Ser Tyr Arg Val Gly Ser Glu Ala Asp Gly Trp Ser Glu Val Gln
145 150 155 160
Thr Phe Asn Thr Gly Thr Tyr Gly Asp Asn Trp Asn Phe Leu Phe Phe
165 170 175
Gly Asp Thr Gln Leu Tyr Asn Thr His Ser Asn Arg Ala Glu Glu Val
180 185 190
Gln Asn Trp Ala Asn Asn Leu Glu Arg Arg Pro Thr Asn Arg Lys Pro
195 200 205
Arg Asn Leu Leu His Pro Leu Arg Gly
210 215

<210> 2471

<211> 673

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(673)

<223> RXA01858

<400> 2471

cgtgtgtttg ttttgactgg aacagcgtcg gcttttcggc cacgcggcct gcggacagta 60
gcggaatcac gcgggacatt gatccccgga cgtaaagccg atg ttt atg aca ccg 115

	Met	Phe	Met	Thr	Pro	
	1				5	
cgg gcg ttg acc gaa gat aat gag ttg acc ctg gct ttg aaa tca ctc						163
Arg Ala Leu Thr Glu Asp Asn Glu Leu Thr Leu Ala Leu Lys Ser Leu						
	10			15	20	
gga ggg ctt atg gtg tca ccc aat gag tgc tca gta gtg aca gaa gtg						211
Gly Gly Leu Met Val Ser Pro Asn Glu Cys Ser Val Val Thr Glu Val						
	25			30	35	
atg ccg act tgg aga gaa tta tgg cat caa agg ctt cga tgg caa cgc						259
Met Pro Thr Trp Arg Glu Leu Trp His Gln Arg Leu Arg Trp Gln Arg						
	40			45	50	
ggt gcg ctg gaa aac ctc ggt gct tat ggc atc aca cca caa acg aca						307
Gly Ala Leu Glu Asn Leu Gly Ala Tyr Gly Ile Thr Pro Gln Thr Thr						
	55			60	65	
cgg tat tgg ttc cag cag ctg gga atc ggt tac ggc gca tta gcc ttg						355
Arg Tyr Trp Phe Gln Gln Leu Gly Ile Gly Tyr Gly Ala Leu Ala Leu						
	70			75	80	85
gtc gcc tat ttc gca gtc att atc att acg ttt ctc gcc cgc gat caa						403
Val Ala Tyr Phe Ala Val Ile Ile Ile Thr Phe Leu Ala Arg Asp Gln						
	90			95	100	
tgg atc tgg tat cca ttc tgg atg ctg ctg gga ctg ttg ttc atg att						451
Trp Ile Trp Tyr Pro Phe Trp Met Leu Leu Gly Leu Leu Phe Met Ile						
	105			110	115	
gaa cgc gtg cta acg gtg tgg aga tcc aca tgg ttt gcc agg ttt gtt						499
Glu Arg Val Leu Thr Val Trp Arg Ser Thr Trp Phe Ala Arg Phe Val						
	120			125	130	
gct gcg tta tta atc cca gag ctc atc tac gcc agc tat ctc aac ctg						547
Ala Ala Leu Leu Ile Pro Glu Leu Ile Tyr Ala Ser Tyr Leu Asn Leu						
	135			140	145	
gta ttt ctc aaa ggc gtt gtg gat att cta ttg gcc aag caa gct cac						595
Val Phe Leu Lys Gly Val Val Asp Ile Leu Leu Ala Lys Gln Ala His						
	150			155	160	165
tgg ggt gag cat ggt gac aag aca atg cag gta gcc gat gca gct gcc						643
Trp Gly Glu His Gly Asp Lys Thr Met Gln Val Ala Asp Ala Ala Ala						
	170			175	180	
gaa att aac gat gaa ggg gag gaa cgc cga						673
Glu Ile Asn Asp Glu Gly Glu Glu Arg Arg						
	185			190		

<210> 2472

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 2472

Met	Phe	Met	Thr	Pro	Arg	Ala	Leu	Thr	Glu	Asp	Asn	Glu	Leu	Thr	Leu
1				5					10					15	

Ala Leu Lys Ser Leu Gly Gly Leu Met Val Ser Pro Asn Glu Cys Ser
 20 25 30
 Val Val Thr Glu Val Met Pro Thr Trp Arg Glu Leu Trp His Gln Arg
 35 40 45
 Leu Arg Trp Gln Arg Gly Ala Leu Glu Asn Leu Gly Ala Tyr Gly Ile
 50 55 60
 Thr Pro Gln Thr Thr Arg Tyr Trp Phe Gln Gln Leu Gly Ile Gly Tyr
 65 70 75 80
 Gly Ala Leu Ala Leu Val Ala Tyr Phe Ala Val Ile Ile Ile Thr Phe
 85 90 95
 Leu Ala Arg Asp Gln Trp Ile Trp Tyr Pro Phe Trp Met Leu Leu Gly
 100 105 110
 Leu Leu Phe Met Ile Glu Arg Val Leu Thr Val Trp Arg Ser Thr Trp
 115 120 125
 Phe Ala Arg Phe Val Ala Ala Leu Leu Ile Pro Glu Leu Ile Tyr Ala
 130 135 140
 Ser Tyr Leu Asn Leu Val Phe Leu Lys Gly Val Val Asp Ile Leu Leu
 145 150 155 160
 Ala Lys Gln Ala His Trp Gly Glu His Gly Asp Lys Thr Met Gln Val
 165 170 175
 Ala Asp Ala Ala Ala Glu Ile Asn Asp Glu Gly Glu Glu Arg Arg
 180 185 190

<210> 2473

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXA01870

<400> 2473

ggatcatgtc caccccagaa ggtagcctgt cagtgtgagc gtaatcgagg gcaagtacca 60

gctgaaacct caaggccgag gtggcctgtg gtgggtcaatc gtg ggt gtg gca gtt 115
 Val Gly Val Ala Val
 1 5

gtt ttg ttg ctg ctt cca acg ttg atc aac ctg gtg gtt ccg gat aaa 163
 Val Leu Leu Leu Leu Pro Thr Leu Ile Asn Leu Val Val Pro Asp Lys
 10 15 20

gcc aat gac tac aag cag cta gaa atc gat ctt ctg ggt gtg gat tgg 211
 Ala Asn Asp Tyr Lys Gln Leu Glu Ile Asp Leu Leu Gly Val Asp Trp
 25 30 35

tca gtg cca atc acc acg gag gaa tcc gct gcg gtg ctg tgt gag gaa 259
 Ser Val Pro Ile Thr Thr Glu Glu Ser Ala Ala Val Leu Cys Glu Glu

40	45	50	
aca tct gat gaa atc aca cag aag tat tgg gac tgc aac ggg gac acc			307
Thr Ser Asp Glu Ile Thr Gln Lys Tyr Trp Asp Cys Asn Gly Asp Thr			
55	60	65	
acg gtg gtg acc atg atc gtc gag ggc gtg aaa gat ccg tcc aat acg			355
Thr Val Val Thr Met Ile Val Glu Gly Val Lys Asp Pro Ser Asn Thr			
70	75	80	85
ttg cgt cgc atg gtg ggt tca tcg ctg ata acc agt gtg gat gac agc			403
Leu Arg Arg Met Val Gly Ser Ser Leu Ile Thr Ser Val Asp Asp Ser			
90	95	100	
cta gag gca gta tct agc gaa gat ggc cgt gcg cat gcg ttg tat gtg			451
Leu Glu Ala Val Ser Ser Glu Asp Gly Arg Ala His Ala Leu Tyr Val			
105	110	115	
cca ggt cag caa gaa gga tct ttg tgg acg ctg cct atc gtg gca ctg			499
Pro Gly Gln Gln Glu Gly Ser Leu Trp Thr Leu Pro Ile Val Ala Leu			
120	125	130	
agc gtg cag ggt tcg ggt gat tat gaa gac ctc aca gcg atc gca att			547
Ser Val Gln Gly Ser Gly Asp Tyr Glu Asp Leu Thr Ala Ile Ala Ile			
135	140	145	
atc aac ggc acc tcg ttg gat tat tac agc acc cac att tgg tcc agc			595
Ile Asn Gly Thr Ser Leu Asp Tyr Tyr Ser Thr His Ile Trp Ser Ser			
150	155	160	165
atg gcc gct gac cgc ggg ttg ccg tac cag cag gac ttc ccc ctg atg			643
Met Ala Ala Asp Arg Gly Leu Pro Tyr Gln Gln Asp Phe Pro Leu Met			
170	175	180	
ctg gaa gag gag cca tgg caa gac acc ccc ggc ggg gat cgt ccc ttc			691
Leu Glu Glu Glu Pro Trp Gln Asp Thr Pro Gly Gly Asp Arg Pro Phe			
185	190	195	
gag ctg ccc aat gat ttc ttt gat cag tac ccc gat ctt ttt ggc cca			739
Glu Leu Pro Asn Asp Phe Phe Asp Gln Tyr Pro Asp Leu Phe Gly Pro			
200	205	210	
ggc tcc gtc att ccc aac ctt gaa gga gaa tcc cta tgagtcgcat			785
Gly Ser Val Ile Pro Asn Leu Glu Gly Glu Ser Leu			
215	220	225	
gttttagcatc acc			798

<210> 2474

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 2474

Val Gly Val Ala Val Val Leu Leu Leu Leu Pro Thr Leu Ile Asn Leu
1 5 10 15

Val Val Pro Asp Lys Ala Asn Asp Tyr Lys Gln Leu Glu Ile Asp Leu
20 25 30

Leu	Gly	Val 35	Asp	Trp	Ser	Val	Pro 40	Ile	Thr	Thr	Glu	Glu 45	Ser	Ala	Ala
Val	Leu 50	Cys	Glu	Glu	Thr	Ser 55	Asp	Glu	Ile	Thr	Gln 60	Lys	Tyr	Trp	Asp
Cys 65	Asn	Gly	Asp	Thr	Thr 70	Val	Val	Thr	Met	Ile 75	Val	Glu	Gly	Val	Lys 80
Asp	Pro	Ser	Asn	Thr 85	Leu	Arg	Arg	Met	Val 90	Gly	Ser	Ser	Leu	Ile 95	Thr
Ser	Val	Asp	Asp 100	Ser	Leu	Glu	Ala	Val 105	Ser	Ser	Glu	Asp	Gly 110	Arg	Ala
His	Ala 115	Leu	Tyr	Val	Pro	Gly	Gln 120	Gln	Glu	Gly	Ser	Leu 125	Trp	Thr	Leu
Pro	Ile 130	Val	Ala	Leu	Ser	Val 135	Gln	Gly	Ser	Gly	Asp 140	Tyr	Glu	Asp	Leu
Thr 145	Ala	Ile	Ala	Ile	Ile 150	Asn	Gly	Thr	Ser	Leu 155	Asp	Tyr	Tyr	Ser	Thr 160
His	Ile	Trp	Ser	Ser 165	Met	Ala	Ala	Asp	Arg 170	Gly	Leu	Pro	Tyr	Gln 175	Gln
Asp	Phe	Pro	Leu 180	Met	Leu	Glu	Glu	Glu 185	Pro	Trp	Gln	Asp	Thr 190	Pro	Gly
Gly	Asp	Arg 195	Pro	Phe	Glu	Leu	Pro 200	Asn	Asp	Phe	Phe	Asp 205	Gln	Tyr	Pro
Asp	Leu 210	Phe	Gly	Pro	Gly	Ser 215	Val	Ile	Pro	Asn 220	Leu	Glu	Gly	Glu	Ser

Leu
225

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<210> 2475
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1063)  
<223> RXA01871
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<400> 2475
gcgggggatcg tcccttcgag ctgcccaatg atttctttga tcagtacccc gatctttttg 60
gccagggtc cgtcattccc aaccttgaag gagaatccct atg agt cgc atg ttt      115
                                         Met Ser Arg Met Phe
                                           1           5
agc atc acc ttg tgg gtt gcc atc ctc ctc tca acc ccg gcg ctg ttt      163
Ser Ile Thr Leu Trp Val Ala Ile Leu Leu Ser Thr Pro Ala Leu Phe
                        10                      15                    20
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ttg agc ttg gcc acg ttc atc ttc gtg gat ggc atc tct gtc ctc gtg	211
Leu Ser Leu Ala Thr Phe Ile Phe Val Asp Gly Ile Ser Val Leu Val	
25 30 35	
aat ata gtg ttc gcg gtg ctc tac ttg gta gtc att gtt ttc ctg tta	259
Asn Ile Val Phe Ala Val Leu Tyr Leu Val Val Ile Val Phe Leu Leu	
40 45 50	
agt cgc acc ccg ctg tgg cca cgt ttt aaa ggc tcc ggc agc aag aag	307
Ser Arg Thr Pro Leu Trp Pro Arg Phe Lys Gly Ser Gly Ser Lys Lys	
55 60 65	
gga ggc gga ttc gcg tgg gcg gcg tca tca ttg ttg tgg ggc gcg ttc	355
Gly Gly Gly Phe Ala Trp Ala Ala Ser Ser Leu Leu Trp Gly Ala Phe	
70 75 80 85	
gtt ggt ttc ggc atc gtc atg ttg ttt gcc ggt ccg gtc atg gat ctc	403
Val Gly Phe Gly Ile Val Met Leu Phe Ala Gly Pro Val Met Asp Leu	
90 95 100	
acg gac aaa ctc ggc tgg gat ttc gtt gcc atg agt ttc acc gga gcg	451
Thr Asp Lys Leu Gly Trp Asp Phe Val Ala Met Ser Phe Thr Gly Ala	
105 110 115	
tat cca gaa gaa atc gcc aaa gcg tta ggc gtt gcc atc atc ttg ttg	499
Tyr Pro Glu Ile Ala Lys Ala Leu Gly Val Ala Ile Ile Leu Leu	
120 125 130	
agc ttc cgc caa ctc aac cgt ccg tgg cat gga ttt atc acc ggc gcg	547
Ser Phe Arg Gln Leu Asn Arg Pro Trp His Gly Phe Ile Thr Gly Ala	
135 140 145	
cta gtg ggc tta ggt ttt gag gtc aac gaa aac ctc ctc tat ggc gcc	595
Leu Val Gly Leu Gly Phe Glu Val Asn Glu Asn Leu Leu Tyr Gly Ala	
150 155 160 165	
acc ggt gca atc atg gac ccc aac gct gac ctc gac ggc gtc ctt atg	643
Thr Gly Ala Ile Met Asp Pro Asn Ala Asp Leu Asp Gly Val Leu Met	
170 175 180	
atg tgg caa tac cgc acc atg ttg ggc cca ctc atc cat acg ttg ctc	691
Met Trp Gln Tyr Arg Thr Met Leu Gly Pro Leu Ile His Thr Leu Leu	
185 190 195	
acc gga ttc gca ggt tac ggc atc gcg ttg gca ttc ttc cgc gca cga	739
Thr Gly Phe Ala Gly Tyr Gly Ile Ala Leu Ala Phe Phe Arg Ala Arg	
200 205 210	
aaa aca gtc gcc tgg cgc tgg ggc gtg gcg atc ggt tgg act ctc atc	787
Lys Thr Val Ala Trp Arg Trp Gly Val Ala Ile Gly Trp Thr Leu Ile	
215 220 225	
gcc ttc gca ctg cat ttt tca tgg aac ctg atg tgg gaa aac gta atc	835
Ala Phe Ala Leu His Phe Ser Trp Asn Leu Met Trp Glu Asn Val Ile	
230 235 240 245	
ggt tcc tat gtc acc atc atc gtg gtc agc gtt gtc atg tac ggt ctg	883
Gly Ser Tyr Val Thr Ile Ile Val Val Ser Val Val Met Tyr Gly Leu	
250 255 260	
gct atc tac atc ctc tgg agt aat tgg gcc gaa gcc cgc aac gac tcc	931

Ala Ile Tyr Ile Leu Trp Ser Asn Trp Ala Glu Ala Arg Asn Asp Ser
 265 270 275
 agc tac gct ttc gtc ccg gga atc atc aca aac acc aaa gat tta tcg 979
 Ser Tyr Ala Phe Val Pro Gly Ile Ile Thr Asn Thr Lys Asp Leu Ser
 280 285 290
 ctt ctt gac gcc ccc att cca gta ggc gct gag gtt ccc gag tcg cgc 1027
 Leu Leu Asp Ala Pro Ile Pro Val Gly Ala Glu Val Pro Glu Ser Arg
 295 300 305
 att ccc caa cag ata gag gaa ccc aag gcg gag aac tagctttcac 1073
 Ile Pro Gln Gln Ile Glu Glu Pro Lys Ala Glu Asn
 310 315 320
 tcgctctcca tcc 1086

<210> 2476

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 2476

Met Ser Arg Met Phe Ser Ile Thr Leu Trp Val Ala Ile Leu Leu Ser
 1 5 10 15
 Thr Pro Ala Leu Phe Leu Ser Leu Ala Thr Phe Ile Phe Val Asp Gly
 20 25 30
 Ile Ser Val Leu Val Asn Ile Val Phe Ala Val Leu Tyr Leu Val Val
 35 40 45
 Ile Val Phe Leu Leu Ser Arg Thr Pro Leu Trp Pro Arg Phe Lys Gly
 50 55 60
 Ser Gly Ser Lys Lys Gly Gly Gly Phe Ala Trp Ala Ala Ser Ser Leu
 65 70 75 80
 Leu Trp Gly Ala Phe Val Gly Phe Gly Ile Val Met Leu Phe Ala Gly
 85 90 95
 Pro Val Met Asp Leu Thr Asp Lys Leu Gly Trp Asp Phe Val Ala Met
 100 105 110
 Ser Phe Thr Gly Ala Tyr Pro Glu Glu Ile Ala Lys Ala Leu Gly Val
 115 120 125
 Ala Ile Ile Leu Leu Ser Phe Arg Gln Leu Asn Arg Pro Trp His Gly
 130 135 140
 Phe Ile Thr Gly Ala Leu Val Gly Leu Gly Phe Glu Val Asn Glu Asn
 145 150 155 160
 Leu Leu Tyr Gly Ala Thr Gly Ala Ile Met Asp Pro Asn Ala Asp Leu
 165 170 175
 Asp Gly Val Leu Met Met Trp Gln Tyr Arg Thr Met Leu Gly Pro Leu
 180 185 190
 Ile His Thr Leu Leu Thr Gly Phe Ala Gly Tyr Gly Ile Ala Leu Ala

195					200					205					
Phe	Phe	Arg	Ala	Arg	Lys	Thr	Val	Ala	Trp	Arg	Trp	Gly	Val	Ala	Ile
210						215					220				
Gly	Trp	Thr	Leu	Ile	Ala	Phe	Ala	Leu	His	Phe	Ser	Trp	Asn	Leu	Met
225					230					235					240
Trp	Glu	Asn	Val	Ile	Gly	Ser	Tyr	Val	Thr	Ile	Ile	Val	Val	Ser	Val
				245					250					255	
Val	Met	Tyr	Gly	Leu	Ala	Ile	Tyr	Ile	Leu	Trp	Ser	Asn	Trp	Ala	Glu
			260					265					270		
Ala	Arg	Asn	Asp	Ser	Ser	Tyr	Ala	Phe	Val	Pro	Gly	Ile	Ile	Thr	Asn
		275					280					285			
Thr	Lys	Asp	Leu	Ser	Leu	Leu	Asp	Ala	Pro	Ile	Pro	Val	Gly	Ala	Glu
	290					295					300				
Val	Pro	Glu	Ser	Arg	Ile	Pro	Gln	Gln	Ile	Glu	Glu	Pro	Lys	Ala	Glu
305					310					315					320

Asn

<210> 2477

<211> 302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(279)

<223> RXA01903

<400> 2477

gct	cac	ctt	gat	gac	cgt	ggc	atc	tat	atc	atc	cca	gct	caa	tat	cct	48
Ala	His	Leu	Asp	Asp	Arg	Gly	Ile	Tyr	Ile	Ile	Pro	Ala	Gln	Tyr	Pro	
1				5					10					15		

tgg	gga	tac	gag	gaa	atc	att	aac	cta	ccg	gca	cgc	gct	acc	tct	aca	96
Trp	Gly	Tyr	Glu	Ile	Ile	Asn	Leu	Pro	Ala	Arg	Ala	Thr	Ser	Thr		
			20				25					30				

cct	gct	gtt	gct	cct	cgc	act	gag	gct	gct	cca	gct	aca	gta	tct	gat	144
Pro	Ala	Val	Ala	Pro	Arg	Thr	Glu	Ala	Ala	Pro	Ala	Thr	Val	Ser	Asp	
		35					40					45				

gct	gag	gtc	cag	agc	ctg	ctt	gag	tac	ttg	cgt	act	aat	gct	ttc	gta	192
Ala	Glu	Val	Gln	Ser	Leu	Leu	Glu	Tyr	Leu	Arg	Thr	Asn	Ala	Phe	Val	
	50					55				60						

agt	cgt	cac	gac	ggc	gac	acc	acg	aag	gcc	gac	atc	ttc	aac	aag	cac	240
Ser	Arg	His	Asp	Gly	Asp	Thr	Thr	Lys	Ala	Asp	Ile	Phe	Asn	Lys	His	
	65				70				75					80		

gcg	gat	act	gtc	aac	aag	ctt	gca	gca	cta	cgt	gca	ccc	taa	cccc	aca	289
Ala	Asp	Thr	Val	Asn	Lys	Leu	Ala	Ala	Leu	Arg	Ala	Pro				
				85					90							

ccgcataacc ccc

302

<210> 2478

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 2478

Ala His Leu Asp Asp Arg Gly Ile Tyr Ile Ile Pro Ala Gln Tyr Pro
 1 5 10 15

Trp Gly Tyr Glu Glu Ile Ile Asn Leu Pro Ala Arg Ala Thr Ser Thr
 20 25 30

Pro Ala Val Ala Pro Arg Thr Glu Ala Ala Pro Ala Thr Val Ser Asp
 35 40 45

Ala Glu Val Gln Ser Leu Leu Glu Tyr Leu Arg Thr Asn Ala Phe Val
 50 55 60

Ser Arg His Asp Gly Asp Thr Thr Lys Ala Asp Ile Phe Asn Lys His
 65 70 75 80

Ala Asp Thr Val Asn Lys Leu Ala Ala Leu Arg Ala Pro
 85 90

<210> 2479

<211> 546

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(523)

<223> RXA01904

<400> 2479

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acacttgagg taatacagtt acgaggctaa ggagtatgta atg agc att tcg ccg 115
 Met Ser Ile Ser Pro
 1 5

aag aat tcc ggt aca cca aac gag aac gcc gca gca gcg cag gtg gca 163
 Lys Asn Ser Gly Thr Pro Asn Glu Asn Ala Ala Ala Ala Gln Val Ala
 10 15 20

gca aat ctg gct aat tta acg tcg cag gct aca ggg tcc atg gac gaa 211
 Ala Asn Leu Ala Asn Leu Thr Ser Gln Ala Thr Gly Ser Met Asp Glu
 25 30 35

act aat gag caa gtc att aaa agt aac gag cat ggc tct gat gct tat 259
 Thr Asn Glu Gln Val Ile Lys Ser Asn Glu His Gly Ser Asp Ala Tyr
 40 45 50

ttg gcg gat att aaa gcc agt cga gag atg tgg gca aaa att gcg ctc 307
 Leu Ala Asp Ile Lys Ala Ser Arg Glu Met Trp Ala Lys Ile Ala Leu
 55 60 65

gat ccg aat caa tct gaa gaa act agg aaa gaa gct cgg gag aat atg 355
 Asp Pro Asn Gln Ser Glu Glu Thr Arg Lys Glu Ala Arg Glu Asn Met
 70 75 80 85

gcg cgg ata gat gag tac gct cgt gag cac gat aaa gac aac aag ggt 403
 Ala Arg Ile Asp Glu Tyr Ala Arg Glu His Asp Lys Asp Asn Lys Gly
 90 95 100

ttg ttg cag aag tta gcg aaa aac aaa gca gag ctc atc ggg act gtt 451
 Leu Leu Gln Lys Leu Ala Lys Asn Lys Ala Glu Leu Ile Gly Thr Val
 105 110 115

gcg gtt gca acc tta ggt gta gtg gca gcc att gct aac aat ggc aag 499
 Ala Val Ala Thr Leu Gly Val Val Ala Ala Ile Ala Asn Asn Gly Lys
 120 125 130

ata ccg atg att cag ttg aaa aaa taacccccgc acaggctgga cat 546
 Ile Pro Met Ile Gln Leu Lys Lys
 135 140

<210> 2480

<211> 141

<212> PRT

<213> Corynebacterium glutamicum

<400> 2480

Met Ser Ile Ser Pro Lys Asn Ser Gly Thr Pro Asn Glu Asn Ala Ala
 1 5 10 15

Ala Ala Gln Val Ala Ala Asn Leu Ala Asn Leu Thr Ser Gln Ala Thr
 20 25 30

Gly Ser Met Asp Glu Thr Asn Glu Gln Val Ile Lys Ser Asn Glu His
 35 40 45

Gly Ser Asp Ala Tyr Leu Ala Asp Ile Lys Ala Ser Arg Glu Met Trp
 50 55 60

Ala Lys Ile Ala Leu Asp Pro Asn Gln Ser Glu Glu Thr Arg Lys Glu
 65 70 75 80

Ala Arg Glu Asn Met Ala Arg Ile Asp Glu Tyr Ala Arg Glu His Asp
 85 90 95

Lys Asp Asn Lys Gly Leu Leu Gln Lys Leu Ala Lys Asn Lys Ala Glu
 100 105 110

Leu Ile Gly Thr Val Ala Val Ala Thr Leu Gly Val Val Ala Ala Ile
 115 120 125

Ala Asn Asn Gly Lys Ile Pro Met Ile Gln Leu Lys Lys
 130 135 140

<210> 2481

<211> 654

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(631)

<223> RXA01905

<400> 2481

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caaaaaacct cactactttc tacagaaagg cgtcttcctc atg aag gct tct cag 115
                                         Met Lys Ala Ser Gln
                                         1                               5

acc ctc acc cgc aac act cgt gca cgc aag ctc ggc atg ggt att ctc 163
Thr Leu Thr Arg Asn Thr Arg Ala Arg Lys Leu Gly Met Gly Ile Leu
                        10                        15                        20

gca gca act att atg gct acc ggt gca ctt gct ggc act gct cca cag 211
Ala Ala Thr Ile Met Ala Thr Gly Ala Leu Ala Gly Thr Ala Pro Gln
                        25                        30                        35

gcg aca gca gca gta gat acc act gcg cca tac gtg tcc tat gtc gtt 259
Ala Thr Ala Ala Val Asp Thr Thr Ala Pro Tyr Val Ser Tyr Val Val
                        40                        45                        50

gac att cct ggc aag gtt ggt gaa cca atc aag cct cag tac ctc acc 307
Asp Ile Pro Gly Lys Val Gly Glu Pro Ile Lys Pro Gln Tyr Leu Thr
                        55                        60                        65

atc tcc gat cag tcc gcc tac acc gtg acc ttc aag tac atg cca tcc 355
Ile Ser Asp Gln Ser Ala Tyr Thr Val Thr Phe Lys Tyr Met Pro Ser
                        70                        75                        80                        85

tgg ttg aag tac gac gca aac aag aag atg ctg tac ggt acc cca acc 403
Trp Leu Lys Tyr Asp Ala Asn Lys Lys Met Leu Tyr Gly Thr Pro Thr
                        90                        95                        100

gag gtt gat gtc tgg act cct gag gta cat gtt gtt gat gct cat ggc 451
Glu Val Asp Val Trp Thr Pro Glu Val His Val Val Asp Ala His Gly
                        105                        110                        115

aac aag act gtc cgt tac ttc acc gtt gta gca gtc cca gca aac act 499
Asn Lys Thr Val Arg Tyr Phe Thr Val Val Ala Val Pro Ala Asn Thr
                        120                        125                        130

gga cca acc acc acc acg cca tct act tca aag cca tct acc ccg cag 547
Gly Pro Thr Thr Thr Thr Pro Ser Thr Ser Lys Pro Ser Thr Pro Gln
                        135                        140                        145

gtg acc acc cca act act ccg aag gcg cct acc ttg cca aag tcc acc 595
Val Thr Thr Pro Thr Thr Pro Lys Ala Pro Thr Leu Pro Lys Ser Thr
                        150                        155                        160                        165

ttc gac tgg acc ttg tgg ggc tcc atc ttt ggt ttc tagttctcac 641
Phe Asp Trp Thr Leu Trp Gly Ser Ile Phe Gly Phe
                        170                        175

tagcacctca aaa 654

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<210> 2482

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

<400> 2482

Met Lys Ala Ser Gln Thr Leu Thr Arg Asn Thr Arg Ala Arg Lys Leu
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Gly Met Gly Ile Leu Ala Ala Thr Ile Met Ala Thr Gly Ala Leu Ala
 20 25 30

Gly Thr Ala Pro Gln Ala Thr Ala Ala Val Asp Thr Thr Ala Pro Tyr
 35 40 45

Val Ser Tyr Val Val Asp Ile Pro Gly Lys Val Gly Glu Pro Ile Lys
 50 55 60

Pro Gln Tyr Leu Thr Ile Ser Asp Gln Ser Ala Tyr Thr Val Thr Phe
 65 70 75 80

Lys Tyr Met Pro Ser Trp Leu Lys Tyr Asp Ala Asn Lys Lys Met Leu
 85 90 95

Tyr Gly Thr Pro Thr Glu Val Asp Val Trp Thr Pro Glu Val His Val
 100 105 110

Val Asp Ala His Gly Asn Lys Thr Val Arg Tyr Phe Thr Val Val Ala
 115 120 125

Val Pro Ala Asn Thr Gly Pro Thr Thr Thr Thr Pro Ser Thr Ser Lys
 130 135 140

Pro Ser Thr Pro Gln Val Thr Thr Pro Thr Thr Pro Lys Ala Pro Thr
 145 150 155 160

Leu Pro Lys Ser Thr Phe Asp Trp Thr Leu Trp Gly Ser Ile Phe Gly
 165 170 175

Phe

<210> 2483

<211> 588

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(565)

<223> RXA01906

<400> 2483

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gcaccacaac aaccacatt aaagaaaggt ttttcacccc atg tcc gaa ttc cct 115
 Met Ser Glu Phe Pro
 1 5

aca cct acg act ttt cac gtc gaa cca gaa acg ctt agc tcc gcc acc. 163
 Thr Pro Thr Thr Phe His Val Glu Pro Glu Thr Leu Ser Ser Ala Thr
 10 15 20

gat ctc act gtt gat gca cat aaa atc gca gaa ctg ctg ctc agc acc 211
Asp Leu Thr Val Asp Ala His Lys Ile Ala Glu Leu Leu Leu Ser Thr
25 30 35

act gat tac cgt gtg ttc tac atg ccg cgt ctc gcc ggt gtg act cct 259
Thr Asp Tyr Arg Val Phe Tyr Met Pro Arg Leu Ala Gly Val Thr Pro
40 45 50

atc gtg tcc tac ctc tat gtc tac gat ggt gaa aac ttc ctc att gtt 307
Ile Val Ser Tyr Leu Tyr Val Tyr Asp Gly Glu Asn Phe Leu Ile Val
55 60 65

ggg cgc tcc act cat gtg ccg tgg gag tac tac gtt cac tac ccc atc 355
Gly Arg Ser Thr His Val Pro Trp Glu Tyr Tyr Val His Tyr Pro Ile
70 75 80 85

aag cca tca cgt gaa ttt ggc tct gct att gct gtg cct ctc gat gat 403
Lys Pro Ser Arg Glu Phe Gly Ser Ala Ile Ala Val Pro Leu Asp Asp
90 95 100

tct gat gac cct tat gat gca gca gaa gtt gtt gct cta gta aag cag 451
Ser Asp Asp Pro Tyr Asp Ala Ala Glu Val Val Ala Leu Val Lys Gln
105 110 115

tac atg acg ccc acg ctc act cct ggt gag ggt tat atg cag ggc ttt 499
Tyr Met Thr Pro Thr Leu Thr Pro Gly Glu Gly Tyr Met Gln Gly Phe
120 125 130

tac aag ggt ctc acc ttc acc aac cac ctc gat ata cat cga cca ctg 547
Tyr Lys Gly Leu Thr Phe Thr Asn His Leu Asp Ile His Arg Pro Leu
135 140 145

acc cag att atc tca gac taacagctat attcaccac cta 588
Thr Gln Ile Ile Ser Asp
150 155

<210> 2484

<211> 155

<212> PRT

<213> Corynebacterium glutamicum

<400> 2484

Met Ser Glu Phe Pro Thr Pro Thr Thr Phe His Val Glu Pro Glu Thr
1 5 10 15

Leu Ser Ser Ala Thr Asp Leu Thr Val Asp Ala His Lys Ile Ala Glu
20 25 30

Leu Leu Leu Ser Thr Thr Asp Tyr Arg Val Phe Tyr Met Pro Arg Leu
35 40 45

Ala Gly Val Thr Pro Ile Val Ser Tyr Leu Tyr Val Tyr Asp Gly Glu
50 55 60

Asn Phe Leu Ile Val Gly Arg Ser Thr His Val Pro Trp Glu Tyr Tyr
65 70 75 80

Val His Tyr Pro Ile Lys Pro Ser Arg Glu Phe Gly Ser Ala Ile Ala
85 90 95

Val Pro Leu Asp Asp Ser Asp Asp Pro Tyr Asp Ala Ala Glu Val Val
 100 105 110

Ala Leu Val Lys Gln Tyr Met Thr Pro Thr Leu Thr Pro Gly Glu Gly
 115 120 125

Tyr Met Gln Gly Phe Tyr Lys Gly Leu Thr Phe Thr Asn His Leu Asp
 130 135 140

Ile His Arg Pro Leu Thr Gln Ile Ile Ser Asp
 145 150 155

<210> 2485
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> RXA01907

<400> 2485
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ttttcctact tttcctcata actacagaag ggacgccctc atg tct gct ttt gat 115
 Met Ser Ala Phe Asp
 1 5

gaa ctc cgc aag aac tac cgc tac aag ttc act gac acc tgg ccg gcc 163
 Glu Leu Arg Lys Asn Tyr Arg Tyr Lys Phe Thr Asp Thr Trp Pro Ala
 10 15 20

aac gct gtt acc ggc acc ggc tac tac gcc aac cca gct ttt atc atc 211
 Asn Ala Val Thr Gly Thr Gly Tyr Tyr Ala Asn Pro Ala Phe Ile Ile
 25 30 35

atc tcc gct gat gcc atg acg cag aac acc cat gcc gat tcc aat ctc 259
 Ile Ser Ala Asp Ala Met Thr Gln Asn Thr His Ala Asp Ser Asn Leu
 40 45 50

atc acg gtt aaa gag cac ctt aac acc ctg ttt ccg tac agc gta caa 307
 Ile Thr Val Lys Glu His Leu Asn Thr Leu Phe Pro Tyr Ser Val Gln
 55 60 65

cgc aag gat cgt gcc ttt gtc tct gag atc tac acc cct att aac ctg 355
 Arg Lys Asp Arg Ala Phe Val Ser Glu Ile Tyr Thr Pro Ile Asn Leu
 70 75 80 85

ctc gaa gat aat cca gaa cta gct caa gaa ata ctc gat gtg ctc gac 403
 Leu Glu Asp Asn Pro Glu Leu Ala Gln Glu Ile Leu Asp Val Leu Asp
 90 95 100

acc ctg agc aac aac gct gtt ttt aac gat gcg cac tac agc gag ctt 451
 Thr Leu Ser Asn Asn Ala Val Phe Asn Asp Ala His Tyr Ser Glu Leu
 105 110 115

gaa cta gag cgc ctc aat gaa tat gtc atc gac acc ttg gcc tat gac 499
 Glu Leu Glu Arg Leu Asn Glu Tyr Val Ile Asp Thr Leu Ala Tyr Asp

120	125	130	
atg aag tcc gac atg atg cgc gcc ctc gtt aag gcc cga cca gag gcc			547
Met Lys Ser Asp Met Met Arg Ala Leu Val Lys Ala Arg Pro Glu Ala			
135	140	145	
gat ctt gag gcg atg gaa gaa ctc gac att gcc aat atc cag agc tgg			595
Asp Leu Glu Ala Met Glu Glu Leu Asp Ile Ala Asn Ile Gln Ser Trp			
150	155	160	165
att aat ctc cac tcc tcc act gtg agc gaa cac aac gat ggc agc gtt			643
Ile Asn Leu His Ser Ser Thr Val Ser Glu His Asn Asp Gly Ser Val			
170	175	180	
gat gat gca ccg ttt aat tct ctc gca tta gct gag att tat ttg caa			691
Asp Asp Ala Pro Phe Asn Ser Leu Ala Leu Ala Glu Ile Tyr Leu Gln			
185	190	195	
cag ctt gca gac cac act gtc taagcacgct gtgtaactac cac			735
Gln Leu Ala Asp His Thr Val			
200			

<210> 2486

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 2486

Met Ser Ala Phe Asp Glu Leu Arg Lys Asn Tyr Arg Tyr Lys Phe Thr	
1 5 10 15	
Asp Thr Trp Pro Ala Asn Ala Val Thr Gly Thr Gly Tyr Tyr Ala Asn	
20 25 30	
Pro Ala Phe Ile Ile Ile Ser Ala Asp Ala Met Thr Gln Asn Thr His	
35 40 45	
Ala Asp Ser Asn Leu Ile Thr Val Lys Glu His Leu Asn Thr Leu Phe	
50 55 60	
Pro Tyr Ser Val Gln Arg Lys Asp Arg Ala Phe Val Ser Glu Ile Tyr	
65 70 75 80	
Thr Pro Ile Asn Leu Leu Glu Asp Asn Pro Glu Leu Ala Gln Glu Ile	
85 90 95	
Leu Asp Val Leu Asp Thr Leu Ser Asn Asn Ala Val Phe Asn Asp Ala	
100 105 110	
His Tyr Ser Glu Leu Glu Leu Glu Arg Leu Asn Glu Tyr Val Ile Asp	
115 120 125	
Thr Leu Ala Tyr Asp Met Lys Ser Asp Met Met Arg Ala Leu Val Lys	
130 135 140	
Ala Arg Pro Glu Ala Asp Leu Glu Ala Met Glu Glu Leu Asp Ile Ala	
145 150 155 160	
Asn Ile Gln Ser Trp Ile Asn Leu His Ser Ser Thr Val Ser Glu His	
165 170 175	

Asn Asp Gly Ser Val Asp Asp Ala Pro Phe Asn Ser Leu Ala Leu Ala
 180 185 190

Glu Ile Tyr Leu Gln Gln Leu Ala Asp His Thr Val
 195 200

<210> 2487

<211> 529

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXA01923

<400> 2487

ccaaagtgaat taccctcgact gcagcagcgc aaaagttcaa gtactttggg atgcaaattct 60

agtagcacgt cccatgtttc tcacactctc aggagctgac atg tct gca ctt att 115
 Met Ser Ala Leu Ile
 1 5

aaa ggt tca gga cct cat cat gtg gtt gtc tta aat ggt tgg ttt ggt 163
 Lys Gly Ser Gly Pro His His Val Val Leu Asn Gly Trp Phe Gly
 10 15 20

cat gct gcg ggc tgg gga gct ttc gct gac tat ctt gac ctc ggc aac 211
 His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr Leu Asp Leu Gly Asn
 25 30 35

tac acc tgg cac ttt tgg gat tac cga ggt tac ggc aac aga aaa gac 259
 Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr Gly Asn Arg Lys Asp
 40 45 50

gac gca gga gaa ttt act ctg gag gaa att tca gcg gat atc gtt gca 307
 Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser Ala Asp Ile Val Ala
 55 60 65

tac atc gac tcg att gag gca gaa aag gtt tcc atc ctg ggc cat tcc 355
 Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser Ile Leu Gly His Ser
 70 75 80 85

atg ggt gga gtg ttc atg cag aaa gtc ctt gca gac agc gcc acc ccc 403
 Met Gly Gly Val Phe Met Gln Lys Val Leu Ala Asp Ser Ala Thr Pro
 90 95 100

atc gct tca ctg gtt gga att tct gcc gtt gct gca gct gga aca cca 451
 Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala Ala Gly Thr Pro
 105 110 115

ttc gat gag gat tct cgg aag ctt ttc acc tca gca ggg cac aac ccg 499
 Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser Ala Gly His Asn Pro
 120 125 130

gac tcg agg cga gcc atc atc gat ttc acc 529
 Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr
 135 140

<210> 2488

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 2488

Met Ser Ala Leu Ile Lys Gly Ser Gly Pro His His Val Val Val Leu
 1 5 10 15
 Asn Gly Trp Phe Gly His Ala Ala Gly Trp Gly Ala Phe Ala Asp Tyr
 20 25 30
 Leu Asp Leu Gly Asn Tyr Thr Trp His Phe Trp Asp Tyr Arg Gly Tyr
 35 40 45
 Gly Asn Arg Lys Asp Asp Ala Gly Glu Phe Thr Leu Glu Glu Ile Ser
 50 55 60
 Ala Asp Ile Val Ala Tyr Ile Asp Ser Ile Glu Ala Glu Lys Val Ser
 65 70 75 80
 Ile Leu Gly His Ser Met Gly Gly Val Phe Met Gln Lys Val Leu Ala
 85 90 95
 Asp Ser Ala Thr Pro Ile Ala Ser Leu Val Gly Ile Ser Ala Val Ala
 100 105 110
 Ala Ala Gly Thr Pro Phe Asp Glu Asp Ser Arg Lys Leu Phe Thr Ser
 115 120 125
 Ala Gly His Asn Pro Asp Ser Arg Arg Ala Ile Ile Asp Phe Thr
 130 135 140

<210> 2489

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> RXA01931

<400> 2489

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 accaaggcgt acatctaccc ggcactttta gatcagtggc atg agc act tct ttt 115
 Met Ser Thr Ser Phe
 1 5
 gag tcc att ccc gga gtt act atc tcc gct cga aaa gcc ttg agc act 163
 Glu Ser Ile Pro Gly Val Thr Ile Ser Ala Arg Lys Ala Leu Ser Thr
 10 15 20
 gcg ggg ttt aaa gat ctg gaa tcg ctt gca ggt acc aat tac gaa gaa 211
 Ala Gly Phe Lys Asp Leu Glu Ser Leu Ala Gly Thr Asn Tyr Glu Glu
 25 30 35
 gtg gct ggt ctg tca gga att ggc gca cgt act ttg gag cga ttg caa 259

Val Ala Gly Leu Ser Gly Ile Gly Ala Arg Thr Leu Glu Arg Leu Gln
 40 45 50
 gca gcg ctg gtg gag aag aga atg agc ttt ggc ggt aaa gtg cca gag 307
 Ala Ala Leu Val Glu Lys Arg Met Ser Phe Gly Gly Lys Val Pro Glu
 55 60 65
 gca gaa cag cgc acc gcg acg tgg aca acg cta gat tct gca gca cca 355
 Ala Glu Gln Arg Thr Ala Thr Trp Thr Thr Leu Asp Ser Ala Ala Pro
 70 75 80 85
 gag gca aca gaa acc tca gaa tcc cca gag tac ttc att caa aac cta 403
 Glu Ala Thr Glu Thr Ser Glu Ser Pro Glu Tyr Phe Ile Gln Asn Leu
 90 95 100
 gac att cct cgc aga att acc cac ggc cgg ttg ttg ttg gaa att ttc 451
 Asp Ile Pro Arg Arg Ile Thr His Gly Arg Leu Leu Leu Glu Ile Phe
 105 110 115
 aac aga gcg aca ggc cag aaa cct tat gta gca ggg tct tgc att gtt 499
 Asn Arg Ala Thr Gly Gln Lys Pro Tyr Val Ala Gly Ser Ser Ile Val
 120 125 130
 ggt tat ggg cga gtt cat tat cgc tat gcc acg ggt agg gaa ggg atc 547
 Gly Tyr Gly Arg Val His Tyr Arg Tyr Ala Thr Gly Arg Glu Gly Ile
 135 140 145
 act att cgt gtg ggt ttc agt ccg cga aag gca aag att tca ctt tat 595
 Thr Ile Arg Val Gly Phe Ser Pro Arg Lys Ala Lys Ile Ser Leu Tyr
 150 155 160 165
 gga cta acc agt gcg cct gcg tct cga gaa ctt ctg aag aaa ttg ggt 643
 Gly Leu Thr Ser Ala Pro Ala Ser Arg Glu Leu Leu Lys Lys Leu Gly
 170 175 180
 aag cat tct gtt ggt gtg tcc tgc cta tat atc aac aaa cca gag gat 691
 Lys His Ser Val Gly Val Ser Cys Leu Tyr Ile Asn Lys Pro Glu Asp
 185 190 195
 gtt gat ctt gag gtg ctt gag gaa atg atc cgt att tct tgg gaa gcg 739
 Val Asp Leu Glu Val Leu Glu Glu Met Ile Arg Ile Ser Trp Glu Ala
 200 205 210
 gaa cct ggc gaa tgt taaatctcaa cctttaacaa agt 777
 Glu Pro Gly Glu Cys
 215

<210> 2490

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 2490

Met Ser Thr Ser Phe Glu Ser Ile Pro Gly Val Thr Ile Ser Ala Arg
 1 5 10 15
 Lys Ala Leu Ser Thr Ala Gly Phe Lys Asp Leu Glu Ser Leu Ala Gly
 20 25 30
 Thr Asn Tyr Glu Glu Val Ala Gly Leu Ser Gly Ile Gly Ala Arg Thr

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<210> 2491
<211> 558
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(535)
<223> RXA01941
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<400> 2491
ccggacttgc cgctggttta gtcacttttt gctcagcagc gtattttattg gtcgatttca 60
ccagcgcagc gttgaaaaac gttgggcgcc agtcacccac atg gcc ttg act tca 115
Met Ala Leu Thr Ser
1 5
ctt ttg cac cag ctt gca gat aaa aaa cac agt gac ctc agc cgg gaa 163
Leu Leu His Gln Leu Ala Asp Lys Lys His Ser Asp Leu Ser Arg Glu
10 15 20
gac atc gta ccg cgg gcc ttt act gtc ccg acc tct act gac gcc cac 211
Asp Ile Val Pro Arg Ala Phe Thr Val Pro Thr Ser Thr Asp Ala His
25 30 35

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<210> 2492
<211> 145
<212> PRT
<213> Corynebacterium glutamicum
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<400> 2492																
Met	Ala	Leu	Thr	Ser	Leu	Leu	His	Gln	Leu	Ala	Asp	Lys	Lys	His	Ser	
1				5					10					15		
Asp	Leu	Ser	Arg	Glu	Asp	Ile	Val	Pro	Arg	Ala	Phe	Thr	Val	Pro	Thr	
			20					25					30			
Ser	Thr	Asp	Ala	His	Ala	Ile	His	Gln	Asp	Leu	Glu	Lys	Leu	Arg	Asn	
		35					40					45				
Ser	Val	Leu	Lys	Glu	Gln	Asn	His	Leu	Thr	Thr	Val	Leu	Gly	Thr	Trp	
	50					55					60					
Ser	Glu	Phe	Leu	Thr	Ser	Asn	Ser	Asp	Asn	Ser	Asp	Ile	Leu	Arg	Ser	
65					70					75					80	
Ser	Ala	Glu	Leu	Gly	Leu	Gln	Leu	Glu	Gln	Val	Arg	Asp	Lys	Ala	Leu	
				85					90					95		
Glu	Val	Glu	Gln	Arg	Ile	Lys	Ala	Ser	Ala	Gln	Val	Asp	Leu	Thr	Asp	
			100					105					110			
Leu	Ala	His	Glu	Ile	Glu	Ile	Cys	Asn	Gln	His	His	Ala	Thr	Leu	Ile	
		115					120					125				

Ser Ala Ile Gln Val Arg Leu Gln Ser His Thr Ala Glu Leu Arg Ala
 130 135 140

Gly
 145

<210> 2493
 <211> 723
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(700)
 <223> RXA01942

<400> 2493
 gccgcgaaat tccgtgaaat tgaaggtatt cctgcagatc aggcaaattc ttccacgact 60
 gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115
 Met Leu Arg Ile Gly
 1 5
 cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
 Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
 10 15 20
 tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
 Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
 25 30 35
 atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259
 Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe
 40 45 50
 ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
 Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
 55 60 65
 gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
 Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
 70 75 80 85
 att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
 Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
 90 95 100
 gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
 Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
 105 110 115
 gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
 Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp
 120 125 130
 gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc 547
 Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu
 135 140 145
 aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac 595

Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp
 150 155 160 165
 gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta 643
 Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu
 170 175 180
 gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt 691
 Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser
 185 190 195
 cgc gtg aat tagcactaaa acatcgtcaa agt 723
 Arg Val Asn
 200

<210> 2494

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 2494

Met Leu Arg Ile Gly Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr
 1 5 10 15
 Val Ala Asp Leu Leu Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp
 20 25 30
 Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu
 35 40 45
 Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu
 50 55 60
 Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr
 65 70 75 80
 Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala
 85 90 95
 Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr
 100 105 110
 Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu
 115 120 125
 Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val
 130 135 140
 Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser
 145 150 155 160
 Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp
 165 170 175
 Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
 180 185 190
 Ala Glu Ile Leu Ser Arg Val Asn
 195 200

<210> 2495
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> RXA01957

<400> 2495
acctcaactc cacagagcgt tggtatcaga tgctgatatg gctcgccttg cagcacaact 60

gaccgacaaa cactaaaacc tccacaacaa ggacatcatc atg act act cgc acc 115
Met Thr Thr Arg Thr
1 5

gta tct act tct gca ccc cat gtc act gtc aac atc aat acc gcg cac 163
Val Ser Thr Ser Ala Pro His Val Thr Val Asn Ile Asn Thr Ala His
10 15 20

aac aaa aca cgc act gtt acc aat ggc gcc aga aaa act aat gca gag 211
Asn Lys Thr Arg Thr Val Thr Asn Gly Ala Arg Lys Thr Asn Ala Glu
25 30 35

cgt ggc aag agc tgc atc tca ttt cgt gta ggg cca gaa ttg ttt gat 259
Arg Gly Lys Ser Cys Ile Ser Phe Arg Val Gly Pro Glu Leu Phe Asp
40 45 50

gaa ttc aaa gcg acc tgc atc gac aac gat att tcc atg acc aag gcg 307
Glu Phe Lys Ala Thr Cys Ile Asp Asn Asp Ile Ser Met Thr Lys Ala
55 60 65

ttt gag aaa gag ctt cgc acc tgg gtt gat gag cac aac gct ggt gca 355
Phe Glu Lys Glu Leu Arg Thr Trp Val Asp Glu His Asn Ala Gly Ala
70 75 80 85

aca aag aaa aga aac acc cat cgc acc tac gta caa gca ccc gtt ggt 403
Thr Lys Lys Arg Asn Thr His Arg Thr Tyr Val Gln Ala Pro Val Gly
90 95 100

act gtc gcc acc agc tct att cca ggt ctt ggg tta ttt act gtg ttc 451
Thr Val Ala Thr Ser Ser Ile Pro Gly Leu Gly Leu Phe Thr Val Phe
105 110 115

aag aag agc tct gat cag atg tgg tac gac ctg gaa agc agc ccg ctg 499
Lys Lys Ser Ser Asp Gln Met Trp Tyr Asp Leu Glu Ser Ser Pro Leu
120 125 130

atc gca caa gag ccc atg tcg aat atg gac atg cat cgt aac ggc tct 547
Ile Ala Gln Glu Pro Met Ser Asn Met Asp Met His Arg Asn Gly Ser
135 140 145

ttt gag ctg cac ctg tagatctctc tctcgaccac aca 585
Phe Glu Leu His Leu
150

<210> 2496
<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 2496

Met Thr Thr Arg Thr Val Ser Thr Ser Ala Pro His Val Thr Val Asn
 1 5 10 15

Ile Asn Thr Ala His Asn Lys Thr Arg Thr Val Thr Asn Gly Ala Arg
 20 25 30

Lys Thr Asn Ala Glu Arg Gly Lys Ser Cys Ile Ser Phe Arg Val Gly
 35 40 45

Pro Glu Leu Phe Asp Glu Phe Lys Ala Thr Cys Ile Asp Asn Asp Ile
 50 55 60

Ser Met Thr Lys Ala Phe Glu Lys Glu Leu Arg Thr Trp Val Asp Glu
 65 70 75 80

His Asn Ala Gly Ala Thr Lys Lys Arg Asn Thr His Arg Thr Tyr Val
 85 90 95

Gln Ala Pro Val Gly Thr Val Ala Thr Ser Ser Ile Pro Gly Leu Gly
 100 105 110

Leu Phe Thr Val Phe Lys Lys Ser Ser Asp Gln Met Trp Tyr Asp Leu
 115 120 125

Glu Ser Ser Pro Leu Ile Ala Gln Glu Pro Met Ser Asn Met Asp Met
 130 135 140

His Arg Asn Gly Ser Phe Glu Leu His Leu
 145 150

<210> 2497

<211> 630

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> RXA01958

<400> 2497

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cacacagctc tcaccacctc ctagaaagga cggtttcacc atg tct aaa aaa cgc 115
 Met Ser Lys Lys Arg
 1 5

gac cac ctc acc gtc att cct gac ctt gag tca cgc acc cat cac agc 163
 Asp His Leu Thr Val Ile Pro Asp Leu Glu Ser Arg Thr His His Ser
 10 15 20

cgc agt aca caa ccg cca act acg ctg ccc gca cca cag ctg act att 211
 Arg Ser Thr Gln Pro Pro Thr Thr Leu Pro Ala Pro Gln Leu Thr Ile
 25 30 35

atc acc gca cca gac aag cat caa cca cag ctt cgg gtt gtt aaa aac 259

100	105	110
Val Arg Ala Ala Asp Gln Leu Leu Ser Pro Phe Asp Ala Tyr Ile Leu		
115	120	125
Asp Asn Gly Asp Val Tyr Thr Lys Thr Pro Arg Ala Ile Ser Ala Ala		
130	135	140
Glu Gln Glu Glu Ile Leu Glu His Leu His Glu His His Ile Cys Trp		
145	150	155
Asp Glu Glu Ala Glu Phe Leu Leu Arg		
165		

<210> 2499

<211> 481

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(481)

<223> RXA01959

<400> 2499

cccaactact atgcacagcc cgtaaccatc gagccggcta aaatctatca acagaaaaac 60

cactgcctat ttgaccattc ttgtgcaaga aagtacacct atg ccc cac gac gtt	115
Met Pro His Asp Val	
1	5

tac gat gtc gaa cac atc att tcc aag caa cct ttc tgc tcc atc ttt	163
Tyr Asp Val Glu His Ile Ile Ser Lys Gln Pro Phe Cys Ser Ile Phe	
10	15
20	

ttc cag ctc ccc gct gca gcg ctg aaa cct act att caa aaa gct gcc	211
Phe Gln Leu Pro Ala Ala Ala Leu Lys Pro Thr Ile Gln Lys Ala Ala	
25	30
35	

acc aac cgc gac ctt act aag ctc aac acc gaa cag atc gct gag aac	259
Thr Asn Arg Asp Leu Thr Lys Leu Asn Thr Glu Gln Ile Ala Glu Asn	
40	45
50	

cta cag cgc tac ctc gac acc tac agt gtc atg tct cac cag cgt gtc	307
Leu Gln Arg Tyr Leu Asp Thr Tyr Ser Val Met Ser His Gln Arg Val	
55	60
65	

acc att gaa gag gtc act cat gtg cgc aac cct cat gag cct gat tat	355
Thr Ile Glu Glu Val Thr His Val Arg Asn Pro His Glu Pro Asp Tyr	
70	75
80	85

gag ttt tca cca cag tac ggt gca cat atc tcg ctc atc ggt gag tct	403
Glu Phe Ser Pro Gln Tyr Gly Ala His Ile Ser Leu Ile Gly Glu Ser	
90	95
100	

tat gct gtg aac acg gcc acc aac gag cct tat gcc acc gac tcc gag	451
Tyr Ala Val Asn Thr Ala Thr Asn Glu Pro Tyr Ala Thr Asp Ser Glu	
105	110
115	

ggc cat cct ctc gca ctg tat ttt gaa atg	481
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Gly His Pro Leu Ala Leu Tyr Phe Glu Met
 120 125

<210> 2500

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 2500

Met Pro His Asp Val Tyr Asp Val Glu His Ile Ile Ser Lys Gln Pro
 1 5 10 15

Phe Cys Ser Ile Phe Phe Gln Leu Pro Ala Ala Ala Leu Lys Pro Thr
 20 25 30

Ile Gln Lys Ala Ala Thr Asn Arg Asp Leu Thr Lys Leu Asn Thr Glu
 35 40 45

Gln Ile Ala Glu Asn Leu Gln Arg Tyr Leu Asp Thr Tyr Ser Val Met
 50 55 60

Ser His Gln Arg Val Thr Ile Glu Glu Val Thr His Val Arg Asn Pro
 65 70 75 80

His Glu Pro Asp Tyr Glu Phe Ser Pro Gln Tyr Gly Ala His Ile Ser
 85 90 95

Leu Ile Gly Glu Ser Tyr Ala Val Asn Thr Ala Thr Asn Glu Pro Tyr
 100 105 110

Ala Thr Asp Ser Glu Gly His Pro Leu Ala Leu Tyr Phe Glu Met
 115 120 125

<210> 2501

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> RXA01961

<400> 2501

aacacccagc tagtgccctgt gcttgagcta ccaaagttca atccttttga ggcacttgct 60

atccaccttg aagccgcca caactaagaa agcatccttc atg act gac aac gct 115
 Met Thr Asp Asn Ala
 1 5

gac aac acc aca gat aac gta acc aat aac tca gac acc aat ctc gat 163
 Asp Asn Thr Thr Asp Asn Val Thr Asn Asn Ser Asp Thr Asn Leu Asp
 10 15 20

tac agc ttc gac ccg ctc cct gac gag ccc tat gcc tac ggc ttt gaa 211
 Tyr Ser Phe Asp Pro Leu Pro Asp Glu Pro Tyr Ala Tyr Gly Phe Glu
 25 30 35

ctg gtc gct gct gat gca cac tct gac tca aca aca acc agc acc gat 259

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<210> 2502
<211> 160
<212> PRT
<213> Corynebacterium glutamicum
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Met Thr Asp Asn Ala Asp Asn Thr Thr Asp Asn Val Thr Asn Asn Ser
1 5 10 15

Asp Thr Asn Leu Asp Tyr Ser Phe Asp Pro Leu Pro Asp Glu Pro Tyr
20 25 30

Ala Tyr Gly Phe Glu Leu Val Ala Ala Asp Ala His Ser Asp Ser Thr
35 40 45

Thr Thr Ser Thr Asp Thr Pro Glu Thr Val Ala Val Ala Leu Lys Thr
50 55 60

Arg Glu Asp Thr Ile Asn Trp Val Asn Thr Gln Arg Ala Glu Gly Lys
65 70 75 80

Pro Asp Glu Ile Arg Ile Asn Asn Pro Ile Arg Ser Glu Arg Ile Ala
85 90 95

Glu Phe Val His Glu Met Ile Met His His Gly Leu Val Ala Cys Met
100 105 110

Glu Asp Leu Ala Ile Leu Ile Lys Arg Asp Lys Leu Thr Gln Leu Glu
115 120 125

Ala Glu Asn Ala Ile Thr Ala Trp His Asn Leu Thr Lys Glu Ser Leu
130 135 140

Gly Gln Ile Met Gly Leu Phe Tyr Gln Tyr Val Glu Asn Asn Thr Lys
145 150 155 160

<210> 2503

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXA01962

<400> 2503

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cgctcgaaaac aacacaaaat aggaaagaag aaacaccatc atg tct gac aac act 115
Met Ser Asp Asn Thr
1 5

cag gac aac cct ttc tcc atc cgc tac gca cac cct gac cac cag ctc 163
Gln Asp Asn Pro Phe Ser Ile Arg Tyr Ala His Pro Asp His Gln Leu
10 15 20

gct ctt aat gag ctt gtt gat act gcc gat cta cct gca cca aca agc 211
Ala Leu Asn Glu Leu Val Asp Thr Ala Asp Leu Pro Ala Pro Thr Ser
25 30 35

tat atg aaa aat ccc tgg tcc ggg gac aac acg cct atc gcc gag tgg 259
Tyr Met Lys Asn Pro Trp Ser Gly Asp Asn Thr Pro Ile Ala Glu Trp
40 45 50

cga cgc gag cgc atc acc cag tgg cag cgc acc gag atc att gtc aat 307
Arg Arg Glu Arg Ile Thr Gln Trp Gln Arg Thr Glu Ile Ile Val Asn
55 60 65

caa cgc gat gat gac gat ctc att cac gtc agc ttc ccg aag ctc ggc 355
Gln Arg Asp Asp Asp Asp Leu Ile His Val Ser Phe Pro Lys Leu Gly
70 75 80 85

cag cac att cag ctc aac acc gac gat att ctc gca ttg gtc gca gcc 403
Gln His Ile Gln Leu Asn Thr Asp Asp Ile Leu Ala Leu Val Ala Ala
90 95 100

tgc gtc aca ccc act gct aac gac att gag gca act atc gaa gaa aat 451
Cys Val Thr Pro Thr Ala Asn Asp Ile Glu Ala Thr Ile Glu Glu Asn
105 110 115

ctc cac tca tat ccg cac gat acg gtc atc atg ttt aac gca gat gat 499
Leu His Ser Tyr Pro His Asp Thr Val Ile Met Phe Asn Ala Asp Asp
120 125 130

cta gat gat gcc ctt ggt ctc gtt gtt gcc gtc aaa gac gcg agc ggg 547
Leu Asp Asp Ala Leu Gly Leu Val Val Ala Val Lys Asp Ala Ser Gly

135	140	145	
gaa cac tca ccg cgc gct gtc tgg cgc acc aac acc gat cat gga gct			595
Glu His Ser Pro Arg Ala Val Trp Arg Thr Asn Thr Asp His Gly Ala			
150	155	160	165
ctt gac gag act gaa ctc gcg cgg ctc att ctc aaa ttc ggt ggc agc			643
Leu Asp Glu Thr Glu Leu Ala Arg Leu Ile Leu Lys Phe Gly Gly Ser			
	170	175	180
ttc gat gac tac ggc gtg ctg caa cat taaaccgact cactaagcac			690
Phe Asp Asp Tyr Gly Val Leu Gln His			
	185	190	
cgc			693
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Pro Asp His Gln Leu Ala Leu Asn Glu Leu Val Asp Thr Ala Asp Leu			
	20	25	30
Pro Ala Pro Thr Ser Tyr Met Lys Asn Pro Trp Ser Gly Asp Asn Thr			
	35	40	45
Pro Ile Ala Glu Trp Arg Arg Glu Arg Ile Thr Gln Trp Gln Arg Thr			
	50	55	60
Glu Ile Ile Val Asn Gln Arg Asp Asp Asp Asp Leu Ile His Val Ser			
	65	70	75
Phe Pro Lys Leu Gly Gln His Ile Gln Leu Asn Thr Asp Asp Ile Leu			
	85	90	95
Ala Leu Val Ala Ala Cys Val Thr Pro Thr Ala Asn Asp Ile Glu Ala			
	100	105	110
Thr Ile Glu Glu Asn Leu His Ser Tyr Pro His Asp Thr Val Ile Met			
	115	120	125
Phe Asn Ala Asp Asp Leu Asp Asp Ala Leu Gly Leu Val Val Ala Val			
	130	135	140
Lys Asp Ala Ser Gly Glu His Ser Pro Arg Ala Val Trp Arg Thr Asn			
	145	150	155
Thr Asp His Gly Ala Leu Asp Glu Thr Glu Leu Ala Arg Leu Ile Leu			
	165	170	175
Lys Phe Gly Gly Ser Phe Asp Asp Tyr Gly Val Leu Gln His			
	180	185	190

<210> 2505

Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg Ile His Lys Gly Asp
 185 190 195

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 Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val Val Gly Ile Met Ser
 200 205 210

cac ggc aca ata aat aag aac gac ggg tct ttt gat gac gaa tcc 784
 His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe Asp Asp Glu Ser
 215 220 225

<210> 2506

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 2506

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Val Leu Gly Ile Val Ala Ala His Pro Phe His Ala Ser Ala Val Ile
 20 25 30

Gly Gly Ser Val Pro Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys
 35 40 45

Ile Gly Pro Gly Ala Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser
 50 55 60

Trp Ala Leu Thr Ala Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly
 65 70 75 80

Asp Ile Asp Thr Ile Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu
 85 90 95

Gly Asn Tyr Met Gly Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala
 100 105 110

Leu Ile Asn Ile Asn Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro
 115 120 125

Thr Gln Glu Tyr Pro Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly
 130 135 140

Gly Gly Gly Val Asn Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu
 145 150 155 160

Thr Asp Ile Tyr Ser Val Arg Ser Gly Lys Phe His His Gly Val Gly
 165 170 175

Arg Ser His Tyr Leu Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg
 180 185 190

Ile His Lys Gly Asp Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val
 195 200 205

Val Gly Ile Met Ser His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe
 210 215 220

Asp Asp Glu Ser

225

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<211> 1426

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<223> RXA01964

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				Met	Thr	Ser	Ala	Val		
				1				5		

aat	gtg	cag	aag	aag	acc	aca	cag	aaa	gta	ctt	aag	ccc	att	aat	acg	163
Asn	Val	Gln	Lys	Lys	Thr	Thr	Gln	Lys	Val	Leu	Lys	Pro	Ile	Asn	Thr	
			10					15						20		

aag	aat	tac	tct	gcg	aca	gat	gca	gta	cag	aca	ggc	cag	cac	gga	tct	211
Lys	Asn	Tyr	Ser	Ala	Thr	Asp	Ala	Val	Gln	Thr	Gly	Gln	His	Gly	Ser	
			25				30						35			

gct	tta	ggc	tcg	aat	atc	ggg	gtc	tac	acc	tat	acc	gct	gga	ctc	gat	259
Ala	Leu	Gly	Ser	Asn	Ile	Gly	Val	Tyr	Thr	Tyr	Thr	Ala	Gly	Leu	Asp	
		40				45						50				

att	gga	aac	ggg	tat	gtc	aag	ggc	att	atc	gag	gca	acc	ggg	gat	acg	307
Ile	Gly	Asn	Gly	Tyr	Val	Lys	Gly	Ile	Ile	Glu	Ala	Thr	Gly	Asp	Thr	
	55					60				65						

act	ggc	acg	tct	gtt	gat	gtt	att	gat	atg	ccc	tct	gca	gca	acg	cgc	355
Thr	Gly	Thr	Ser	Val	Asp	Val	Ile	Asp	Met	Pro	Ser	Ala	Ala	Thr	Arg	
	70				75				80						85	

atg	agc	cgg	cca	acg	gaa	gtt	ccc	gaa	cca	gat	gac	acc	gct	gtt	gct	403
Met	Ser	Arg	Pro	Thr	Glu	Val	Pro	Glu	Pro	Asp	Asp	Thr	Ala	Val	Ala	
			90					95						100		

gtc	acc	ggg	gcg	gat	ttc	ttc	aac	cac	att	gat	acc	aat	ttc	aat	tcg	451
Val	Thr	Gly	Ala	Asp	Phe	Phe	Asn	His	Ile	Asp	Thr	Asn	Phe	Asn	Ser	
			105					110					115			

cct	atg	gtg	aaa	ggg	aat	tat	cgt	tac	ctt	tgt	ggc	acg	cgc	agc	ttg	499
Pro	Met	Val	Lys	Gly	Asn	Tyr	Arg	Tyr	Leu	Cys	Gly	Thr	Arg	Ser	Leu	
		120					125					130				

tct	gca	cga	ggg	agc	ttg	gag	gaa	ttt	gat	ctg	gtg	ggg	aac	cgc	tcc	547
Ser	Ala	Arg	Gly	Ser	Leu	Glu	Glu	Phe	Asp	Leu	Val	Gly	Asn	Arg	Ser	
	135					140					145					

aag	gcg	gaa	caa	gaa	ctg	agc	aag	gtg	ctg	gtc	atg	gca	gta	ctt	gcg	595
Lys	Ala	Glu	Gln	Glu	Leu	Ser	Lys	Val	Leu	Val	Met	Ala	Val	Leu	Ala	
150					155				160					165		

gcc	aag	gct	gtg	aaa	gac	ttt	gtg	gca	gca	cat	ggg	cga	atc	cca	cag	643
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Ala Lys Ala Val Lys Asp Phe Val Ala Ala His Gly Arg Ile Pro Gln	
170 175 180	
gtt gct gtt gag ggt gat ccc ggt gtg ctg cgt gtg cat acg tat ctt	691
Val Ala Val Glu Gly Asp Pro Gly Val Leu Arg Val His Thr Tyr Leu	
185 190 195	
gca ctt gcg tta ccg att aat gaa tat gtg ggt cac cgt cat ggg tat	739
Ala Leu Ala Leu Pro Ile Asn Glu Tyr Val Gly His Arg His Gly Tyr	
200 205 210	
aag gca cag ttt atg ggt gat ggg gca gcg aac ccg gct gtg cat gtg	787
Lys Ala Gln Phe Met Gly Asp Gly Ala Ala Asn Pro Ala Val His Val	
215 220 225	
gtg acg gtt aac aac ttt gaa acc cca gca acg gtg cag ctc atc ttt	835
Val Thr Val Asn Asn Phe Glu Thr Pro Ala Thr Val Gln Leu Ile Phe	
230 235 240 245	
gag cgt gtc gag gtc att gcc gag ggc gca tcg gca cag tat gcc att	883
Glu Arg Val Glu Val Ile Ala Glu Gly Ala Ser Ala Gln Tyr Ala Ile	
250 255 260	
acc gca ggt ggc gaa gta ctt atg aac gga atg ctc gcc gat gta cgc	931
Thr Ala Gly Gly Glu Val Leu Met Asn Gly Met Leu Ala Asp Val Arg	
265 270 275	
tcc aaa ggg ctt gct cta gag ggc gtg aca gca ggt gat gtg cta caa	979
Ser Lys Gly Leu Ala Leu Glu Gly Val Thr Ala Gly Asp Val Leu Gln	
280 285 290	
gct cgc cac aca atc ggt gtg gat gtg ggt gaa ggt act gtg aat ttc	1027
Ala Arg His Thr Ile Gly Val Asp Val Gly Glu Gly Thr Val Asn Phe	
295 300 305	
cca gtc ttt acg gat ggg cgg ttt aat cat gat gct tca cgc gcc tat	1075
Pro Val Phe Thr Asp Gly Arg Phe Asn His Asp Ala Ser Arg Ala Tyr	
310 315 320 325	
gac aag ggt tat ggc acc gtc ttg gag tcg gcg att cag gct atg gac	1123
Asp Lys Gly Tyr Gly Thr Val Leu Glu Ser Ala Ile Gln Ala Met Asp	
330 335 340	
gat gct ggg ttg gca cac aac ttt aac tcg cgt aag cag ttg gct gat	1171
Asp Ala Gly Leu Ala His Asn Phe Asn Ser Arg Lys Gln Leu Ala Asp	
345 350 355	
tat ttg cag cga cca ccg agt gca ctc aag cgg aat ttc tat acc cgc	1219
Tyr Leu Gln Arg Pro Pro Ser Ala Leu Lys Arg Asn Phe Tyr Thr Arg	
360 365 370	
gtg gaa cag cat gtt gat cag gag gca gtg ttc ttt gtt cag gat gtg	1267
Val Glu Gln His Val Asp Gln Glu Ala Val Phe Phe Val Gln Asp Val	
375 380 385	
gct gca gag ttc gca cga gtg ttg agc gac gtg ggt gct ctt acc gaa	1315
Ala Ala Glu Phe Ala Arg Val Leu Ser Asp Val Gly Ala Leu Thr Glu	
390 395 400 405	
gta gcc ttt gtc tac ggc ggt ggt tcc ggc ccg ctg cgt gat cga ctg	1363
Val Ala Phe Val Tyr Gly Gly Gly Ser Gly Pro Leu Arg Asp Arg Leu	

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Phe Pro Val Leu Tyr
440

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			20					25					30		
Gly	Gln	His	Gly	Ser	Ala	Leu	Gly	Ser	Asn	Ile	Gly	Val	Tyr	Thr	Tyr
		35					40					45			
Thr	Ala	Gly	Leu	Asp	Ile	Gly	Asn	Gly	Tyr	Val	Lys	Gly	Ile	Ile	Glu
	50					55					60				
Ala	Thr	Gly	Asp	Thr	Thr	Gly	Thr	Ser	Val	Asp	Val	Ile	Asp	Met	Pro
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Ser	Ala	Ala	Thr	Arg	Met	Ser	Arg	Pro	Thr	Glu	Val	Pro	Glu	Pro	Asp
				85					90					95	
Asp	Thr	Ala	Val	Ala	Val	Thr	Gly	Ala	Asp	Phe	Phe	Asn	His	Ile	Asp
			100					105					110		
Thr	Asn	Phe	Asn	Ser	Pro	Met	Val	Lys	Gly	Asn	Tyr	Arg	Tyr	Leu	Cys
		115					120					125			
Gly	Thr	Arg	Ser	Leu	Ser	Ala	Arg	Gly	Ser	Leu	Glu	Glu	Phe	Asp	Leu
	130					135					140				
Val	Gly	Asn	Arg	Ser	Lys	Ala	Glu	Gln	Glu	Leu	Ser	Lys	Val	Leu	Val
145					150					155					160
Met	Ala	Val	Leu	Ala	Ala	Lys	Ala	Val	Lys	Asp	Phe	Val	Ala	Ala	His
				165					170					175	
Gly	Arg	Ile	Pro	Gln	Val	Ala	Val	Glu	Gly	Asp	Pro	Gly	Val	Leu	Arg
			180					185					190		
Val	His	Thr	Tyr	Leu	Ala	Leu	Ala	Leu	Pro	Ile	Asn	Glu	Tyr	Val	Gly
		195					200					205			
His	Arg	His	Gly	Tyr	Lys	Ala	Gln	Phe	Met	Gly	Asp	Gly	Ala	Ala	Asn
210						215					220				
Pro	Ala	Val	His	Val	Val	Thr	Val	Asn	Asn	Phe	Glu	Thr	Pro	Ala	Thr
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Met Ala Gln Lys Gln
1 5

gac acg aca cat gta tca gag gac gat gcc ccg tgg cgt aat gtg cgt 163
Asp Thr Thr His Val Ser Glu Asp Asp Ala Pro Trp Arg Asn Val Arg
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Trp Arg Asn Val Arg Met Arg Phe Pro Glu Thr Asp Ala Ile Val Glu
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Arg Phe Leu Glu Thr Gln Gly Ala Arg Gly Ile Ser Leu Ala Met Arg
      35          40          45

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Gln Leu Ile Tyr Leu Phe Val Ala Glu Tyr Gly Asp Val Glu Val Ala
 50 55 60
 Thr Val Ile Gly Leu Lys Leu Val Glu Ser Leu Gln Ala Gly Ala Glu
 65 70 75 80
 Gly Ser Asp Leu Phe Ala Gln Leu Ala Ala Gly Val Ala Asp Val Asp
 85 90 95
 Ala Val Thr Thr Arg Lys Lys Ala Pro Gln Gln Ile Ala Pro Pro Ser
 100 105 110
 Thr Thr Thr Arg Ala Pro Asp Gln Val Asn Glu Phe Val Ala Glu Ala
 115 120 125
 Glu Ser Gln Pro Val Glu Glu Ser Val Val Glu Ala Lys Val Pro Lys
 130 135 140
 Gln Gln Val Ala Pro Gln Pro Ala Gln Lys Pro Glu Gln Lys Pro Glu
 145 150 155 160
 Gln Lys Ser Ala Gln Pro Ala Gln Ser Glu Pro Asp Asp Gly Phe Asp
 165 170 175
 Met Asp Asp Val Met Gly Gln Ala Phe Gly Arg
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (47)..(703)

<223> RXA01966

<400> 2511

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 Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp Asp Arg Leu Val
 5 10 15 20

tgg gtc gat ctg gaa atg act ggt cta gat ttg aag cgc cac gtg atc 154
 Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys Arg His Val Ile
 25 30 35

gtg gag gtt gcg gcg ttg gtc act gac gct aac ctc aac gtt ttg ggc 202
 Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu Asn Val Leu Gly
 40 45 50

gag ggc gtg gac ttg gtt gtt cac gca act gaa gaa gag ctc gcg cag 250
 Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu Glu Leu Ala Gln
 55 60 65

atg gat gat ttt gtc acc aac atg cac gaa tcc tct ggg ctg act gag 298
 Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser Gly Leu Thr Glu

70	75	80	
cag atc cgg gaa tcc gcg gtc acg ttg aag gaa gcc gaa gat gct gtg			346
Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala Glu Asp Ala Val			
85	90	95	100
ctc gca ttg att gaa aag cac tgc gat cca gcc cat cct gca ccg cta			394
Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His Pro Ala Pro Leu			
	105	110	115
gct ggt aac tcc att gcc act gac cgc gcg ttt atc cgc gaa cat atg			442
Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile Arg Glu His Met			
	120	125	130
cca cgt ctt gat gag gcc ctg cat tac cgc atg gtg gat gtg tcc tcg			490
Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val Asp Val Ser Ser			
	135	140	145
gtg aag gaa ttg gcg cgt cgc tgg tac cca cgc gtg tac tac aag cag			538
Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val Tyr Tyr Lys Gln			
	150	155	160
ccg gag aag ggt ttg gcg cac cgc gcg ttg gcg gac att gtg gag tcg			586
Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp Ile Val Glu Ser			
	165	170	175
att cgg gag ttg gat tac tac cgt cgc tca ttt ttt gtt gca gag cct			634
Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe Val Ala Glu Pro			
	185	190	195
ggt cct acc tct gag cag tgc gca gat gat gcg cag gca gcg gtg gac			682
Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln Ala Ala Val Asp			
	200	205	210
cgt ttt gca ccc tac ttt gat tagagggttt taagcagcct ggt			726
Arg Phe Ala Pro Tyr Phe Asp			
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<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 2512

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	20	25	30
Arg His Val Ile Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu			
	35	40	45
Asn Val Leu Gly Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu			
	50	55	60
Glu Leu Ala Gln Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser			
	65	70	75
Gly Leu Thr Glu Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala			

Thr 70	Asn	Glu	Glu	Gly	Tyr 75	Glu	Val	Glu	Ser	Glu 80	Leu	Ser	Asp	Asp	Gly 85	
cgt	agc	tg	acc	act	gcg	gaa	acc	ctt	ggc	tac	aac	cgc	acg	tac	acc	403
Arg	Ser	Trp	Thr	Thr	Ala	Glu	Thr	Leu	Gly	Tyr	Asn	Arg	Thr	Tyr	Thr	
				90					95					100		
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Ile	Lys	Ala	Thr	Asp	Lys	Asn	Gly	Glu	Thr	Ala	Thr	Ala	Ser	Phe	Ser	
			105					110					115			
act	gca	acc	cct	gca	gct	acc	aca	aac	gtg	gcg	ctt	tct	ccg	ctg	gct	499
Thr	Ala	Thr	Pro	Ala	Ala	Thr	Thr	Asn	Val	Ala	Leu	Ser	Pro	Leu	Ala	
			120				125					130				
gat	tct	gtc	gtt	gg	gtt	ggc	cag	act	atc	ggt	ttc	cgt	ttt	ggt	tcc	547
Asp	Ser	Val	Val	Gly	Val	Gly	Gln	Thr	Ile	Gly	Phe	Arg	Phe	Gly	Ser	
			135			140					145					
cct	gtg	aag	gat	cgc	aag	gcg	gct	cag	gat	gct	att	act	gtg	aca	act	595
Pro	Val	Lys	Asp	Arg	Lys	Ala	Ala	Gln	Asp	Ala	Ile	Thr	Val	Thr	Thr	
					155					160					165	
tca	cca	aag	gtg	gag	gg	ggc	ttt	tac	tg	ttg	aac	aac	agt	gag	ttg	643
Ser	Pro	Lys	Val	Glu	Gly	Gly	Phe	Tyr	Trp	Leu	Asn	Asn	Ser	Glu	Leu	
				170					175					180		
cgc	tg	cgt	cca	gcg	gag	tac	tg	gag	cca	ggt	act	gaa	gtt	acg	gtc	691
Arg	Trp	Arg	Pro	Ala	Glu	Tyr	Trp	Glu	Pro	Gly	Thr	Glu	Val	Thr	Val	
			185					190					195			
gag	gct	gac	att	tac	ggc	aag	gat	ctc	ggc	ggc	ggt	gtc	tg	ggc	gaa	739
Glu	Ala	Asp	Ile	Tyr	Gly	Lys	Asp	Leu	Gly	Gly	Gly	Val	Trp	Gly	Glu	
		200					205					210				
act	gat	aac	gcc	acc	aac	ttc	acc	att	ggt	gac	aag	gtt	gag	gct	gtg	787
Thr	Asp	Asn	Ala	Thr	Asn	Phe	Thr	Ile	Gly	Asp	Lys	Val	Glu	Ala	Val	
						220					225					
gca	gat	gat	gcc	acc	aag	acc	atg	agt	gtg	tac	aag	aac	ggt	gag	ttg	835
Ala	Asp	Asp	Ala	Thr	Lys	Thr	Met	Ser	Val	Tyr	Lys	Asn	Gly	Glu	Leu	
					235				240					245		
ctg	cgc	act	atg	ccg	gta	tcc	ttt	ggt	cgt	gac	acc	tct	gag	tg	gca	883
Leu	Arg	Thr	Met	Pro	Val	Ser	Phe	Gly	Arg	Asp	Thr	Ser	Glu	Trp	Ala	
				250					255					260		
acg	cca	aac	ggt	acc	tac	atc	att	ggt	gat	cgc	aat	gag	tcg	atg	atc	931
Thr	Pro	Asn	Gly	Thr	Tyr	Ile	Ile	Gly	Asp	Arg	Asn	Glu	Ser	Met	Ile	
			265					270					275			
atg	gac	tcc	acc	acc	ttc	ggt	ctg	gga	tat	gag	gag	ggt	ggc	tac	cgc	979
Met	Asp	Ser	Thr	Thr	Phe	Gly	Leu	Gly	Tyr	Glu	Glu	Gly	Gly	Tyr	Arg	
		280					285					290				
act	ccg	gtg	aag	tac	gcg	acc	cag	atg	tcc	tat	tct	gga	att	tac	gtg	1027
Thr	Pro	Val	Lys	Tyr	Ala	Thr	Gln	Met	Ser	Tyr	Ser	Gly	Ile	Tyr	Val	
		295				300					305					
cac	gca	gca	ccg	tg	tct	gta	ggt	gcg	caa	ggt	agc	tac	aac	acc	tca	1075
His	Ala	Ala	Pro	Trp	Ser	Val	Gly	Ala	Gln	Gly	Ser	Tyr	Asn	Thr	Ser	

310 315 320 325
 cat ggt tgc atc aat gta tcc acc gaa aat gct cag tgg ttc cag gag 1123
 His Gly Cys Ile Asn Val Ser Thr Glu Asn Ala Gln Trp Phe Gln Glu
 330 335 340
 gcc gtg aag cgc ggt gac att gtg acc gtg aaa aac acc atc ggt gag 1171
 Ala Val Lys Arg Gly Asp Ile Val Thr Val Lys Asn Thr Ile Gly Glu
 345 350 355
 act ttg agt ggc tac gac gga ctg ggg gac tgg aac att cca tgg tct 1219
 Thr Leu Ser Gly Tyr Asp Gly Leu Gly Asp Trp Asn Ile Pro Trp Ser
 360 365 370
 gaa tgg agc aag ggg aac gcg gat caa act tcg gcg tgg taactgcgga 1268
 Glu Trp Ser Lys Gly Asn Ala Asp Gln Thr Ser Ala Trp
 375 380 385
 agtcgcaggt aaa 1281

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 <211> 386
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2514
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 Ser Asp Ala Gln Glu Gln Ser Ser Gln Gln Ser Thr Glu Val Glu Ala
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 Glu Glu Ala Gln Ala Pro Val Ile Ser Val Asp Asp Gly Asp Glu Asp
 35 40 45
 Val Asp Pro Ser Glu Ser Val Ile Val Lys Ser Met Gly Asp Gly Leu
 50 55 60
 Ser Lys Val Thr Met Thr Asn Glu Glu Gly Tyr Glu Val Glu Ser Glu
 65 70 75 80
 Leu Ser Asp Asp Gly Arg Ser Trp Thr Thr Ala Glu Thr Leu Gly Tyr
 85 90 95
 Asn Arg Thr Tyr Thr Ile Lys Ala Thr Asp Lys Asn Gly Glu Thr Ala
 100 105 110
 Thr Ala Ser Phe Ser Thr Ala Thr Pro Ala Ala Thr Thr Asn Val Ala
 115 120 125
 Leu Ser Pro Leu Ala Asp Ser Val Val Gly Val Gly Gln Thr Ile Gly
 130 135 140
 Phe Arg Phe Gly Ser Pro Val Lys Asp Arg Lys Ala Ala Gln Asp Ala
 145 150 155 160
 Ile Thr Val Thr Thr Ser Pro Lys Val Glu Gly Gly Phe Tyr Trp Leu
 165 170 175
 Asn Asn Ser Glu Leu Arg Trp Arg Pro Ala Glu Tyr Trp Glu Pro Gly

180										185					190				
Thr	Glu	Val	Thr	Val	Glu	Ala	Asp	Ile	Tyr	Gly	Lys	Asp	Leu	Gly	Gly				
		195					200					205							
Gly	Val	Trp	Gly	Glu	Thr	Asp	Asn	Ala	Thr	Asn	Phe	Thr	Ile	Gly	Asp				
	210					215					220								
Lys	Val	Glu	Ala	Val	Ala	Asp	Asp	Ala	Thr	Lys	Thr	Met	Ser	Val	Tyr				
225					230					235					240				
Lys	Asn	Gly	Glu	Leu	Leu	Arg	Thr	Met	Pro	Val	Ser	Phe	Gly	Arg	Asp				
				245					250					255					
Thr	Ser	Glu	Trp	Ala	Thr	Pro	Asn	Gly	Thr	Tyr	Ile	Ile	Gly	Asp	Arg				
			260					265					270						
Asn	Glu	Ser	Met	Ile	Met	Asp	Ser	Thr	Thr	Phe	Gly	Leu	Gly	Tyr	Glu				
	275						280					285							
Glu	Gly	Gly	Tyr	Arg	Thr	Pro	Val	Lys	Tyr	Ala	Thr	Gln	Met	Ser	Tyr				
	290					295					300								
Ser	Gly	Ile	Tyr	Val	His	Ala	Ala	Pro	Trp	Ser	Val	Gly	Ala	Gln	Gly				
305					310					315					320				
Ser	Tyr	Asn	Thr	Ser	His	Gly	Cys	Ile	Asn	Val	Ser	Thr	Glu	Asn	Ala				
				325					330					335					
Gln	Trp	Phe	Gln	Glu	Ala	Val	Lys	Arg	Gly	Asp	Ile	Val	Thr	Val	Lys				
			340					345					350						
Asn	Thr	Ile	Gly	Glu	Thr	Leu	Ser	Gly	Tyr	Asp	Gly	Leu	Gly	Asp	Trp				
	355					360						365							
Asn	Ile	Pro	Trp	Ser	Glu	Trp	Ser	Lys	Gly	Asn	Ala	Asp	Gln	Thr	Ser				
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Ala	Trp																		
385																			

<210> 2515

<211> 497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(474)

<223> RXA01969

<400> 2515

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Lys	Cys	Gln	Arg	Arg	Gly	Leu	Ser	Gln	Asp	Pro	Leu	Tyr	Lys	Asn	Arg		
1				5					10					15			
aat	tcc	ttg	ttg	acc	acg	cag	aag	tgg	ttt	agt	cct	cgt	cag	caa	gaa		96
Asn	Ser	Leu	Leu	Thr	Thr	Gln	Lys	Trp	Phe	Ser	Pro	Arg	Gln	Gln	Glu		
			20					25					30				

agc ttg gag cag ttg tgg gcg tat gac aaa gcc tac ggg gcg tta aag 144
 Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys
 35 40 45
 ctt gcg tgg ctt gcg tat cag gcg att att gat tgt tat cag atg ggt 192
 Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly
 50 55 60
 aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag ctt 240
 Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu
 65 70 75 80
 cgg gtg ttg aag ggg ccg aat aag gaa ctc gcg cag ttg ggt cgt agt 288
 Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser
 85 90 95
 ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt gtc 336
 Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val
 100 105 110
 tcc aac ggt ccg gtc gaa gcg atc aac gga cgg ttg gag cat ttg cgt 384
 Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg
 115 120 125
 ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg tgc 432
 Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys
 130 135 140
 ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc 474
 Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
 145 150 155
 taaaacagga agagccactt aag 497

<210> 2516

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 2516

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 Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys
 35 40 45
 Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly
 50 55 60
 Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu
 65 70 75 80
 Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser
 85 90 95
 Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val
 100 105 110

Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg
 115 120 125

Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys
 130 135 140

Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
 145 150 155

<210> 2517

<211> 605

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(582)

<223> RXA01973

<400> 2517

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 Ser Ala Met Ser Lys Ser Gln Asp Asp Arg Lys Ile Ala Glu Leu Glu
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gca cag ttt cat agt ctt ggt ctt aac aac act gaa cta gtt acc ctt 96
 Ala Gln Phe His Ser Leu Gly Leu Asn Asn Thr Glu Leu Val Thr Leu
 20 25 30

gat gat gca gcg tcg cta ttg ggt gtg ccg gca ggt att cat cag att 144
 Asp Asp Ala Ala Ser Leu Leu Gly Val Pro Ala Gly Ile His Gln Ile
 35 40 45

gag gcc gag gtg atg ttg gtg aat ttc ggt gat ggt gca gat ggc atg 192
 Glu Ala Glu Val Met Leu Val Asn Phe Gly Asp Gly Ala Asp Gly Met
 50 55 60

ggc ggt gac acg acg aag ttt ttg cat tat cag cca gat gag tcg cag 240
 Gly Gly Asp Thr Thr Lys Phe Leu His Tyr Gln Pro Asp Glu Ser Gln
 65 70 75 80

cct tac gtc tgg gtg atg aag cgg gtg tat tcc ttt gag gcg atg aaa 288
 Pro Tyr Val Trp Val Met Lys Arg Val Tyr Ser Phe Glu Ala Met Lys
 85 90 95

aag ctc atg gtc ggg ttg ttt att ggc ttg tgc ata ctc atc gtg ggt 336
 Lys Leu Met Val Gly Leu Phe Ile Gly Leu Cys Ile Leu Ile Val Gly
 100 105 110

ggg cca gct tta ggg ctt atg ctc ggt ggt ttt atc ggt gtg ctt att 384
 Gly Pro Ala Leu Gly Leu Met Leu Gly Gly Phe Ile Gly Val Leu Ile
 115 120 125

ggt cta tgt cta ggt act tcc gca gcc atg att gtt ggc cct ttt ggg 432
 Gly Leu Cys Leu Gly Thr Ser Ala Ala Met Ile Val Gly Pro Phe Gly
 130 135 140

ctt atg cgg atg aag gcg tat cca cca tgt atg gac agt cca tgg gtg 480
 Leu Met Arg Met Lys Ala Tyr Pro Pro Cys Met Asp Ser Pro Trp Val
 145 150 155 160

tat atg tca caa gag cag tgg cgc acc gct atg ggt gcg gca cag cag 528
Tyr Met Ser Gln Glu Gln Trp Arg Thr Ala Met Gly Ala Ala Gln Gln
165 170 175

acc gag gtg tct ttt gtt gag cac tgg gac aat att tac ggg gat aat 576
Thr Glu Val Ser Phe Val Glu His Trp Asp Asn Ile Tyr Gly Asp Asn
180 185 190

ctg cat taacaaatta gttaataaag tgt 605
Leu His

<210> 2518

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 2518

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Ala Gln Phe His Ser Leu Gly Leu Asn Asn Thr Glu Leu Val Thr Leu
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Asp Asp Ala Ala Ser Leu Leu Gly Val Pro Ala Gly Ile His Gln Ile
35 40 45

Glu Ala Glu Val Met Leu Val Asn Phe Gly Asp Gly Ala Asp Gly Met
50 55 60

Gly Gly Asp Thr Thr Lys Phe Leu His Tyr Gln Pro Asp Glu Ser Gln
65 70 75 80

Pro Tyr Val Trp Val Met Lys Arg Val Tyr Ser Phe Glu Ala Met Lys
85 90 95

Lys Leu Met Val Gly Leu Phe Ile Gly Leu Cys Ile Leu Ile Val Gly
100 105 110

Gly Pro Ala Leu Gly Leu Met Leu Gly Gly Phe Ile Gly Val Leu Ile
115 120 125

Gly Leu Cys Leu Gly Thr Ser Ala Ala Met Ile Val Gly Pro Phe Gly
130 135 140

Leu Met Arg Met Lys Ala Tyr Pro Pro Cys Met Asp Ser Pro Trp Val
145 150 155 160

Tyr Met Ser Gln Glu Gln Trp Arg Thr Ala Met Gly Ala Ala Gln Gln
165 170 175

Thr Glu Val Ser Phe Val Glu His Trp Asp Asn Ile Tyr Gly Asp Asn
180 185 190

Leu His

<210> 2519

<211> 1552
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1552)
 <223> RXA01974

<400> 2519

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                                   Met Thr Gln Val Val
                                   1 5

gcg ggt acg ttg gtg gga gag tcg att aat cgt gag att gat gaa gac 163
Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg Glu Ile Asp Glu Asp
                                   10 15 20

aag tac cct tat ttg agc tcg tat gca gcg cct gtt gct gta ccg gtg 211
Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro Val Ala Val Pro Val
                                   25 30 35

cgt gag att att ggg cgc gaa gaa gaa gtc aat aag att atg gcc gcg 259
Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn Lys Ile Met Ala Ala
                                   40 45 50

ctg atg cgt cca gag att tct aat gtc atg ctt gtg ggt cct gct ggt 307
Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu Val Gly Pro Ala Gly
                                   55 60 65

tcg ggt aaa act acg ttg gta cag caa gca ctg gtg aaa gat cca gag 355
Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu Val Lys Asp Pro Glu
                                   70 75 80 85

cgt aac tac atc gag gtc gat gta gcg aaa atg gtt gcg gat ttg agc 403
Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met Val Ala Asp Leu Ser
                                   90 95 100

acc ccg gcg caa atg gct gcg cgt att aaa ggt gtg ttt gag gac gcc 451
Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly Val Phe Glu Asp Ala
                                   105 110 115

att gcc tat cgc aag cac gaa ggt cat gaa ttg gtg ctg ttc gtt gat 499
Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu Val Leu Phe Val Asp
                                   120 125 130

gag ttt cac caa att gtg cag ctg tct aat gct gcg gta gag gca atc 547
Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala Ala Val Glu Ala Ile
                                   135 140 145

aag ccg att ttg gcg atg tct ggt gtc ctt ggt gtg cgc gtt atc gct 595
Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly Val Arg Val Ile Ala
150 155 160 165

gcg aca act ctc gaa gaa ttt cac gaa cac atc agg ccg aac caa gca 643
Ala Thr Thr Leu Glu Glu Phe His Glu His Ile Arg Pro Asn Gln Ala
                                   170 175 180

ttg acg gag cgt ttg cag gaa att cga cta acg ccg acc gat cag aag 691

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Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr Pro Thr Asp Gln Lys	
185 190 195	
acc act gtg gcg att ttg cgt ggt atg gca gat cgt tat ggc gta agt	739
Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp Arg Tyr Gly Val Ser	
200 205 210	
gat cag ttc tat gac gac cac gtt ttt gag cag att tac tcc acc act	787
Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln Ile Tyr Ser Thr Thr	
215 220 225	
gag cgt ttt atg ccg agt tct gtc cag cct cgt aaa tcc att cgt gtc	835
Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg Lys Ser Ile Arg Val	
230 235 240 245	
ctt gat gcg atg gtt ggt tgg cat cga ctt tcc ggc aag ccg atg gat	883
Leu Asp Ala Met Val Gly Trp His Arg Leu Ser Gly Lys Pro Met Asp	
250 255 260	
atg gat ctg ctc ggt gat gtg ctc cac gat gct att ggt gtc gat att	931
Met Asp Leu Leu Gly Asp Val Leu His Asp Ala Ile Gly Val Asp Ile	
265 270 275	
gca ttc aag gtc gat ggt acg agc att aaa gac aag ctt gat gag aag	979
Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp Lys Leu Asp Glu Lys	
280 285 290	
gta atg gcg caa agt ctt gcc acc act gtg gta gca cgt cgt ttg cag	1027
Val Met Ala Gln Ser Leu Ala Thr Thr Val Val Ala Arg Arg Leu Gln	
295 300 305	
ctg gtg gtg gcg gat ctt cat gat aaa tca cgg cca ctg tcg aac ttc	1075
Leu Val Val Ala Asp Leu His Asp Lys Ser Arg Pro Leu Ser Asn Phe	
310 315 320 325	
ttg ttc acc ggg cct act ggt gtc ggt aaa aca gag ctg gtc aag caa	1123
Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Val Lys Gln	
330 335 340	
cta gca cgg gtg ctc ttt ggt gat gac act ggg cga ttg att cgt ttt	1171
Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly Arg Leu Ile Arg Phe	
345 350 355	
gac atg tca gag ttc gcc tta gaa tca agt ctt gac ctt ttc agg tct	1219
Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu Asp Leu Phe Arg Ser	
360 365 370	
gag ctc act cgt cgt gtc gct gac cag ggt aac gct att gtc ctg ctc	1267
Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn Ala Ile Val Leu Leu	
375 380 385	
gat gag gtt gag aaa gct gat cga gct att gcg cgg ttg tta ctg cag	1315
Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala Arg Leu Leu Leu Gln	
390 395 400 405	
gta ctt gat gat ggc cga cta tct gac gat tac aac cgt gag gtg agt	1363
Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr Asn Arg Glu Val Ser	
410 415 420	
ttt ctt aat acc tat atc gtc atg aca act aac gct ggt tct gag att	1411
Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn Ala Gly Ser Glu Ile	

425	430	435	
ttc gag aca att tcg aac tat gcc act gat gac acg ggc gat ggt cgg			1459
Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp Thr Gly Asp Gly Arg			
440	445	450	
gcg atc aaa gac ttt gtg aaa aac att cac acg tcg atc aag aat aag			1507
Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr Ser Ile Lys Asn Lys			
455	460	465	
ggt ttt cca cct gag ctt ctt ggt cgt gta gat gaa att gtg cct			1552
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<210> 2520

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 2520

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Val Ala Val Pro Val Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn			
35	40	45	
Lys Ile Met Ala Ala Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu			
50	55	60	
Val Gly Pro Ala Gly Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu			
65	70	75	80
Val Lys Asp Pro Glu Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met			
85	90	95	
Val Ala Asp Leu Ser Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly			
100	105	110	
Val Phe Glu Asp Ala Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu			
115	120	125	
Val Leu Phe Val Asp Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala			
130	135	140	
Ala Val Glu Ala Ile Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly			
145	150	155	160
Val Arg Val Ile Ala Ala Thr Thr Leu Glu Glu Phe His Glu His Ile			
165	170	175	
Arg Pro Asn Gln Ala Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr			
180	185	190	
Pro Thr Asp Gln Lys Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp			
195	200	205	
Arg Tyr Gly Val Ser Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln			

210	215	220
Ile Tyr Ser Thr Thr Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg 225 230 235 240		
Lys Ser Ile Arg Val Leu Asp Ala Met Val Gly Trp His Arg Leu Ser 245 250 255		
Gly Lys Pro Met Asp Met Asp Leu Leu Gly Asp Val Leu His Asp Ala 260 265 270		
Ile Gly Val Asp Ile Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp 275 280 285		
Lys Leu Asp Glu Lys Val Met Ala Gln Ser Leu Ala Thr Thr Val Val 290 295 300		
Ala Arg Arg Leu Gln Leu Val Val Ala Asp Leu His Asp Lys Ser Arg 305 310 315 320		
Pro Leu Ser Asn Phe Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr 325 330 335		
Glu Leu Val Lys Gln Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly 340 345 350		
Arg Leu Ile Arg Phe Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu 355 360 365		
Asp Leu Phe Arg Ser Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn 370 375 380		
Ala Ile Val Leu Leu Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala 385 390 395 400		
Arg Leu Leu Leu Gln Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr 405 410 415		
Asn Arg Glu Val Ser Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn 420 425 430		
Ala Gly Ser Glu Ile Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp 435 440 445		
Thr Gly Asp Gly Arg Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr 450 455 460		
Ser Ile Lys Asn Lys Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp 465 470 475 480		
Glu Ile Val Pro		

<210> 2521

<211> 1644

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1621)

<223> RXA01976

<400> 2521

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 Met Thr Gln Thr Leu
 1 5

gct ggc gag cgc aga atc gtc acc acg gca gag ctt aaa gcg atg ctg 163
 Ala Gly Glu Arg Arg Ile Val Thr Thr Ala Glu Leu Lys Ala Met Leu
 10 15 20

gca cga ggg gat aag gtg ttt ctg cct ggt gtc gca gcg cgg gcg cca 211
 Ala Arg Gly Asp Lys Val Phe Leu Pro Gly Val Ala Ala Arg Ala Pro
 25 30 35

gag atc ctc gac aac ttc gat cca gca gat cgg gca cgt ctc gac gtg 259
 Glu Ile Leu Asp Asn Phe Asp Pro Ala Asp Arg Ala Arg Leu Asp Val
 40 45 50

ccc gca gca gac aat gaa atc gtc tct gta gaa ttc tcc cgc cgc gat 307
 Pro Ala Ala Asp Asn Glu Ile Val Ser Val Glu Phe Ser Arg Arg Asp
 55 60 65

acc gtg caa tgc atc agc att gcc gac cgt gac cat ctc tac atc act 355
 Thr Val Gln Cys Ile Ser Ile Ala Asp Arg Asp His Leu Tyr Ile Thr
 70 75 80 85

gac gat atg atc ccg acc cac aac acg tcc aac att atc ttc ttg aaa 403
 Asp Asp Met Ile Pro Thr His Asn Thr Ser Asn Ile Ile Phe Leu Lys
 90 95 100

tcc aca gac gaa aca atg att aag acg ttg gtg gat tgg tca ggt gag 451
 Ser Thr Asp Glu Thr Met Ile Lys Thr Leu Val Asp Trp Ser Gly Glu
 105 110 115

cga cat gtt gta cgc aga aat tca aag acc gta acc cgt gac ttg gca 499
 Arg His Val Val Arg Arg Asn Ser Lys Thr Val Thr Arg Asp Leu Ala
 120 125 130

cag tta gtt atg cgc acc gag ggt aaa gtg tcg tac acg tct gca act 547
 Gln Leu Val Met Arg Thr Glu Gly Lys Val Ser Tyr Thr Ser Ala Thr
 135 140 145

gaa aaa gag ccg gtg gtg tct tat aat gac cta aat act ctg cca tcg 595
 Glu Lys Glu Pro Val Val Ser Tyr Asn Asp Leu Asn Thr Leu Pro Ser
 150 155 160 165

cag aac gcc atc gtc ttc cgt gcg ggt cag tat ccg gtg tgg tca cgc 643
 Gln Asn Ala Ile Val Phe Arg Ala Gly Gln Tyr Pro Val Trp Ser Arg
 170 175 180

aat gaa acg att tgg ccg atg tcg ttc atg ttg ttt gct aac cag att 691
 Asn Glu Thr Ile Trp Pro Met Ser Phe Met Leu Phe Ala Asn Gln Ile
 185 190 195

atc caa ccg ggt cgc gaa tac tcg ttg cag act att cca aca ctg tcg 739
 Ile Gln Pro Gly Arg Glu Tyr Ser Leu Gln Thr Ile Pro Thr Leu Ser
 200 205 210

agc gct aat gaa ttc gat gtg aat caa aat gca ccg gac ttt atg gcg Ser Ala Asn Glu Phe Asp Val Asn Gln Asn Ala Pro Asp Phe Met Ala 215 220 225	787
atg ctg gaa aag cgc atg gcg cag tcg att cgt act cag cgt gcc gtc Met Leu Glu Lys Arg Met Ala Gln Ser Ile Arg Thr Gln Arg Ala Val 230 235 240 245	835
gat att tat aaa aag gcg act ggg ctc gat gac tct gat att gca cgc Asp Ile Tyr Lys Lys Ala Thr Gly Leu Asp Asp Ser Asp Ile Ala Arg 250 255 260	883
ctg gat atg gat gtg tat tca gca gaa atc atg gac atc gtg gac acg Leu Asp Met Asp Val Tyr Ser Ala Glu Ile Met Asp Ile Val Asp Thr 265 270 275	931
atg atc gcg aaa gat gag tac gat gac acg ccg gat tat gac gag ggg Met Ile Ala Lys Asp Glu Tyr Asp Asp Thr Pro Asp Tyr Asp Glu Gly 280 285 290	979
gat gag tct gtc atg aat gct cgt gat ttc atg gag tct gaa tat gac Asp Glu Ser Val Met Asn Ala Arg Asp Phe Met Glu Ser Glu Tyr Asp 295 300 305	1027
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ctg gct gat caa ttc ggc cac atc ctg cag gac tca ctc gaa gat gag Leu Ala Asp Gln Phe Gly His Ile Leu Gln Asp Ser Leu Glu Asp Glu 375 380 385	1267
ctc act gca gcc tat gat gag agc ctg cac gct ttt gct caa gat ccg Leu Thr Ala Ala Tyr Asp Glu Ser Leu His Ala Phe Ala Gln Asp Pro 390 395 400 405	1315
aat ttc cgg gtg act gct aac aac ggc ttg gtt aat gct gtc gat ggc Asn Phe Arg Val Thr Ala Asn Asn Gly Leu Val Asn Ala Val Asp Gly 410 415 420	1363
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gcg caa gca gga gtg gag cag tcg cgt gtc tac tct gag ggt gaa gaa Ala Gln Ala Gly Val Glu Gln Ser Arg Val Tyr Ser Glu Gly Glu Glu 440 445 450	1459

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 Ala Leu Ser Gly Thr Glu Asp Asp Pro Leu Ser Ala Met Gly Lys Tyr
 455 460 465

aag acc acc cga gca ttc cgc atc atg ctg gtg gag ctt ccg cat tgg 1555
 Lys Thr Thr Arg Ala Phe Arg Ile Met Leu Val Glu Leu Pro His Trp
 470 475 480 485

cgt gat ctc gcc cag ggt cac ttt gat aaa gaa gtc gcg cga gcc ttt 1603
 Arg Asp Leu Ala Gln Gly His Phe Asp Lys Glu Val Ala Arg Ala Phe
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<210> 2522

<211> 507

<212> PRT

<213> Corynebacterium glutamicum

<400> 2522

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 35 40 45

Ala Arg Leu Asp Val Pro Ala Ala Asp Asn Glu Ile Val Ser Val Glu
 50 55 60

Phe Ser Arg Arg Asp Thr Val Gln Cys Ile Ser Ile Ala Asp Arg Asp
 65 70 75 80

His Leu Tyr Ile Thr Asp Asp Met Ile Pro Thr His Asn Thr Ser Asn
 85 90 95

Ile Ile Phe Leu Lys Ser Thr Asp Glu Thr Met Ile Lys Thr Leu Val
 100 105 110

Asp Trp Ser Gly Glu Arg His Val Val Arg Arg Asn Ser Lys Thr Val
 115 120 125

Thr Arg Asp Leu Ala Gln Leu Val Met Arg Thr Glu Gly Lys Val Ser
 130 135 140

Tyr Thr Ser Ala Thr Glu Lys Glu Pro Val Val Ser Tyr Asn Asp Leu
 145 150 155 160

Asn Thr Leu Pro Ser Gln Asn Ala Ile Val Phe Arg Ala Gly Gln Tyr
 165 170 175

Pro Val Trp Ser Arg Asn Glu Thr Ile Trp Pro Met Ser Phe Met Leu
 180 185 190

Phe Ala Asn Gln Ile Ile Gln Pro Gly Arg Glu Tyr Ser Leu Gln Thr
 195 200 205

Ile Pro Thr Leu Ser Ser Ala Asn Glu Phe Asp Val Asn Gln Asn Ala
210 215 220
Pro Asp Phe Met Ala Met Leu Glu Lys Arg Met Ala Gln Ser Ile Arg
225 230 235 240
Thr Gln Arg Ala Val Asp Ile Tyr Lys Lys Ala Thr Gly Leu Asp Asp
245 250 255
Ser Asp Ile Ala Arg Leu Asp Met Asp Val Tyr Ser Ala Glu Ile Met
260 265 270
Asp Ile Val Asp Thr Met Ile Ala Lys Asp Glu Tyr Asp Asp Thr Pro
275 280 285
Asp Tyr Asp Glu Gly Asp Glu Ser Val Met Asn Ala Arg Asp Phe Met
290 295 300
Glu Ser Glu Tyr Asp Val Phe Asp Asp Glu Phe Glu Asp Ser Ala Gln
305 310 315 320
Gly Phe Pro Val Ala Thr Gly Thr Lys Val Lys Lys Lys Ser Leu Ser
325 330 335
Glu Glu Ala Glu Val Asn Asp Glu Phe Ile His Asp Gln Glu Asn Ala
340 345 350
Glu His Lys Leu Ala Asp Met Arg Leu Lys Arg Tyr Ala Glu Gly Lys
355 360 365
Val Ser Arg Asp Met Leu Ala Asp Gln Phe Gly His Ile Leu Gln Asp
370 375 380
Ser Leu Glu Asp Glu Leu Thr Ala Ala Tyr Asp Glu Ser Leu His Ala
385 390 395
Phe Ala Gln Asp Pro Asn Phe Arg Val Thr Ala Asn Asn Gly Leu Val
405 410 415
Asn Ala Val Asp Gly Thr Val Leu Ile Glu Ala Leu Ser Gln Glu Asp
420 425 430
Ile Ala Leu Met Arg Ala Gln Ala Gly Val Glu Gln Ser Arg Val Tyr
435 440 445
Ser Glu Gly Glu Glu Ala Leu Ser Gly Thr Glu Asp Asp Pro Leu Ser
450 455 460
Ala Met Gly Lys Tyr Lys Thr Thr Arg Ala Phe Arg Ile Met Leu Val
465 470 475 480
Glu Leu Pro His Trp Arg Asp Leu Ala Gln Gly His Phe Asp Lys Glu
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<211> 699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(676)

<223> RXA01977

<400> 2523

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                                         Met Leu Arg Thr Leu
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ttc gtc cgc aag att aga gcg ctg ctg ctg gtt ttg atg att gcg cca 163
Phe Val Arg Lys Ile Arg Ala Leu Leu Val Leu Met Ile Ala Pro
                        10                               15                               20

act cca ttg gtc gaa ggg cta act tcg act gca atg att gta tcc gta 211
Thr Pro Leu Val Glu Gly Leu Thr Ser Thr Ala Met Ile Val Ser Val
                        25                               30                               35

gta atc ctg gcg atc tac atg gcg ata aca atg tat aga gta gtg cac 259
Val Ile Leu Ala Ile Tyr Met Ala Ile Thr Met Tyr Arg Val Val His
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Gly Arg His Glu Phe Ala His Ile Ala Arg Arg Met Ala Leu Tyr Val
                        55                               60                               65

aac aag act tct tct agg ttc agt gtt gtt att gct tat gta gta tta 355
Asn Lys Thr Ser Ser Arg Phe Ser Val Val Ile Ala Tyr Val Val Leu
                        70                               75                               80                               85

att gct att tat gcg cta cta att ccc gga ctt gtc tac tct gtt aca 403
Ile Ala Ile Tyr Ala Leu Leu Ile Pro Gly Leu Val Tyr Ser Val Thr
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Phe Gly Phe Ile Val Pro Ser Thr Pro Asn Thr Phe Ser Asp Ala Pro
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gca tgg att atg tgc gta tcg ctg ctg ctc att gca gtc gcc agt ttc 499
Ala Trp Ile Met Cys Val Ser Leu Leu Leu Ile Ala Val Ala Ser Phe
                        120                               125                               130

atc aca tca atc atg gat gac ttt att gat ggc ata ctc act gat ttt 547
Ile Thr Ser Ile Met Asp Asp Phe Ile Asp Gly Ile Leu Thr Asp Phe
                        135                               140                               145

tat gac gaa gat aat gct gat agc ccc gat agt cct gcc gag gat ata 595
Tyr Asp Glu Asp Asn Ala Asp Ser Pro Asp Ser Pro Ala Glu Asp Ile
                        150                               155                               160                               165

gcc acc cgt cct gtc gag agc gca aca aca agt gct ctt gct gga ttt 643
Ala Thr Arg Pro Val Glu Ser Ala Thr Thr Ser Ala Leu Ala Gly Phe
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gct gtt ggt tat att tgt ggg cgc ttt aat cgc taacacttaa aacacttctc 696
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185

190

aac

699

<210> 2524

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 2524

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20 25 30

Met Ile Val Ser Val Val Ile Leu Ala Ile Tyr Met Ala Ile Thr Met
35 40 45

Tyr Arg Val Val His Gly Arg His Glu Phe Ala His Ile Ala Arg Arg
50 55 60

Met Ala Leu Tyr Val Asn Lys Thr Ser Ser Arg Phe Ser Val Val Ile
65 70 75 80

Ala Tyr Val Val Leu Ile Ala Ile Tyr Ala Leu Leu Ile Pro Gly Leu
85 90 95

Val Tyr Ser Val Thr Phe Gly Phe Ile Val Pro Ser Thr Pro Asn Thr
100 105 110

Phe Ser Asp Ala Pro Ala Trp Ile Met Cys Val Ser Leu Leu Leu Ile
115 120 125

Ala Val Ala Ser Phe Ile Thr Ser Ile Met Asp Asp Phe Ile Asp Gly
130 135 140

Ile Leu Thr Asp Phe Tyr Asp Glu Asp Asn Ala Asp Ser Pro Asp Ser
145 150 155 160

Pro Ala Glu Asp Ile Ala Thr Arg Pro Val Glu Ser Ala Thr Thr Ser
165 170 175

Ala Leu Ala Gly Phe Ala Val Gly Tyr Ile Cys Gly Arg Phe Asn Arg
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<210> 2525

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXA01982

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Met Ala Thr Thr Ser
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ctc ccc acg acg att aca ccg gat tcc gag gag acc gta gaa aag cgt 163
Leu Pro Thr Thr Ile Thr Pro Asp Ser Glu Glu Thr Val Glu Lys Arg
10 15 20

cac tcc ctg acc ccg atc ctg gat tca ctt ccc tgc gag tca gtt ccc 211
His Ser Leu Thr Pro Ile Leu Asp Ser Leu Pro Cys Glu Ser Val Pro
25 30 35

tat gct ctg gct gca ggt gag gga caa caa cac cag ctt ggc ccc tac 259
Tyr Ala Leu Ala Ala Gly Glu Gly Gln Gln His Gln Leu Gly Pro Tyr
40 45 50

cat ctc aca gtt atg tcc cgt ccc gaa gac aac ggt gga ata ttt tcg 307
His Leu Thr Val Met Ser Arg Pro Glu Asp Asn Gly Gly Ile Phe Ser
55 60 65

ctg gct cgt gtg agc gca ggc aag act ccc gcc acc cgg ttc ttc tct 355
Leu Ala Arg Val Ser Ala Gly Lys Thr Pro Ala Thr Arg Phe Phe Ser
70 75 80 85

gtc gca gga ccg acg ttc ctc tac atg atg gag ggg cgg ttg act ctc 403
Val Ala Gly Pro Thr Phe Leu Tyr Met Met Glu Gly Arg Leu Thr Leu
90 95 100

tgg ttc gct gat gga cgt caa gag atc atc gct ggc ggc agt gcc acc 451
Trp Phe Ala Asp Gly Arg Gln Glu Ile Ile Ala Gly Gly Ser Ala Thr
105 110 115

att cct acg aat acg ccc tgg tcc ttc gcc tgt gag ggc cta gta aat 499
Ile Pro Thr Asn Thr Pro Trp Ser Phe Ala Cys Glu Gly Leu Val Asn
120 125 130

tca gct cta gtg tac tac tca tcc tcg aat gca ttc cta cac gcg gca 547
Ser Ala Leu Val Tyr Tyr Ser Ser Ser Asn Ala Phe Leu His Ala Ala
135 140 145

gag aaa ctt ggc acg tcc tcg ttc tcc cac acc ttc cgc gtc agt ggc 595
Glu Lys Leu Gly Thr Ser Ser Phe Ser His Thr Phe Arg Val Ser Gly
150 155 160 165

gag gtc aca ggg att ccc tac gag gaa ctg gag gat tgc gga ttc aca 643
Glu Val Thr Gly Ile Pro Tyr Glu Glu Leu Glu Asp Cys Gly Phe Thr
170 175 180

ttc tat gag cgg gac cac ctt gcc gag ctc ggg ccg cat ttc gat cgc 691
Phe Tyr Glu Arg Asp His Leu Ala Glu Leu Gly Pro His Phe Asp Arg
185 190 195

ctc cca gaa gat atg aag gcg ttt gcc ctg aac gat ggt gag ggg gac 739
Leu Pro Glu Asp Met Lys Ala Phe Ala Leu Asn Asp Gly Glu Gly Asp
200 205 210

cgg ctt gag cag ttc gag cag atc aac agc ttc gtc tgc cgt ccg aga 787
Arg Leu Glu Gln Phe Glu Gln Ile Asn Ser Phe Val Cys Arg Pro Arg
215 220 225

cac acc gga aat cag ttc ctc gct atg cag acc aag ggt gcc aag acg 835

His Thr Gly Asn Gln Phe Leu Ala Met Gln Thr Lys Gly Ala Lys Thr
 230 235 240 245
 cct tat ata cct cgt cat ttc cac cgc ctt cac acc gaa aac ttc atc 883
 Pro Tyr Ile Pro Arg His Phe His Arg Leu His Thr Glu Asn Phe Ile
 250 255 260
 tgt ctg gac ggg cgc gtc aaa ctg cac gtc aac ggt caa gag atc atc 931
 Cys Leu Asp Gly Arg Val Lys Leu His Val Asn Gly Gln Glu Ile Ile
 265 270 275
 ctc tcc cgt ggg gat tac gtt cat gcc cca gcc gga acc atc cac tct 979
 Leu Ser Arg Gly Asp Tyr Val His Ala Pro Ala Gly Thr Ile His Ser
 280 285 290
 ttc gcc ttc gca ggg cac aat acc cag atg ctg gga gtg ctc acc aca 1027
 Phe Ala Phe Ala Gly His Asn Thr Gln Met Leu Gly Val Leu Thr Thr
 295 300 305
 gag gta ttc gag aag ttc ttt gac tac ata aac act ccg act aat gct 1075
 Glu Val Phe Glu Lys Phe Phe Asp Tyr Ile Asn Thr Pro Thr Asn Ala
 310 315 320 325
 cga gtt cag ctg gag gac ggg ggg aag cca ttt ttt cct gct gaa gca 1123
 Arg Val Gln Leu Glu Asp Gly Gly Lys Pro Phe Phe Pro Ala Glu Ala
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 Phe Ala Lys Val Gln Ala Glu Leu Asp Val Val Val Val Gly Pro Pro
 345 350 355
 cga att agt acc ctg gat gtt gtt aca aac tcg cgt ttc gaa cca att 1219
 Arg Ile Ser Thr Leu Asp Val Val Thr Asn Ser Arg Phe Glu Pro Ile
 360 365 370
 aac aga act atc acc tat cgt gcg ctg gac gct aac caa tagtgagtga 1268
 Asn Arg Thr Ile Thr Tyr Arg Ala Leu Asp Ala Asn Gln
 375 380 385
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<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 2526

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 20 25 30
 Cys Glu Ser Val Pro Tyr Ala Leu Ala Ala Gly Glu Gly Gln Gln His
 35 40 45
 Gln Leu Gly Pro Tyr His Leu Thr Val Met Ser Arg Pro Glu Asp Asn
 50 55 60
 Gly Gly Ile Phe Ser Leu Ala Arg Val Ser Ala Gly Lys Thr Pro Ala

65	70	75	80
Thr Arg Phe Phe Ser Val Ala Gly Pro Thr Phe Leu Tyr Met Met Glu	85	90	95
Gly Arg Leu Thr Leu Trp Phe Ala Asp Gly Arg Gln Glu Ile Ile Ala	100	105	110
Gly Gly Ser Ala Thr Ile Pro Thr Asn Thr Pro Trp Ser Phe Ala Cys	115	120	125
Glu Gly Leu Val Asn Ser Ala Leu Val Tyr Tyr Ser Ser Ser Asn Ala	130	135	140
Phe Leu His Ala Ala Glu Lys Leu Gly Thr Ser Ser Phe Ser His Thr	145	150	155
Phe Arg Val Ser Gly Glu Val Thr Gly Ile Pro Tyr Glu Glu Leu Glu	165	170	175
Asp Cys Gly Phe Thr Phe Tyr Glu Arg Asp His Leu Ala Glu Leu Gly	180	185	190
Pro His Phe Asp Arg Leu Pro Glu Asp Met Lys Ala Phe Ala Leu Asn	195	200	205
Asp Gly Glu Gly Asp Arg Leu Glu Gln Phe Glu Gln Ile Asn Ser Phe	210	215	220
Val Cys Arg Pro Arg His Thr Gly Asn Gln Phe Leu Ala Met Gln Thr	225	230	235
Lys Gly Ala Lys Thr Pro Tyr Ile Pro Arg His Phe His Arg Leu His	245	250	255
Thr Glu Asn Phe Ile Cys Leu Asp Gly Arg Val Lys Leu His Val Asn	260	265	270
Gly Gln Glu Ile Ile Leu Ser Arg Gly Asp Tyr Val His Ala Pro Ala	275	280	285
Gly Thr Ile His Ser Phe Ala Phe Ala Gly His Asn Thr Gln Met Leu	290	295	300
Gly Val Leu Thr Thr Glu Val Phe Glu Lys Phe Phe Asp Tyr Ile Asn	305	310	315
Thr Pro Thr Asn Ala Arg Val Gln Leu Glu Asp Gly Gly Lys Pro Phe	325	330	335
Phe Pro Ala Glu Ala Phe Ala Lys Val Gln Ala Glu Leu Asp Val Val	340	345	350
Val Val Gly Pro Pro Arg Ile Ser Thr Leu Asp Val Val Thr Asn Ser	355	360	365
Arg Phe Glu Pro Ile Asn Arg Thr Ile Thr Tyr Arg Ala Leu Asp Ala	370	375	380
Asn Gln			
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<211> 1022

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(999)

<223> RXA01990

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acg ttg ccg gac agt att gtg acc agt gtt tct tat acg ttg aac ggg	96
Thr Leu Pro Asp Ser Ile Val Thr Ser Val Ser Tyr Thr Leu Asn Gly	
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ctg tca ttt tct gac ccg gtt gag ctg ggt atc agt gac aac gac aag	144
Leu Ser Phe Ser Asp Pro Val Glu Leu Gly Ile Ser Asp Asn Asp Lys	
35 40 45	
cgt gaa gag ctt cta gga gac atc acc aag ggt gaa ctg cga ttg cag	192
Arg Glu Glu Leu Leu Gly Asp Ile Thr Lys Gly Glu Leu Arg Leu Gln	
50 55 60	
atg gag ttt tcg atc ccg gat tca gca act gcc gag gat gag tac gtc	240
Met Glu Phe Ser Ile Pro Asp Ser Ala Thr Ala Glu Asp Glu Tyr Val	
65 70 75 80	
ttt aat ctc acc ggc gat gga ctt cgg ttt ttc aat tca aac gat cgc	288
Phe Asn Leu Thr Gly Asp Gly Leu Arg Phe Phe Asn Ser Asn Asp Arg	
85 90 95	
acc gtc cct gta cgc aat gat gca ggt att cgt gtc gca gat ctt ttg	336
Thr Val Pro Val Arg Asn Asp Ala Gly Ile Arg Val Ala Asp Leu Leu	
100 105 110	
gtg agc aac ggt ggt acg cgc ggt acg ttg aca aac ttt agt tcg gat	384
Val Ser Asn Gly Gly Thr Arg Gly Thr Leu Thr Asn Phe Ser Ser Asp	
115 120 125	
gct ggc act act tct cgc acc gca gct ctt gat atg gaa ctg tac ggg	432
Ala Gly Thr Thr Ser Arg Thr Ala Ala Leu Asp Met Glu Leu Tyr Gly	
130 135 140	
tgg gtg agt agc gcc cag cag acg ggt gag cga cca att caa gac tgg	480
Trp Val Ser Ser Ala Gln Gln Thr Gly Glu Arg Pro Ile Gln Asp Trp	
145 150 155 160	
act gtg ggt aag act gag ggt cag gtt gag aac aag gta gtc cgc tac	528
Thr Val Gly Lys Thr Glu Gly Gln Val Glu Asn Lys Val Val Arg Tyr	
165 170 175	
ggc gtt gct gga cac ccg tgg att atc agt act gtc cag cac acg tgg	576
Gly Val Ala Gly His Pro Trp Ile Ile Ser Thr Val Gln His Thr Trp	
180 185 190	

gtt aag tct acg cag acc gtg tcg cat ttc cga agt gaa caa gac tgg 624
 Val Lys Ser Thr Gln Thr Val Ser His Phe Arg Ser Glu Gln Asp Trp
 195 200 205

aag att aat caa cca cca gct gtt gat atg ggc gca tta gca tac gca 672
 Lys Ile Asn Gln Pro Pro Ala Val Asp Met Gly Ala Leu Ala Tyr Ala
 210 215 220

gct cca ctt ggc gtc gtg gtc ggg cac gcc aat gtt gtc att agc aat 720
 Ala Pro Leu Gly Val Val Val Gly His Ala Asn Val Val Ile Ser Asn
 225 230 235 240

aac aac ggt gct gga ttc cgg ggt gcg ctt gtc aat acc aca ccc acc 768
 Asn Asn Gly Ala Gly Phe Arg Gly Ala Leu Val Asn Thr Thr Pro Thr
 245 250 255

aca cgc gac gtg ata ctt aat ttc aca gcc gca gac gga gcc act tta 816
 Thr Arg Asp Val Ile Leu Asn Phe Thr Ala Ala Asp Gly Ala Thr Leu
 260 265 270

cgc gaa cgt tcc gga ggt gga ttt gag gat ttc gac gtt ttc tcg gaa 864
 Arg Glu Arg Ser Gly Gly Gly Phe Glu Asp Phe Asp Val Phe Ser Glu
 275 280 285

gtt cct cgg gta gag gaa aca tcg acg agg atc agc tat tct tac aaa 912
 Val Pro Arg Val Glu Glu Thr Ser Thr Arg Ile Ser Tyr Ser Tyr Lys
 290 295 300

aat tca ttt gaa tat gac gaa ttt gtt gcc gca ttt ccc gag tac cga 960
 Asn Ser Phe Glu Tyr Asp Glu Phe Val Ala Ala Phe Pro Glu Tyr Arg
 305 310 315 320

cgt agc tgc gtg gga acc aac cgt tgt gta ttc agc gga taagaccaca 1009
 Arg Ser Cys Val Gly Thr Asn Arg Cys Val Phe Ser Gly
 325 330

gcaacagcga cgt 1022

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 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
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 35 40 45
 Arg Glu Glu Leu Leu Gly Asp Ile Thr Lys Gly Glu Leu Arg Leu Gln
 50 55 60
 Met Glu Phe Ser Ile Pro Asp Ser Ala Thr Ala Glu Asp Glu Tyr Val
 65 70 75 80
 Phe Asn Leu Thr Gly Asp Gly Leu Arg Phe Phe Asn Ser Asn Asp Arg

85										90					95				
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			100					105					110						
Val	Ser	Asn	Gly	Gly	Thr	Arg	Gly	Thr	Leu	Thr	Asn	Phe	Ser	Ser	Asp				
		115					120					125							
Ala	Gly	Thr	Thr	Ser	Arg	Thr	Ala	Ala	Leu	Asp	Met	Glu	Leu	Tyr	Gly				
	130					135					140								
Trp	Val	Ser	Ser	Ala	Gln	Gln	Thr	Gly	Glu	Arg	Pro	Ile	Gln	Asp	Trp				
145					150					155					160				
Thr	Val	Gly	Lys	Thr	Glu	Gly	Gln	Val	Glu	Asn	Lys	Val	Val	Arg	Tyr				
			165						170					175					
Gly	Val	Ala	Gly	His	Pro	Trp	Ile	Ile	Ser	Thr	Val	Gln	His	Thr	Trp				
		180						185					190						
Val	Lys	Ser	Thr	Gln	Thr	Val	Ser	His	Phe	Arg	Ser	Glu	Gln	Asp	Trp				
	195						200					205							
Lys	Ile	Asn	Gln	Pro	Pro	Ala	Val	Asp	Met	Gly	Ala	Leu	Ala	Tyr	Ala				
	210					215					220								
Ala	Pro	Leu	Gly	Val	Val	Val	Gly	His	Ala	Asn	Val	Val	Ile	Ser	Asn				
225					230					235					240				
Asn	Asn	Gly	Ala	Gly	Phe	Arg	Gly	Ala	Leu	Val	Asn	Thr	Thr	Pro	Thr				
			245						250					255					
Thr	Arg	Asp	Val	Ile	Leu	Asn	Phe	Thr	Ala	Ala	Asp	Gly	Ala	Thr	Leu				
		260						265					270						
Arg	Glu	Arg	Ser	Gly	Gly	Gly	Phe	Glu	Asp	Phe	Asp	Val	Phe	Ser	Glu				
	275						280					285							
Val	Pro	Arg	Val	Glu	Glu	Thr	Ser	Thr	Arg	Ile	Ser	Tyr	Ser	Tyr	Lys				
	290					295					300								
Asn	Ser	Phe	Glu	Tyr	Asp	Glu	Phe	Val	Ala	Ala	Phe	Pro	Glu	Tyr	Arg				
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<211> 573

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(550)

<223> RXA01992

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Val Tyr Cys Pro Phe
1 5

tgc caa cat gat cat tca aaa gtc att gac tcc cgc gtc att gac gcc 163
Cys Gln His Asp His Ser Lys Val Ile Asp Ser Arg Val Ile Asp Ala
10 15 20

gga agc gcc att cgc agg cgc cgc gag tgc agc aaa tgc gaa ggc cgt 211
Gly Ser Ala Ile Arg Arg Arg Arg Glu Cys Ser Lys Cys Glu Gly Arg
25 30 35

ttc acc acc atc gaa aaa gct gtt ctc ctc gtt gtt aaa aga aac ggc 259
Phe Thr Thr Ile Glu Lys Ala Val Leu Leu Val Val Lys Arg Asn Gly
40 45 50

gtc act gaa ccg ttc agt cga gaa aaa gta gtc acc ggt gtc cgt cgt 307
Val Thr Glu Pro Phe Ser Arg Glu Lys Val Val Thr Gly Val Arg Arg
55 60 65

gca tgc caa ggc cgc gac gta tca gat gac gcg ttg aaa cgc cta gct 355
Ala Cys Gln Gly Arg Asp Val Ser Asp Asp Ala Leu Lys Arg Leu Ala
70 75 80 85

cag caa gtg gaa gaa aca gtc cgc agc aac gga agc tct caa gta cgc 403
Gln Gln Val Glu Glu Thr Val Arg Ser Asn Gly Ser Ser Gln Val Arg
90 95 100

gct aac gat att ggt tta gcc att ctc gat cca ctg aga gaa ctc gac 451
Ala Asn Asp Ile Gly Leu Ala Ile Leu Asp Pro Leu Arg Glu Leu Asp
105 110 115

gag gta gcg tac cta cgc ttt gcc tct gtg tat aag tct ttt gac agt 499
Glu Val Ala Tyr Leu Arg Phe Ala Ser Val Tyr Lys Ser Phe Asp Ser
120 125 130

gct gac gac ttt gaa aaa gaa atc cgc ctc atg cgc aga cgc gga agg 547
Ala Asp Asp Phe Glu Lys Glu Ile Arg Leu Met Arg Arg Arg Gly Arg
135 140 145

gac tagcagacac aaagtcttaa cta 573
Asp
150

<210> 2530

<211> 150

<212> PRT

<213> Corynebacterium glutamicum

<400> 2530

Val Tyr Cys Pro Phe Cys Gln His Asp His Ser Lys Val Ile Asp Ser
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Arg Val Ile Asp Ala Gly Ser Ala Ile Arg Arg Arg Arg Glu Cys Ser
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Lys Cys Glu Gly Arg Phe Thr Thr Ile Glu Lys Ala Val Leu Leu Val
35 40 45

Val Lys Arg Asn Gly Val Thr Glu Pro Phe Ser Arg Glu Lys Val Val

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Met Thr Leu Pro Thr																115
1 5																
cct aca cat tcc acc aaa ggc agt tca ggc cgc atg aaa cga atg gcc																163
Pro Thr His Ser Thr Lys Gly Ser Ser Gly Arg Met Lys Arg Met Ala																
10 15 20																
ctt atc ggc tcc tcg ctc att att tcc atg gga ctt att act gcg tgc																211
Leu Ile Gly Ser Ser Leu Ile Ile Ser Met Gly Leu Ile Thr Ala Cys																
25 30 35																
ggt tcg gcc gct gca gaa ccc gaa gcc cct gca cca aca gtt acc gaa																259
Gly Ser Ala Ala Ala Glu Pro Glu Ala Pro Ala Pro Thr Val Thr Glu																
40 45 50																
act gta aca gcc acg gtg aca acc aca gct aaa gcc agc acg atc acc																307
Thr Val Thr Ala Thr Val Thr Thr Ala Lys Ala Ser Thr Ile Thr																
55 60 65																
tcg aca gtg acg gaa act acc tcc gcg gaa gat ctt gcc caa gaa att																355
Ser Thr Val Thr Glu Thr Thr Ser Ala Glu Asp Leu Ala Gln Glu Ile																
70 75 80 85																
gtg aag cca gcg gcc gtg gag gaa tat tca gag cct cag gta aat acg																403
Val Lys Pro Ala Val Glu Glu Tyr Ser Glu Pro Gln Val Asn Thr																
90 95 100																

cca cag cag ttt gcg gcc atc ccg gaa cct gca ccg gcg gtt gca cca 451
 Pro Gln Gln Phe Ala Ala Ile Pro Glu Pro Ala Pro Ala Val Ala Pro
 105 110 115

gct caa acg tat tac gcc aac tgc gcg gca gtt cgt gcg gcg ggt gca 499
 Ala Gln Thr Tyr Tyr Ala Asn Cys Ala Ala Val Arg Ala Ala Gly Ala
 120 125 130

gct ccc ctt tat gcg gga tca cct gga tat agt tcc aag ctt gat cgc 547
 Ala Pro Leu Tyr Ala Gly Ser Pro Gly Tyr Ser Ser Lys Leu Asp Arg
 135 140 145

gat ggc gac gga att gcc tgc gaa taaataggaa tagttaaaaa cac 594
 Asp Gly Asp Gly Ile Ala Cys Glu
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<210> 2532

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 2532

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Met Lys Arg Met Ala Leu Ile Gly Ser Ser Leu Ile Ile Ser Met Gly
 20 25 30

Leu Ile Thr Ala Cys Gly Ser Ala Ala Ala Glu Pro Glu Ala Pro Ala
 35 40 45

Pro Thr Val Thr Glu Thr Val Thr Ala Thr Val Thr Thr Thr Ala Lys
 50 55 60

Ala Ser Thr Ile Thr Ser Thr Val Thr Glu Thr Thr Ser Ala Glu Asp
 65 70 75 80

Leu Ala Gln Glu Ile Val Lys Pro Ala Ala Val Glu Glu Tyr Ser Glu
 85 90 95

Pro Gln Val Asn Thr Pro Gln Gln Phe Ala Ala Ile Pro Glu Pro Ala
 100 105 110

Pro Ala Val Ala Pro Ala Gln Thr Tyr Tyr Ala Asn Cys Ala Ala Val
 115 120 125

Arg Ala Ala Gly Ala Ala Pro Leu Tyr Ala Gly Ser Pro Gly Tyr Ser
 130 135 140

Ser Lys Leu Asp Arg Asp Gly Asp Gly Ile Ala Cys Glu
 145 150 155

<210> 2533

<211> 572

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (1)..(549)
 <223> RXA02001

<400> 2533

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  1             5             10             15

acg ata gtc agc cgg aat cac aat ccg gtc gag gac ctt gtc gtg tcg 96
Thr Ile Val Ser Arg Asn His Asn Pro Val Glu Asp Leu Val Val Ser
             20             25             30

gtc acg caa atc cac acc ggc agc gcc gat aat atc atc ccc gaa acc 144
Val Thr Gln Ile His Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr
             35             40             45

gcc tat atc aac ggc act gtc cgc acc ttc aac aaa gac gtg cag gcc 192
Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala
             50             55             60

atg gtc atc acg cgg atg gaa gaa atc gtc gcg gcc caa gct gca gcc 240
Met Val Ile Thr Arg Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala
             65             70             75             80

tat ggg gtc gag gcg acg ctg acc tac aac cgc aac tat ccc gcc acc 288
Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr
             85             90             95

att aac gac gcc gcc aaa gcc gcc atc gct gcc gaa gtc gcg gcc gag 336
Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu
             100             105             110

gtc gcc ctc ggg gtc aac ccg aac gcc tcg cgc ggg atg ggg gcc gag 384
Val Gly Leu Gly Val Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu
             115             120             125

gat ttc tcg tat ttc ctc gaa aag cgc ccg ggt gcc tac ctg ttc gtc 432
Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val
             130             135             140

ggt aat gcc gac agc gcg gcc ctt cac aac ccc gcc tat aat ttc aac 480
Gly Asn Gly Asp Ser Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn
             145             150             155             160

gac gag gcc gcg ccc tac gcc gca tcg ttc ttg gcc cgc atg gca gaa 528
Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu
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cgc ccc ttg ccg tta aag gcc tgatccatgg cgctcgaaga tgc 572
Arg Pro Leu Pro Leu Lys Gly
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<211> 183

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<400> 2534

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 Thr Ile Val Ser Arg Asn His Asn Pro Val Glu Asp Leu Val Val Ser
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 Val Thr Gln Ile His Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr
 35 40 45
 Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala
 50 55 60
 Met Val Ile Thr Arg Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala
 65 70 75 80
 Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr
 85 90 95
 Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu
 100 105 110
 Val Gly Leu Gly Val Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu
 115 120 125
 Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val
 130 135 140
 Gly Asn Gly Asp Ser Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn
 145 150 155 160
 Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu
 165 170 175
 Arg Pro Leu Pro Leu Lys Gly
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<220>
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 <222> (1)..(207)
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 1 5 10 15
 cgg aag ttc aag cgc acg acc ggc agc gat cat acc ttc aac atc gca 96
 Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
 20 25 30
 ccg aac ttt ctg cag cag gac ttt atg gcg agc agg ccg aac cag aag 144
 Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
 35 40 45
 tgg gcg ggc gac atc acc tat gtc tgg acg cgc gag ggc ctg ggt cta 192
 Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu

50

55

60

tct ggc cga cat tct tgacctttat ccccgccggg tga
 Ser Gly Arg His Ser
 65

230

<210> 2536

<211> 69

<212> PRT

<213> Corynebacterium glutamicum

<400> 2536

Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
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Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
 20 25 30

Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
 35 40 45

Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
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Ser Gly Arg His Ser
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<210> 2537

<211> 565

<212> DNA

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<220>

<221> CDS

<222> (71)..(565)

<223> RXA02006

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gggagactca atg aca gtt gca cac aaa cga agt ctg aca tgg atc aag 109
 Met Thr Val Ala His Lys Arg Ser Leu Thr Trp Ile Lys
 1 5 10

aga cta tct gcg act aca ttt gca gct ttt ctt ggc att cag ctt gtg 157
 Arg Leu Ser Ala Thr Thr Phe Ala Ala Phe Leu Gly Ile Gln Leu Val
 15 20 25

acc ccc gct cac tca att gaa aac acg acg cag att cca gaa agc gaa 205
 Thr Pro Ala His Ser Ile Glu Asn Thr Thr Gln Ile Pro Glu Ser Glu
 30 35 40 45

ttg cac aac ctc ggg ctc aca gac gaa gaa att caa gaa ttc aat caa 253
 Leu His Asn Leu Gly Leu Thr Asp Glu Glu Ile Gln Glu Phe Asn Gln
 50 55 60

tat ctc att gac gag tca ctc ttt caa gag act gta gaa acc tct ccg 301
 Tyr Leu Ile Asp Glu Ser Leu Phe Gln Glu Thr Val Glu Thr Ser Pro
 65 70 75

atc gta gtc agc gac aat gaa gat gca gcc caa gat ccc ggt ttc ggc 349
Ile Val Val Ser Asp Asn Glu Asp Ala Ala Gln Asp Pro Gly Phe Gly
80 85 90

ctt ttc acc aca aat cct gtg aaa cac aca gat gag cac att ggc gct 397
 Leu Phe Thr Thr Asn Pro Val Lys His Thr Asp Glu His Ile Gly Ala
 95 100 105

cta tac ttc tcc gac cta cca ggt att tcc aat ctt acg tgc act gcc 445
Leu Tyr Phe Ser Asp Leu Pro Gly Ile Ser Asn Leu Thr Cys Thr Ala
110 115 120 125

aac tac atc ggt gga aaa ttc tgg acc aca gca cat cat tgt gtt gaa 493
Asn Tyr Ile Gly Gly Lys Phe Trp Thr Thr Ala His His Cys Val Glu
130 135 140

ggc cgc agt cgc ttc gtc ggc ttc atc gag cag tcg gac gga caa tat 541
Gly Arg Ser Arg Phe Val Gly Phe Ile Glu Gln Ser Asp Gly Gln Tyr
145 150 155

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Ala Gly Ile Glu His Val Tyr Thr
160 165

<210> 2538

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 2538

Met Thr Val Ala His Lys Arg Ser Leu Thr Trp Ile Lys Arg Leu Ser
1 5 10 15

Ala Thr Thr Phe Ala Ala Phe Leu Gly Ile Gln Leu Val Thr Pro Ala
20 25 30

His Ser Ile Glu Asn Thr Thr Gln Ile Pro Glu Ser Glu Leu His Asn
35 40 45

Leu Gly Leu Thr Asp Glu Glu Ile Gln Glu Phe Asn Gln Tyr Leu Ile
50 55 60

Asp Glu Ser Leu Phe Gln Glu Thr Val Glu Thr Ser Pro Ile Val Val
65 70 75 80

Ser Asp Asn Glu Asp Ala Ala Gln Asp Pro Gly Phe Gly Leu Phe Thr
85 90 95

Thr Asn Pro Val Lys His Thr Asp Glu His Ile Gly Ala Leu Tyr Phe
100 105 110

Ser Asp Leu Pro Gly Ile Ser Asn Leu Thr Cys Thr Ala Asn Tyr Ile
115 120 125

Gly Gly Lys Phe Trp Thr Thr Ala His His Cys Val Glu Gly Arg Ser
130 135 140

Arg Phe Val Gly Phe Ile Glu Gln Ser Asp Gly Gln Tyr Ala Gly Ile
145 150 155 160

Glu His Val Tyr Thr
165

<210> 2539
<211> 223
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(223)
<223> RXA02009

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Met Thr Met Tyr Asn
1 5
gcc gca aag acc ctt gtt ccc cag att gtt gct ttc gat gac aca gca 163
Ala Ala Lys Thr Leu Val Pro Gln Ile Val Ala Phe Asp Asp Thr Ala
10 15 20
atc atc gca ctc gac caa gcc gcg gaa gat gaa ttc cgc aag gct aac 211
Ile Ile Ala Leu Asp Gln Ala Ala Glu Asp Glu Phe Arg Lys Ala Asn
25 30 35
tac ccc gag gtt 223
Tyr Pro Glu Val
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<210> 2540
<211> 41
<212> PRT
<213> Corynebacterium glutamicum

<400> 2540
Met Thr Met Tyr Asn Ala Ala Lys Thr Leu Val Pro Gln Ile Val Ala
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Phe Asp Asp Thr Ala Ile Ile Ala Leu Asp Gln Ala Ala Glu Asp Glu
20 25 30
Phe Arg Lys Ala Asn Tyr Pro Glu Val
35 40

<210> 2541
<211> 649
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(649)
<223> RXA02013

<400> 2541

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tccggtctta aacacggcat gatggctaac atcggagaac atg acg gaa agt cct 115
                                         Met Thr Glu Ser Pro
                                         1 5

gat cta gca gtt tcc ttt tta gcc gcc ttc aat gac atc gaa gcg cac 163
Asp Leu Ala Val Ser Phe Leu Ala Ala Phe Asn Asp Ile Glu Ala His
                        10 15 20

ctt cga acc cag ctc cgc gct aaa cgc tcc gac agt ttc aga tgg atg 211
Leu Arg Thr Gln Leu Arg Ala Lys Arg Ser Asp Ser Phe Arg Trp Met
                        25 30 35

gta cgt atc gcc gag aaa cag cat ctg att tcc aaa gaa caa gca gaa 259
Val Arg Ile Ala Glu Lys Gln His Leu Ile Ser Lys Glu Gln Ala Glu
                        40 45 50

acc ctt gat gct ttt gcg gag ctg cgc aac gca att agc cac ggc caa 307
Thr Leu Asp Ala Phe Ala Glu Leu Arg Asn Ala Ile Ser His Gly Gln
                        55 60 65

tac aac gat cta cgc ccg att gcc gat ccc cgc ccc gac acc gtg gac 355
Tyr Asn Asp Leu Arg Pro Ile Ala Asp Pro Arg Pro Asp Thr Val Asp
                        70 75 80 85

acc att gag aag att cgc tcc ctc ctt ctc aat cct cca att gcg tta 403
Thr Ile Glu Lys Ile Arg Ser Leu Leu Leu Asn Pro Pro Ile Ala Leu
                        90 95 100

aac gtc ctc ccg gag caa aag gtc cgc tcc tac tca ctt gaa gat cca 451
Asn Val Leu Pro Glu Gln Lys Val Arg Ser Tyr Ser Leu Glu Asp Pro
                        105 110 115

gtg agt agg gcc tta gaa gtt gtg cac acc acg gag atc tcc caa ttc 499
Val Ser Arg Ala Leu Glu Val Val His Thr Thr Glu Ile Ser Gln Phe
                        120 125 130

ccc ata tat aag gga acg gaa tac gtg gca ctg cta act acc aac aca 547
Pro Ile Tyr Lys Gly Thr Glu Tyr Val Ala Leu Leu Thr Thr Asn Thr
                        135 140 145

atc gct cgc tgg gtt gcc tcc gat tta cat gac aat gcc cag ctg gat 595
Ile Ala Arg Trp Val Ala Ser Asp Leu His Asp Asn Ala Gln Leu Asp
                        150 155 160 165

gca cgt tct atc aaa gag gtt ctg gat tat gca gaa tcc tct gac act 643
Ala Arg Ser Ile Lys Glu Val Leu Asp Tyr Ala Glu Ser Ser Asp Thr
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Ala Val

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<210> 2542

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 2542

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 20 25 30
 Ser Phe Arg Trp Met Val Arg Ile Ala Glu Lys Gln His Leu Ile Ser
 35 40 45
 Lys Glu Gln Ala Glu Thr Leu Asp Ala Phe Ala Glu Leu Arg Asn Ala
 50 55 60
 Ile Ser His Gly Gln Tyr Asn Asp Leu Arg Pro Ile Ala Asp Pro Arg
 65 70 75 80
 Pro Asp Thr Val Asp Thr Ile Glu Lys Ile Arg Ser Leu Leu Leu Asn
 85 90 95
 Pro Pro Ile Ala Leu Asn Val Leu Pro Glu Gln Lys Val Arg Ser Tyr
 100 105 110
 Ser Leu Glu Asp Pro Val Ser Arg Ala Leu Glu Val Val His Thr Thr
 115 120 125
 Glu Ile Ser Gln Phe Pro Ile Tyr Lys Gly Thr Glu Tyr Val Ala Leu
 130 135 140
 Leu Thr Thr Asn Thr Ile Ala Arg Trp Val Ala Ser Asp Leu His Asp
 145 150 155 160
 Asn Ala Gln Leu Asp Ala Arg Ser Ile Lys Glu Val Leu Asp Tyr Ala
 165 170 175
 Glu Ser Ser Asp Thr Ala Val
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<210> 2543

<211> 1071

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1048)

<223> RXA02021

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 Met Ser Glu Asn Ile 5
 cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163
 Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr 20
 atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag 211
 Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln

25										30										35										
ttg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca	259																													
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala																														
40 45 50																														
aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat	307																													
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp																														
55 60 65																														
cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct	355																													
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser																														
70 75 80 85																														
caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt	403																													
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu																														
90 95 100																														
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Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu																														
105 110 115																														
gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct	499																													
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro																														
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Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile																														
135 140 145																														
cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt	595																													
His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val																														
150 155 160 165																														
ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca	643																													
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala																														
170 175 180																														
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Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe																														
185 190 195																														
aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc	739																													
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser																														
200 205 210																														
ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att	787																													
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile																														
215 220 225																														
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Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly																														
230 235 240 245																														
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Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu																														
250 255 260																														
gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc	931																													
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			20					25					30		
Phe	Asn	Pro	Asp	Gln	Trp	Ala	Glu	Arg	Tyr	Pro	Leu	Glu	Val	Gly	Thr
		35					40					45			
Thr	Arg	Leu	Gly	Ala	Asn	Glu	Leu	Thr	Pro	Arg	Met	Leu	Gln	Leu	Val
	50					55					60				
Lys	Leu	Asp	Gln	Asp	Arg	Leu	Val	Glu	Gln	Val	Ala	Val	Arg	Thr	Val
65					70					75					80
Ile	Pro	Asp	Leu	Ser	Gln	Pro	Pro	Val	Asp	Ala	His	Asp	Val	Tyr	Leu
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Arg	Leu	His	Leu	Leu	Ser	His	Arg	Leu	Val	Arg	Pro	His	Glu	Met	His
			100					105					110		
Met	Gln	Asn	Thr	Leu	Glu	Leu	Leu	Ser	Asp	Val	Val	Trp	Thr	Asn	Lys
		115					120					125			
Gly	Pro	Cys	Leu	Pro	Glu	Asn	Phe	Glu	Trp	Val	Arg	Gly	Ala	Leu	Arg
	130					135					140				
Ser	Arg	Gly	Leu	Ile	His	Val	Tyr	Cys	Val	Asp	Arg	Leu	Pro	Arg	Met
145					150					155					160
Val	Asp	Tyr	Val	Val	Pro	Pro	Gly	Val	Arg	Ile	Ser	Glu	Ala	Glu	Arg
				165					170					175	
Val	Arg	Leu	Gly	Ala	Tyr	Leu	Ala	Pro	Gly	Thr	Ser	Val	Leu	Arg	Glu
			180					185					190		
Gly	Phe	Val	Ser	Phe	Asn	Ser	Gly	Thr	Leu	Gly	Ala	Ala	Lys	Val	Glu
		195					200					205			
Gly	Arg	Leu	Ser	Ser	Gly	Val	Val	Ile	Gly	Glu	Gly	Ser	Glu	Ile	Gly
	210					215					220				

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
 225 230 235 240
 Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
 245 250 255
 Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
 260 265 270
 Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
 275 280 285
 Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
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 Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
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<211> 504

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(481)

<223> RXA02036

<400> 2545

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 Val His Ile Pro Phe
 1 5
 ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
 Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
 10 15 20
 gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
 25 30 35
 acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
 40 45 50
 ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307
 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
 55 60 65
 cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355
 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
 70 75 80 85
 gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
 90 95 100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451
Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
105 110 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501
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120 125

ttt 504

<210> 2546

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 2546

Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys
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20 25 30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
35 40 45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala
50 55 60

Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala
65 70 75 80

Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile
85 90 95

Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg
100 105 110

Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
115 120 125

<210> 2547

<211> 551

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(528)

<223> RXA02040

<400> 2547

tac ata cct ttt gtc att tgg tcc gat ctc ggt gag gct gcc gaa ggt 48
Tyr Ile Pro Phe Val Ile Trp Ser Asp Leu Gly Glu Ala Ala Glu Gly
1 5 10 15

gag aac ttt gct cgc ttc tgg tcc tgg ctg aaa tcg cgc cgg gac aaa 96
Glu Asn Phe Ala Arg Phe Trp Ser Trp Leu Lys Ser Arg Arg Asp Lys
20 25 30

gct cgc cag cag gga caa acc ttc ggt gtg ttc tgc tat gcc agc aac 144
 Ala Arg Gln Gln Gly Gln Thr Phe Gly Val Phe Cys Tyr Ala Ser Asn
 35 40 45

ggc gaa aac cac tgg atg ctc tcc act gct cgc aga ttc ttc ggc aaa 192
 Gly Glu Asn His Trp Met Leu Ser Thr Ala Arg Arg Phe Phe Gly Lys
 50 55 60

gtc aaa ggt gtg ccc gac gag caa gaa atc cgc agc ttc att agc tct 240
 Val Lys Gly Val Pro Asp Glu Gln Glu Ile Arg Ser Phe Ile Ser Ser
 65 70 75 80

gac caa tgg aat gac atg ttt gct gtc gcg cgc tcc caa ctt gtt ggc 288
 Asp Gln Trp Asn Asp Met Phe Ala Val Ala Arg Ser Gln Leu Val Gly
 85 90 95

ccc ggt ggt tta ggt ctg aaa caa ctc gcg ccg gca gct gga ttc cat 336
 Pro Gly Gly Leu Gly Leu Lys Gln Leu Ala Pro Ala Ala Gly Phe His
 100 105 110

tgg gag gaa gaa gac ttc gca ggt gaa gat agc ctc cac gca tat ctc 384
 Trp Glu Glu Glu Asp Phe Ala Gly Glu Asp Ser Leu His Ala Tyr Leu
 115 120 125

att gct tcc acg gct gcc gaa cca gaa gct gag gcc gct cgt gct caa 432
 Ile Ala Ser Thr Ala Ala Glu Pro Glu Ala Glu Ala Ala Arg Ala Gln
 130 135 140

ttg ctc agc tac aac ggc gat gat tgc agg gcc acc gca gcg gtt cgc 480
 Leu Leu Ser Tyr Asn Gly Asp Asp Cys Arg Ala Thr Ala Ala Val Arg
 145 150 155 160

cat tgg ctt cga caa ggt gcg cgc acg gca cct gtg ctg ggg aat att 528
 His Trp Leu Arg Gln Gly Ala Arg Thr Ala Pro Val Leu Gly Asn Ile
 165 170 175

taaaccaagg aaggattctc cag 551

<210> 2548

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 2548

Tyr Ile Pro Phe Val Ile Trp Ser Asp Leu Gly Glu Ala Ala Glu Gly
 1 5 10 15

Glu Asn Phe Ala Arg Phe Trp Ser Trp Leu Lys Ser Arg Arg Asp Lys
 20 25 30

Ala Arg Gln Gln Gly Gln Thr Phe Gly Val Phe Cys Tyr Ala Ser Asn
 35 40 45

Gly Glu Asn His Trp Met Leu Ser Thr Ala Arg Arg Phe Phe Gly Lys
 50 55 60

Val Lys Gly Val Pro Asp Glu Gln Glu Ile Arg Ser Phe Ile Ser Ser
 65 70 75 80

Asp Gln Trp Asn Asp Met Phe Ala Val Ala Arg Ser Gln Leu Val Gly

85	90	95
Pro Gly Gly Leu Gly Leu Lys Gln Leu Ala Pro Ala Ala Gly Phe His 100 105 110		
Trp Glu Glu Glu Asp Phe Ala Gly Glu Asp Ser Leu His Ala Tyr Leu 115 120 125		
Ile Ala Ser Thr Ala Ala Glu Pro Glu Ala Glu Ala Ala Arg Ala Gln 130 135 140		
Leu Leu Ser Tyr Asn Gly Asp Asp Cys Arg Ala Thr Ala Ala Val Arg 145 150 155 160		
His Trp Leu Arg Gln Gly Ala Arg Thr Ala Pro Val Leu Gly Asn Ile 165 170 175		

<210> 2549

<211> 364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(364)

<223> RXA02046

<400> 2549

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aaattattaa catccgacgc aacgcttcag gagagtcctc atg aaa gag aca ctg 115
                                         Met Lys Glu Thr Leu
                                         1 5
acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc 163
Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg
                        10 15 20
aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca 211
Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro
                        25 30 35
gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc 259
Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys
                        40 45 50
atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc 307
Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly
                        55 60 65
act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg 355
Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr
                        70 75 80 85
gtc acc atc
Val Thr Ile

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<210> 2550

<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 2550

Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile
 1 5 10 15

Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu
 20 25 30

Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
 35 40 45

Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
 50 55 60

Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
 65 70 75 80

Val Pro Gly Ser Thr Val Thr Ile
 85

<210> 2551

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXA02051

<400> 2551

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gcagacatca tcttcaactc gcacaacagt caatgactcc atg gtc atc aga gct 115
 Met Val Ile Arg Ala
 1 5

ctc cag cgc gaa gaa gaa atc gtc ctt ctc agc gcc gga gca ctt gga 163
 Leu Gln Arg Glu Glu Glu Ile Val Leu Leu Ser Ala Gly Ala Leu Gly
 10 15 20

atc cat gag aaa acc gtt gaa cgt aca att cgt gga aaa cgt att cct 211
 Ile His Glu Lys Thr Val Glu Arg Thr Ile Arg Gly Lys Arg Ile Pro
 25 30 35

ggc acg caa aag acc gtg cac gtc caa tac agc tac acc gga aaa ctc 259
 Gly Thr Gln Lys Thr Val His Val Gln Tyr Ser Tyr Thr Gly Lys Leu
 40 45 50

gga atc gat gcc tca gat gtt gaa atc aaa tcc gca ggt gac aat aag 307
 Gly Ile Asp Ala Ser Asp Val Glu Ile Lys Ser Ala Gly Asp Asn Lys
 55 60 65

ctt tcc atc act atc cct gag ttc atc ttc atc gga tac gac gat cta 355
 Leu Ser Ile Thr Ile Pro Glu Phe Ile Phe Ile Gly Tyr Asp Asp Leu
 70 75 80 85

aag ttt aag acc ata gcc gaa gat gac ggt tgg atc agt ttc agc act 403
Lys Phe Lys Thr Ile Ala Glu Asp Asp Gly Trp Ile Ser Phe Ser Thr
90 95 100
gac gat atc gat act gca gaa gta gtt tct gag atc atg agc caa gag 451
Asp Asp Ile Asp Thr Ala Glu Val Val Ser Glu Ile Met Ser Gln Glu
105 110 115
aac ttc gtc gag caa gta acc act aac cgg gaa atg ttg gaa gat caa 499
Asn Phe Val Glu Gln Val Thr Thr Asn Arg Glu Met Leu Glu Asp Gln
120 125 130
gcg gtt gat ttc tac aac gac ctg ctc cac gaa ttc acc gag aaa ctc 547
Ala Val Asp Phe Tyr Asn Asp Leu Leu His Glu Phe Thr Glu Lys Leu
135 140 145
gat aca gat cga tac gaa gac acc aag att gag ctc gaa ttc gag ttt 595
Asp Thr Asp Arg Tyr Glu Asp Thr Lys Ile Glu Leu Glu Phe Glu Phe
150 155 160 165
gag tagatagtgc ttcgaagaca gtt 621
Glu

<210> 2552

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 2552

Met Val Ile Arg Ala Leu Gln Arg Glu Glu Glu Ile Val Leu Leu Ser
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Ala Gly Ala Leu Gly Ile His Glu Lys Thr Val Glu Arg Thr Ile Arg
20 25 30
Gly Lys Arg Ile Pro Gly Thr Gln Lys Thr Val His Val Gln Tyr Ser
35 40 45
Tyr Thr Gly Lys Leu Gly Ile Asp Ala Ser Asp Val Glu Ile Lys Ser
50 55 60
Ala Gly Asp Asn Lys Leu Ser Ile Thr Ile Pro Glu Phe Ile Phe Ile
65 70 75 80
Gly Tyr Asp Asp Leu Lys Phe Lys Thr Ile Ala Glu Asp Asp Gly Trp
85 90 95
Ile Ser Phe Ser Thr Asp Asp Ile Asp Thr Ala Glu Val Val Ser Glu
100 105 110
Ile Met Ser Gln Glu Asn Phe Val Glu Gln Val Thr Thr Asn Arg Glu
115 120 125
Met Leu Glu Asp Gln Ala Val Asp Phe Tyr Asn Asp Leu Leu His Glu
130 135 140
Phe Thr Glu Lys Leu Asp Thr Asp Arg Tyr Glu Asp Thr Lys Ile Glu
145 150 155 160

Leu Glu Phe Glu Phe Glu
165

<210> 2553
<211> 702
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(679)
<223> RXA02053

<400> 2553
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ctaccatgac tctgtttcca acacataaaa aggataaaaa atg tca ctt tca gtc 115
Met Ser Leu Ser Val
1 5
gtc gag gcg att acc aac cgc cgc gcc acc cgc aaa tac acc gat gaa 163
Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg Lys Tyr Thr Asp Glu
10 15 20
gct cct acc cct gag ctg atc gac aaa atc gtt gac ctt gcc ctg gag 211
Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val Asp Leu Ala Leu Glu
25 30 35
gca ccc agt gcg ttc aat gcg cag caa cgt gaa att gtt gtg att act 259
Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu Ile Val Val Ile Thr
40 45 50
gat ccc gca cag aag cag aag ctt tac gag gcc tcc cat cag aaa caa 307
Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala Ser His Gln Lys Gln
55 60 65
ttc ctc acc gca cct gta act ttc att gcg gtt gcc cgc gtg gaa aac 355
Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val Ala Arg Val Glu Asn
70 75 80 85
gag cct gag gat ttg gaa gag att ctt ggt acg gaa agg gct gaa cgt 403
Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr Glu Arg Ala Glu Arg
90 95 100
gtc gcg gga ttc atc aac ggt cgc agc att cag cag gca cgc gaa gca 451
Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln Gln Ala Arg Glu Ala
105 110 115
acg ttg agg gat gcc agc ctc gcg gcg gct ttt cta att ctg gct gcc 499
Thr Leu Arg Asp Ala Ser Leu Ala Ala Phe Leu Ile Leu Ala Ala
120 125 130
cag gcg gag ggt ttg agt acc agc ccg act act ggt tgg gat gag gaa 547
Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr Gly Trp Asp Glu Glu
135 140 145
aaa gtg aag gaa gca atc ggt ctc ggc ggg cgt gag gat cgt gca atc 595
Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Glu Asp Arg Ala Ile
150 155 160 165

gcc ctt gtt att gct acc gga ttc cct aat gaa cag ccg gag cac cct 643
 Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu Gln Pro Glu His Pro
 170 175 180

ggt cgt ttg cag aat agg cgc atc gac aac agc tac taactctgcc 689
 Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser Tyr
 185 190

agctcgcccg gac 702

<210> 2554
 <211> 193
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2554
 Met Ser Leu Ser Val Val Glu Ala Ile Thr Asn Arg Arg Ala Thr Arg
 1 5 10 15
 Lys Tyr Thr Asp Glu Ala Pro Thr Pro Glu Leu Ile Asp Lys Ile Val
 20 25 30
 Asp Leu Ala Leu Glu Ala Pro Ser Ala Phe Asn Ala Gln Gln Arg Glu
 35 40 45
 Ile Val Val Ile Thr Asp Pro Ala Gln Lys Gln Lys Leu Tyr Glu Ala
 50 55 60
 Ser His Gln Lys Gln Phe Leu Thr Ala Pro Val Thr Phe Ile Ala Val
 65 70 75 80
 Ala Arg Val Glu Asn Glu Pro Glu Asp Leu Glu Glu Ile Leu Gly Thr
 85 90 95
 Glu Arg Ala Glu Arg Val Ala Gly Phe Ile Asn Gly Arg Ser Ile Gln
 100 105 110
 Gln Ala Arg Glu Ala Thr Leu Arg Asp Ala Ser Leu Ala Ala Ala Phe
 115 120 125
 Leu Ile Leu Ala Ala Gln Ala Glu Gly Leu Ser Thr Ser Pro Thr Thr
 130 135 140
 Gly Trp Asp Glu Glu Lys Val Lys Glu Ala Ile Gly Leu Gly Gly Arg
 145 150 155 160
 Glu Asp Arg Ala Ile Ala Leu Val Ile Ala Thr Gly Phe Pro Asn Glu
 165 170 175
 Gln Pro Glu His Pro Gly Arg Leu Gln Asn Arg Arg Ile Asp Asn Ser
 180 185 190

Tyr

<210> 2555
 <211> 654
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(631)

<223> RXA02057

<400> 2555

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aagtctttat agtcctgcac tagcctagaa gggccttatg ccgtgtgaat cacacagcat 60

acggcccttt ttgctgccgt ggttgccctaa ggtggaaggt atg aaa cga atc tgt 115
Met Lys Arg Ile Cys
1 5

gcg gtc gcg atc tct tca gta ctt ttg tta agt ggc tgc tcc tcc act 163
Ala Val Ala Ile Ser Ser Val Leu Leu Leu Ser Gly Cys Ser Ser Thr
10 15 20

tcc aca acg cag ctc gag gga ttc gat gga cgc tca gcg cag gag atc 211
Ser Thr Thr Gln Leu Glu Gly Phe Asp Gly Arg Ser Ala Gln Glu Ile
25 30 35

atc aca gaa ctt gat caa acc cca gtc gca gac aga gca act aac ctc 259
Ile Thr Glu Leu Asp Gln Thr Pro Val Ala Asp Arg Ala Thr Asn Leu
40 45 50

atg gcc tcc att cgg gca gat gag tta att ctg tgc gat caa agc gga 307
Met Ala Ser Ile Arg Ala Asp Glu Leu Ile Leu Ser Asp Gln Ser Gly
55 60 65

cag ctc agc att gac atg cct gca gat gag ttc tat atc tcc gca gcc 355
Gln Leu Ser Ile Asp Met Pro Ala Asp Glu Phe Tyr Ile Ser Ala Ala
70 75 80 85

ccg tac acc acc aca acc cac gag tgc ttc tat cac agc ctc acc aca 403
Pro Tyr Thr Thr Thr Thr His Glu Cys Phe Tyr His Ser Leu Thr Thr
90 95 100

tgt act ggt gaa ctc gcc aac acc cca gtg aaa gta acg gtg gtg gca 451
Cys Thr Gly Glu Leu Ala Asn Thr Pro Val Lys Val Thr Val Val Ala
105 110 115

gat aat gga gaa acc atc ctc gaa gag gac acc atc acc tac gat aat 499
Asp Asn Gly Glu Thr Ile Leu Glu Glu Asp Thr Ile Thr Tyr Asp Asn
120 125 130

gga ttt gtt ggg atg tgg ctc ccc cgc aac att gat gcc aca ctc acc 547
Gly Phe Val Gly Met Trp Leu Pro Arg Asn Ile Asp Ala Thr Leu Thr
135 140 145

atc gaa cat gac ggc ctg aaa tcc acc cag ccg atc tct acg ggt gat 595
Ile Glu His Asp Gly Leu Lys Ser Thr Gln Pro Ile Ser Thr Gly Asp
150 155 160 165

gac gcc ccc acg tgc atc acc acg gct gaa cta gcg tgaaaatcct 641
Asp Ala Pro Thr Cys Ile Thr Thr Ala Glu Leu Ala
170 175

ttagacaata aga 654

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<210> 2556

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

<400> 2556

Met Lys Arg Ile Cys Ala Val Ala Ile Ser Ser Val Leu Leu Leu Ser
 1 5 10 15

Gly Cys Ser Ser Thr Ser Thr Thr Gln Leu Glu Gly Phe Asp Gly Arg
 20 25 30

Ser Ala Gln Glu Ile Ile Thr Glu Leu Asp Gln Thr Pro Val Ala Asp
 35 40 45

Arg Ala Thr Asn Leu Met Ala Ser Ile Arg Ala Asp Glu Leu Ile Leu
 50 55 60

Ser Asp Gln Ser Gly Gln Leu Ser Ile Asp Met Pro Ala Asp Glu Phe
 65 70 75 80

Tyr Ile Ser Ala Ala Pro Tyr Thr Thr Thr Thr His Glu Cys Phe Tyr
 85 90 95

His Ser Leu Thr Thr Cys Thr Gly Glu Leu Ala Asn Thr Pro Val Lys
 100 105 110

Val Thr Val Val Ala Asp Asn Gly Glu Thr Ile Leu Glu Glu Asp Thr
 115 120 125

Ile Thr Tyr Asp Asn Gly Phe Val Gly Met Trp Leu Pro Arg Asn Ile
 130 135 140

Asp Ala Thr Leu Thr Ile Glu His Asp Gly Leu Lys Ser Thr Gln Pro
 145 150 155 160

Ile Ser Thr Gly Asp Asp Ala Pro Thr Cys Ile Thr Thr Ala Glu Leu
 165 170 175

Ala

<210> 2557

<211> 675

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(652)

<223> RXA02058

<400> 2557

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agaaccttca ccacctgttc cgttgggaaa cgttgatact gtg cag att gtc tct 115
 Val Gln Ile Val Ser
 1 5

ccc aat ggg gag att gag tct ttt gtg ctg ggg aag ctg tat gag acc 163
 Pro Asn Gly Glu Ile Glu Ser Phe Val Leu Gly Lys Leu Tyr Glu Thr

	10	15	20	
gca tta gtg gaa cgt ggc aga tct gca tca gtt cag ctg att gac ggc				211
Ala Leu Val Glu Arg Gly Arg Ser Ala Ser Val Gln Leu Ile Asp Gly	25	30	35	
gac ttg gat gag caa cta tct atg ctg cga gat gac agc act gat ttg				259
Asp Leu Asp Glu Gln Leu Ser Met Leu Arg Asp Asp Ser Thr Asp Leu	40	45	50	
gtg att gct tgc tca gga caa tta ctg gaa tat tac aac cca gat tta				307
Val Ile Ala Cys Ser Gly Gln Leu Leu Glu Tyr Tyr Asn Pro Asp Leu	55	60	65	
gcc tcc gag ttt gcc gtc gaa tac gct aat cag aca gcc ttt gat aaa				355
Ala Ser Glu Phe Ala Val Glu Tyr Ala Asn Gln Thr Ala Phe Asp Lys	70	75	80	85
aac tct ggt gaa tgg cgc gaa aaa gtc tac gat gct ctc caa gga tcg				403
Asn Ser Gly Glu Trp Arg Glu Lys Val Tyr Asp Ala Leu Gln Gly Ser	90	95	100	
ctg ccg gac tcc atc gtg gcc acc gat cct tcc aat gct att ggt tgt				451
Leu Pro Asp Ser Ile Val Ala Thr Asp Pro Ser Asn Ala Ile Gly Cys	105	110	115	
aag gac gat acg tcg ctg cct caa aac atc gtg cca att tat aga aag				499
Lys Asp Asp Thr Ser Leu Pro Gln Asn Ile Val Pro Ile Tyr Arg Lys	120	125	130	
ccc aat ctg gat agg gac aat cgg gac acc ctg aac ttt gtg agc ggt				547
Pro Asn Leu Asp Arg Asp Asn Arg Asp Thr Leu Asn Phe Val Ser Gly	135	140	145	
tct ttg ggt aca agc gat ttg gaa gca ttg gtc aag gac gcc caa aca				595
Ser Leu Gly Thr Ser Asp Leu Glu Ala Leu Val Lys Asp Ala Gln Thr	150	155	160	165
aca ggc aca acc tct gaa act gcg ctg gat ttc tta ttg tct aaa gga				643
Thr Gly Thr Thr Ser Glu Thr Ala Leu Asp Phe Leu Leu Ser Lys Gly	170	175	180	
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Phe Ser Arg				

<210> 2558

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 2558

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Lys	Leu	Tyr	Glu	Thr	Ala	Leu	Val	Glu	Arg	Gly	Arg	Ser	Ala	Ser	Val
			20					25					30		

Gln	Leu	Ile	Asp	Gly	Asp	Leu	Asp	Glu	Gln	Leu	Ser	Met	Leu	Arg	Asp
	35						40					45			

Asp Ser Thr Asp Leu Val Ile Ala Cys Ser Gly Gln Leu Leu Glu Tyr
 50 55 60
 Tyr Asn Pro Asp Leu Ala Ser Glu Phe Ala Val Glu Tyr Ala Asn Gln
 65 70 75 80
 Thr Ala Phe Asp Lys Asn Ser Gly Glu Trp Arg Glu Lys Val Tyr Asp
 85 90 95
 Ala Leu Gln Gly Ser Leu Pro Asp Ser Ile Val Ala Thr Asp Pro Ser
 100 105 110
 Asn Ala Ile Gly Cys Lys Asp Asp Thr Ser Leu Pro Gln Asn Ile Val
 115 120 125
 Pro Ile Tyr Arg Lys Pro Asn Leu Asp Arg Asp Asn Arg Asp Thr Leu
 130 135 140
 Asn Phe Val Ser Gly Ser Leu Gly Thr Ser Asp Leu Glu Ala Leu Val
 145 150 155 160
 Lys Asp Ala Gln Thr Thr Gly Thr Thr Ser Glu Thr Ala Leu Asp Phe
 165 170 175
 Leu Leu Ser Lys Gly Phe Ser Arg
 180

<210> 2559

<211> 702

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(679)

<223> RXA02069

<400> 2559

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 Met Ala Asp Phe Asn 5
 cgc tct gaa tta gac agc cca ctt ttt gga tcc cgc aaa cga ttt aaa 163
 Arg Ser Glu Leu Asp Ser Pro Leu Phe Gly Ser Arg Lys Arg Phe Lys 20
 ttc gac gat gac acc att ggt gcc tac gcc gaa aaa gta gcc cgg ttc 211
 Phe Asp Asp Thr Ile Gly Ala Tyr Ala Glu Lys Val Ala Arg Phe 35
 25
 ttt ggc acg gga cag tac ctg ttt tgg caa acc att ttc gtg gtg gtg 259
 Phe Gly Thr Gly Gln Tyr Leu Phe Trp Gln Thr Ile Phe Val Val Val 50
 40
 tgg att ttc ctc aac atc ggt ggt tgg gcc tgg agt tgg gac ccc tac 307
 Trp Ile Phe Leu Asn Ile Gly Gly Trp Ala Trp Ser Trp Asp Pro Tyr 65
 55 60

cct ttc atc ctg ctc aac ctg gca ttc tcc acg cag gct gct tat gct 355
 Pro Phe Ile Leu Leu Asn Leu Ala Phe Ser Thr Gln Ala Ala Tyr Ala
 70 75 80 85

 gct ccg ctg atc ctg ttg gcg caa aac cgt caa gaa gac cgc gat aag 403
 Ala Pro Leu Ile Leu Leu Ala Gln Asn Arg Gln Glu Asp Arg Asp Lys
 90 95 100

 cac acc att ttg gcg gat cgt cgg cgt gct gaa gag aca aaa gcc gat 451
 His Thr Ile Leu Ala Asp Arg Arg Arg Ala Glu Glu Thr Lys Ala Asp
 105 110 115

 act gaa ttc ctc gca cgg gaa ctc gca ggc gtt cgc tta gcc ttg gga 499
 Thr Glu Phe Leu Ala Arg Glu Leu Ala Gly Val Arg Leu Ala Leu Gly
 120 125 130

 gat act gtc aca cgt gac tat ttg cgc cat gag tta gaa gat ctc cgc 547
 Asp Thr Val Thr Arg Asp Tyr Leu Arg His Glu Leu Glu Asp Leu Arg
 135 140 145

 gga ctt ctt gac cgc att gaa gcc aag ctc gac gac gag gca gcg tcc 595
 Gly Leu Leu Asp Arg Ile Glu Ala Lys Leu Asp Asp Glu Ala Ala Ser
 150 155 160 165

 cgt att gca gac cgc cac gaa cag cac gga tca gga cct caa gat ttg 643
 Arg Ile Ala Asp Arg His Glu Gln His Gly Ser Gly Pro Gln Asp Leu
 170 175 180

 tct gac ccc act cag ggt gat gtt gca gac gaa ttt tagggagtat 689
 Ser Asp Pro Thr Gln Gly Asp Val Ala Asp Glu Phe
 185 190

 caaaaacttgg gac 702

<210> 2560

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 2560

Met Ala Asp Phe Asn Arg Ser Glu Leu Asp Ser Pro Leu Phe Gly Ser
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Arg Lys Arg Phe Lys Phe Asp Asp Asp Thr Ile Gly Ala Tyr Ala Glu
 20 25 30

Lys Val Ala Arg Phe Phe Gly Thr Gly Gln Tyr Leu Phe Trp Gln Thr
 35 40 45

Ile Phe Val Val Val Trp Ile Phe Leu Asn Ile Gly Gly Trp Ala Trp
 50 55 60

Ser Trp Asp Pro Tyr Pro Phe Ile Leu Leu Asn Leu Ala Phe Ser Thr
 65 70 75 80

Gln Ala Ala Tyr Ala Ala Pro Leu Ile Leu Leu Ala Gln Asn Arg Gln
 85 90 95

Glu Asp Arg Asp Lys His Thr Ile Leu Ala Asp Arg Arg Arg Ala Glu

100	105	110
Glu Thr Lys Ala Asp Thr Glu Phe Leu Ala Arg Glu Leu Ala Gly Val		
115	120	125
Arg Leu Ala Leu Gly Asp Thr Val Thr Arg Asp Tyr Leu Arg His Glu		
130	135	140
Leu Glu Asp Leu Arg Gly Leu Leu Asp Arg Ile Glu Ala Lys Leu Asp		
145	150	155
Asp Glu Ala Ala Ser Arg Ile Ala Asp Arg His Glu Gln His Gly Ser		
165	170	175
Gly Pro Gln Asp Leu Ser Asp Pro Thr Gln Gly Asp Val Ala Asp Glu		
180	185	190
Phe		

<210> 2561
 <211> 1221
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1198)
 <223> RXA02070

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 Met Thr Gln Val Thr 5
 gaa tcc gct gtc cgc agc gcg cta tcc cgc gta gag gat cca gag atc 163
 Glu Ser Ala Val Arg Ser Ala Leu Ser Arg Val Glu Asp Pro Glu Ile 20
 ggt aag ccc atc aca gag ctg ggc atg gtc aaa tca gtg tcc atc gac 211
 Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys Ser Val Ser Ile Asp 35
 ggc tct gat gtc cag gtg gag gtc tac ctg acg atc gcg gct tgc ccg 259
 Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr Ile Ala Ala Cys Pro 50
 atg aaa acc acc att gtc acc aac act gaa gca gct ctc aaa gac atc 307
 Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala Ala Leu Lys Asp Ile 65
 gac ggg gtt ggc caa gtt cat gtc acc acc gat gtc atg agt gat gaa 355
 Asp Gly Val Gly Gln Val His Val Thr Thr Asp Val Met Ser Asp Glu 85
 cag cgc cgt gcg ctg cgc gtc tcc ctg cgc ggt gaa act tct gag cca 403
 Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly Glu Thr Ser Glu Pro 100

gtg att cca ttc gct cag cct ggt tcc act acc cgc gtt tac gct gtt	451
Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr Arg Val Tyr Ala Val	
105 110 115	
gct tcc ggc aaa ggt ggc gta gga aaa tcc tcc atg acg gtg aac ttg	499
Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser Met Thr Val Asn Leu	
120 125 130	
gct gca gcc cta gcc aag cgc ggg ctg tct gtg gga att ttg gat gcc	547
Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val Gly Ile Leu Asp Ala	
135 140 145	
gat att tac gga cac tca gtg ccc gga atg ctc ggc tcg gac caa cgc	595
Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu Gly Ser Asp Gln Arg	
150 155 160 165	
cca cac cag gtc gat gac atg atc atg cct ccc cag gcg cac ggc gtg	643
Pro His Gln Val Asp Asp Met Ile Met Pro Pro Gln Ala His Gly Val	
170 175 180	
aag atg ata tcc att gct cac ttc acc gaa gga aat gct cct gtg gtg	691
Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly Asn Ala Pro Val Val	
185 190 195	
tgg cgt gga cca atg ctg cac cgt gcc atc cag caa ttc ctc act gac	739
Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln Gln Phe Leu Thr Asp	
200 205 210	
gtg ttc tgg ggc gac ctg gat att ttg ctg ctg gat ctt cct cca gga	787
Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu Asp Leu Pro Pro Gly	
215 220 225	
act ggt gac atc gcc atc acc gtt gcc caa ttg atc ccg aat gct gag	835
Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu Ile Pro Asn Ala Glu	
230 235 240 245	
ttg ctc att gtg acc act cct cag gct gcc gca gct gag gtt gcc gag	883
Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala Ala Glu Val Ala Glu	
250 255 260	
cga gca gga acg atc tct gtg cag acc aac cag aag gtt gct ggc gtg	931
Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln Lys Val Ala Gly Val	
265 270 275	
att gaa aac atg tct gcc atg gtg ctt cct gat ggc acc acc atg gat	979
Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp Gly Thr Thr Met Asp	
280 285 290	
gtt ttc ggc acc ggc ggc ggt caa aag att gct gat cgt ctt acc gct	1027
Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala Asp Arg Leu Thr Ala	
295 300 305	
gtg aca ggt gaa gag gtc aag gtt atc gga tct gtt cca ttg gat ccg	1075
Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser Val Pro Leu Asp Pro	
310 315 320 325	
aac ctg cgt atc ggt ggc gat gtg gga aat cct att gcg att tct gaa	1123
Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro Ile Ala Ile Ser Glu	
330 335 340	

cca cac tcc cca acc gct gca gcg atc aat gag atc gct gaa cac cta 1171
Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu Ile Ala Glu His Leu
345 350 355

gct cac cgc aag gta tgc ccc acc aaa tgacccagaa ccacaccgca 1218
Ala His Arg Lys Val Ser Pro Thr Lys
360 365

aac 1221

<210> 2562

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 2562

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Glu Asp Pro Glu Ile Gly Lys Pro Ile Thr Glu Leu Gly Met Val Lys
20 25 30

Ser Val Ser Ile Asp Gly Ser Asp Val Gln Val Glu Val Tyr Leu Thr
35 40 45

Ile Ala Ala Cys Pro Met Lys Thr Thr Ile Val Thr Asn Thr Glu Ala
50 55 60

Ala Leu Lys Asp Ile Asp Gly Val Gly Gln Val His Val Thr Thr Asp
65 70 75 80

Val Met Ser Asp Glu Gln Arg Arg Ala Leu Arg Val Ser Leu Arg Gly
85 90 95

Glu Thr Ser Glu Pro Val Ile Pro Phe Ala Gln Pro Gly Ser Thr Thr
100 105 110

Arg Val Tyr Ala Val Ala Ser Gly Lys Gly Gly Val Gly Lys Ser Ser
115 120 125

Met Thr Val Asn Leu Ala Ala Ala Leu Ala Lys Arg Gly Leu Ser Val
130 135 140

Gly Ile Leu Asp Ala Asp Ile Tyr Gly His Ser Val Pro Gly Met Leu
145 150 155 160

Gly Ser Asp Gln Arg Pro His Gln Val Asp Asp Met Ile Met Pro Pro
165 170 175

Gln Ala His Gly Val Lys Met Ile Ser Ile Ala His Phe Thr Glu Gly
180 185 190

Asn Ala Pro Val Val Trp Arg Gly Pro Met Leu His Arg Ala Ile Gln
195 200 205

Gln Phe Leu Thr Asp Val Phe Trp Gly Asp Leu Asp Ile Leu Leu Leu
210 215 220

Asp Leu Pro Pro Gly Thr Gly Asp Ile Ala Ile Thr Val Ala Gln Leu
225 230 235 240

Ile Pro Asn Ala Glu Leu Leu Ile Val Thr Thr Pro Gln Ala Ala Ala
 245 250 255
 Ala Glu Val Ala Glu Arg Ala Gly Thr Ile Ser Val Gln Thr Asn Gln
 260 265 270
 Lys Val Ala Gly Val Ile Glu Asn Met Ser Ala Met Val Leu Pro Asp
 275 280 285
 Gly Thr Thr Met Asp Val Phe Gly Thr Gly Gly Gly Gln Lys Ile Ala
 290 295 300
 Asp Arg Leu Thr Ala Val Thr Gly Glu Glu Val Lys Val Ile Gly Ser
 305 310 315 320
 Val Pro Leu Asp Pro Asn Leu Arg Ile Gly Gly Asp Val Gly Asn Pro
 325 330 335
 Ile Ala Ile Ser Glu Pro His Ser Pro Thr Ala Ala Ala Ile Asn Glu
 340 345 350
 Ile Ala Glu His Leu Ala His Arg Lys Val Ser Pro Thr Lys
 355 360 365

<210> 2563

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> RXA02080

<400> 2563

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 Met Ser Ile Glu Trp
 1 5
 tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163
 Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala
 10 15 20
 gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct 211
 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro
 25 30 35
 att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac 259
 Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn
 40 45 50
 acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga 307
 Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg
 55 60 65
 cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca 355
 Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala

70	75	80	85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc				403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser				
	90	95	100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg				451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr				
	105	110	115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat				499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His				
	120	125	130	
act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc				547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser				
	135	140	145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg				595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met				
	150	155	160	165
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg				643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu				
	170	175	180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa				691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys				
	185	190	195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata				739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile				
	200	205	210	
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg				787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala				
	215	220	225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga				835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg				
	230	235	240	245
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc				883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr				
	250	255	260	
acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc				930
Thr Val Ile Val Met Thr Ile Gly				
	265			

<210> 2564

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 2564

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Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr

20										25										30									
Leu	Val	Ser	Phe	Pro	Ile	Leu	Val	Phe	Leu	Gly	Leu	Pro	Pro	Leu	Thr														
		35					40					45																	
Ala	Thr	Ile	Ala	Asn	Thr	Ile	Gly	Ile	Val	Pro	Gly	Ser	Ile	Ser	Gly														
	50					55					60																		
Val	Val	Ala	Tyr	Arg	Arg	Glu	Leu	His	Ala	His	Val	Lys	Thr	Ile	Arg														
	65				70					75					80														
Phe	Leu	Leu	Pro	Ala	Ser	Ile	Leu	Gly	Gly	Ile	Thr	Gly	Ala	Ser	Leu														
				85				90						95															
Leu	Leu	His	Phe	Ser	Ala	Asp	Val	Phe	Thr	Ala	Val	Ile	Pro	Trp	Leu														
			100					105					110																
Ile	Gly	Phe	Gly	Thr	Leu	Leu	Val	Ile	Ala	Gly	Pro	Ser	Ile	Lys	Lys														
	115					120						125																	
His	Val	Gly	Ala	His	Thr	Ser	Gly	Gly	Ile	Ser	Ala	Gly	Phe	Arg	Gln														
	130					135					140																		
Leu	Pro	Phe	Pro	Ser	Arg	Thr	Thr	Phe	Ile	Val	Ser	Val	Cys	Gly	Ala														
	145				150					155					160														
Leu	Leu	Leu	Gly	Met	Tyr	Gly	Gly	Tyr	Phe	Ser	Ala	Ala	Gln	Gly	Ile														
				165				170						175															
Leu	Leu	Ile	Ala	Leu	Leu	Gly	Ile	Thr	Ser	Thr	Leu	Gln	Met	Gln	Glu														
			180					185					190																
Leu	Asn	Ala	Ile	Lys	Asn	Leu	Thr	Val	Ala	Ala	Val	Asn	Leu	Ile	Ala														
	195					200						205																	
Ala	Ser	Val	Phe	Ile	Ile	Ile	Ser	Pro	Glu	Leu	Ile	Ser	Trp	Pro	Thr														
	210					215					220																		
Val	Ala	Leu	Ile	Ala	Leu	Gly	Ser	Ala	Leu	Gly	Gly	Tyr	Ile	Gly	Gly														
	225				230					235					240														
Arg	Tyr	Ala	Arg	Arg	Leu	Arg	Pro	Ser	Val	Phe	Arg	Ala	Phe	Val	Val														
				245					250					255															
Ile	Val	Gly	Ile	Thr	Thr	Val	Ile	Val	Met	Thr	Ile	Gly																	
			260					265																					

<210> 2565

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXA02081

<400> 2565

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	Met Thr Leu Ser Gly	
	1 5	
ttg gag ctt tta gag ttc gag cgt cga aca gct gcg atg gaa acc agg	163	
Leu Glu Leu Leu Glu Phe Glu Arg Arg Thr Ala Ala Met Glu Thr Arg		
10 15 20		
ctt ggt cgg cat aat cgg gga gcg ggt ggc gca ttt cct gag gcg gtg	211	
Leu Gly Arg His Asn Arg Gly Ala Gly Gly Ala Phe Pro Glu Ala Val		
25 30 35		
gtg tct cga agc gtg gag ttg cca ctt ttt gta cag gcc cgg aat ttc	259	
Val Ser Arg Ser Val Glu Leu Pro Leu Phe Val Gln Ala Arg Asn Phe		
40 45 50		
ctc aac aat cag cag atc aga gct caa gtg cat cgc cgt att ttg gag	307	
Leu Asn Asn Gln Gln Ile Arg Ala Gln Val His Arg Arg Ile Leu Glu		
55 60 65		
cag ctt cca acc gag gga gag att gtg ctg ttg ggg cac agt ttg ggg	355	
Gln Leu Pro Thr Glu Gly Glu Ile Val Leu Leu Gly His Ser Leu Gly		
70 75 80 85		
tcg gta att gct gca gac ctt ttg agg cga ttg ccg cca gag ctt acg	403	
Ser Val Ile Ala Ala Asp Leu Leu Arg Arg Leu Pro Pro Glu Leu Thr		
90 95 100		
gtg aag gga ttt gtc acc atc ggt agt ccg ttg gca aat ggt caa ttc	451	
Val Lys Gly Phe Val Thr Ile Gly Ser Pro Leu Ala Asn Gly Gln Phe		
105 110 115		
aat gtg gat gat ttg ttt aag ttg ctg cgc acg ccg ttg agc aat gtg	499	
Asn Val Asp Asp Leu Phe Lys Leu Leu Arg Thr Pro Leu Ser Asn Val		
120 125 130		
tcg tgg tgg gtg aat ttt tgg agt gga tct gat cct gtt gca gca aaa	547	
Ser Trp Trp Val Asn Phe Trp Ser Gly Ser Asp Pro Val Ala Ala Lys		
135 140 145		
cgc gga gtg tcg gtg gct gtt ccg tgg gta ttg gat ttt cgt gtg aaa	595	
Arg Gly Val Ser Val Ala Val Pro Trp Val Leu Asp Phe Arg Val Lys		
150 155 160 165		
acc tca ctg gtc cca ggc cct ggg cat tct tcg ccg gaa tac tgt gcc	643	
Thr Ser Leu Val Pro Gly Pro Gly His Ser Ser Arg Glu Tyr Cys Ala		
170 175 180		
aat gat gca gtg gcg gaa gca att ggg ttt ggg ctg ttc gga tcg cgc	691	
Asn Asp Ala Val Ala Glu Ala Ile Gly Phe Gly Leu Phe Gly Ser Arg		
185 190 195		
agc aaa gaa atc gtc ctt gcg gag aaa aat ctg cag att ccg ctc aat	739	
Ser Lys Glu Ile Val Leu Ala Glu Lys Asn Leu Gln Ile Pro Leu Asn		
200 205 210		
gac gcg gag att ttt gtg ctg cag gcg ctg cgt tat tgt tac ctc att	787	
Asp Ala Glu Ile Phe Val Leu Gln Ala Leu Arg Tyr Cys Tyr Leu Ile		
215 220 225		
ttg caa cgg ctc aaa ggc gat gaa gcc tta agg tat gag tac gca ctt	835	

Leu Gln Arg Leu Lys Gly Asp Glu Ala Leu Arg Tyr Glu Tyr Ala Leu 230 235 240 245	
cgg gag act cag gat cgc ctg att gag gag att aaa tcc aga aac gcc Arg Glu Thr Gln Asp Arg Leu Ile Glu Glu Ile Lys Ser Arg Asn Ala 250 255 260	883
gaa gag ggc cgg ccg att ccg aag gaa atc gca cgc ctg gat ttt gat Glu Glu Gly Arg Pro Ile Pro Lys Glu Ile Ala Arg Leu Asp Phe Asp 265 270 275	931
aac ggt gat cca aac gca gca gct cct gtt cca ggt ttg agc cca ttt Asn Gly Asp Pro Asn Ala Ala Ala Pro Val Pro Gly Leu Ser Pro Phe 280 285 290	979
atg ccc aaa gag cag gca att gag cgg ctt tta gag atc att gga cag Met Pro Lys Glu Gln Ala Ile Glu Arg Leu Leu Glu Ile Ile Gly Gln 295 300 305	1027
aac ctg ctg ctg cct ttt gag atc gag gtg ccg gag aaa att cag cgg Asn Leu Leu Leu Pro Phe Glu Ile Glu Val Pro Glu Lys Ile Gln Arg 310 315 320 325	1075
gaa gca ctg agg gat ttc acg gcg gaa act caa ttg ggt tcc acc gtg Glu Ala Leu Arg Asp Phe Thr Ala Glu Thr Gln Leu Gly Ser Thr Val 330 335 340	1123
ggc gct gat att ttt gat gca ttg caa atg gct gtt ggg gtg gtg tcg Gly Ala Asp Ile Phe Asp Ala Leu Gln Met Ala Val Gly Val Val Ser 345 350 355	1171
gga agc gcg aag agc aat tgg cgc aaa tgg gga gcg ttt ggt gtg ggg Gly Ser Ala Lys Ser Asn Trp Arg Lys Trp Gly Ala Phe Gly Val Gly 360 365 370	1219
gct gca gct ttg acc gct gca acg ggt ggt ttg gct ttg gcg gct gtg Ala Ala Ala Leu Thr Ala Ala Thr Gly Gly Leu Ala Leu Ala Ala Val 375 380 385	1267
ccg act gtt gct gga gta gcc act gtt gcc tcg aca ctc gca gca ttt Pro Thr Val Ala Gly Val Ala Thr Val Ala Ser Thr Leu Ala Ala Phe 390 395 400 405	1315
ggt cca ggt ggg atg atg ggc ggt ttg gtc act gca gga aca ctg ctc Gly Pro Gly Gly Met Met Gly Gly Leu Val Thr Ala Gly Thr Leu Leu 410 415 420	1363
aca gtt ggt ggc ggc agt tta acc gct ggg gtg ttg agc tcg gtg aac Thr Val Gly Gly Gly Ser Leu Thr Ala Gly Val Leu Ser Ser Val Asn 425 430 435	1411
acc acg gaa gag atc gaa gcg ctc gtt gta cag aag cta agt ttg gct Thr Thr Glu Glu Ile Glu Ala Leu Val Val Gln Lys Leu Ser Leu Ala 440 445 450	1459
att ttg tgg cag cgc cat gag ata gat aga act cat gag gtg tgg gaa Ile Leu Trp Gln Arg His Glu Ile Asp Arg Thr His Glu Val Trp Glu 455 460 465	1507
gaa ttc gcg gag gca gaa cgt ctg att gtg cgg gag cac acg cgt gtg Glu Phe Ala Glu Ala Glu Arg Leu Ile Val Arg Glu His Thr Arg Val 470 475 480 485	1555

470 475 480 485
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 Lys Asn Val Ser Asp Ser Ser Ser Pro Ile Leu Lys Ala Phe Glu Gln
 490 495 500
 cag cgt tcg act att gag cgg gcg ttg aag tat ttg agc gat cat ggg 1651
 Gln Arg Ser Thr Ile Glu Arg Ala Leu Lys Tyr Leu Ser Asp His Gly
 505 510 515
 atg gaa cct ggc tgg ttt gaa gaa ctg gaa cca cca gcc cca aca cgg 1699
 Met Glu Pro Gly Trp Phe Glu Glu Leu Glu Pro Pro Ala Pro Thr Pro
 520 525 530
 ttt cta aaa ctg cgg gct aag aaa act gat taggagaaac acaatggaga 1749
 Phe Leu Lys Leu Arg Ala Lys Lys Thr Asp
 535 540
 aag 1752

<210> 2566
 <211> 543
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2566
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 Phe Pro Glu Ala Val Val Ser Arg Ser Val Glu Leu Pro Leu Phe Val
 35 40 45
 Gln Ala Arg Asn Phe Leu Asn Asn Gln Gln Ile Arg Ala Gln Val His
 50 55 60
 Arg Arg Ile Leu Glu Gln Leu Pro Thr Glu Gly Glu Ile Val Leu Leu
 65 70 75 80
 Gly His Ser Leu Gly Ser Val Ile Ala Ala Asp Leu Leu Arg Arg Leu
 85 90 95
 Pro Pro Glu Leu Thr Val Lys Gly Phe Val Thr Ile Gly Ser Pro Leu
 100 105 110
 Ala Asn Gly Gln Phe Asn Val Asp Asp Leu Phe Lys Leu Leu Arg Thr
 115 120 125
 Pro Leu Ser Asn Val Ser Trp Trp Val Asn Phe Trp Ser Gly Ser Asp
 130 135 140
 Pro Val Ala Ala Lys Arg Gly Val Ser Val Ala Val Pro Trp Val Leu
 145 150 155 160
 Asp Phe Arg Val Lys Thr Ser Leu Val Pro Gly Pro Gly His Ser Ser
 165 170 175
 Arg Glu Tyr Cys Ala Asn Asp Ala Val Ala Glu Ala Ile Gly Phe Gly

180					185					190					
Leu	Phe	Gly	Ser	Arg	Ser	Lys	Glu	Ile	Val	Leu	Ala	Glu	Lys	Asn	Leu
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Gln	Ile	Pro	Leu	Asn	Asp	Ala	Glu	Ile	Phe	Val	Leu	Gln	Ala	Leu	Arg
		210				215					220				
Tyr	Cys	Tyr	Leu	Ile	Leu	Gln	Arg	Leu	Lys	Gly	Asp	Glu	Ala	Leu	Arg
225					230					235					240
Tyr	Glu	Tyr	Ala	Leu	Arg	Glu	Thr	Gln	Asp	Arg	Leu	Ile	Glu	Glu	Ile
				245					250					255	
Lys	Ser	Arg	Asn	Ala	Glu	Glu	Gly	Arg	Pro	Ile	Pro	Lys	Glu	Ile	Ala
			260					265					270		
Arg	Leu	Asp	Phe	Asp	Asn	Gly	Asp	Pro	Asn	Ala	Ala	Ala	Pro	Val	Pro
		275					280					285			
Gly	Leu	Ser	Pro	Phe	Met	Pro	Lys	Glu	Gln	Ala	Ile	Glu	Arg	Leu	Leu
		290				295					300				
Glu	Ile	Ile	Gly	Gln	Asn	Leu	Leu	Leu	Pro	Phe	Glu	Ile	Glu	Val	Pro
305				310						315					320
Glu	Lys	Ile	Gln	Arg	Glu	Ala	Leu	Arg	Asp	Phe	Thr	Ala	Glu	Thr	Gln
				325					330					335	
Leu	Gly	Ser	Thr	Val	Gly	Ala	Asp	Ile	Phe	Asp	Ala	Leu	Gln	Met	Ala
			340					345					350		
Val	Gly	Val	Val	Ser	Gly	Ser	Ala	Lys	Ser	Asn	Trp	Arg	Lys	Trp	Gly
		355					360					365			
Ala	Phe	Gly	Val	Gly	Ala	Ala	Ala	Leu	Thr	Ala	Ala	Thr	Gly	Gly	Leu
		370				375					380				
Ala	Leu	Ala	Ala	Val	Pro	Thr	Val	Ala	Gly	Val	Ala	Thr	Val	Ala	Ser
385				390						395					400
Thr	Leu	Ala	Ala	Phe	Gly	Pro	Gly	Gly	Met	Met	Gly	Gly	Leu	Val	Thr
				405					410					415	
Ala	Gly	Thr	Leu	Leu	Thr	Val	Gly	Gly	Gly	Ser	Leu	Thr	Ala	Gly	Val
			420				425						430		
Leu	Ser	Ser	Val	Asn	Thr	Thr	Glu	Glu	Ile	Glu	Ala	Leu	Val	Val	Gln
			435				440					445			
Lys	Leu	Ser	Leu	Ala	Ile	Leu	Trp	Gln	Arg	His	Glu	Ile	Asp	Arg	Thr
					455						460				
His	Glu	Val	Trp	Glu	Glu	Phe	Ala	Glu	Ala	Glu	Arg	Leu	Ile	Val	Arg
465				470						475					480
Glu	His	Thr	Arg	Val	Lys	Asn	Val	Ser	Asp	Ser	Ser	Ser	Pro	Ile	Leu
				485					490					495	
Lys	Ala	Phe	Glu	Gln	Gln	Arg	Ser	Thr	Ile	Glu	Arg	Ala	Leu	Lys	Tyr
			500					505					510		

Leu Ser Asp His Gly Met Glu Pro Gly Trp Phe Glu Glu Leu Glu Pro
 515 520 525

Pro Ala Pro Thr Pro Phe Leu Lys Leu Arg Ala Lys Lys Thr Asp
 530 535 540

<210> 2567

<211> 468

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(445)

<223> RXA02084

<400> 2567

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 Val Ile Ile Ile Ala
 1 5

agc gtt gtt ttc ctc ctc gtt ggc gca atg ttg gcg aat gct gcc gct 163
 Ser Val Val Phe Leu Leu Val Gly Ala Met Leu Ala Asn Ala Ala Ala
 10 15 20

gcg ctc ttt agt gcc agc gag cca ttc gga cga att tcc tac ctc att 211
 Ala Leu Phe Ser Ala Ser Glu Pro Phe Gly Arg Ile Ser Tyr Leu Ile
 25 30 35

ggc cta cct aac gaa gac gac ttc gtg ccg tac tca cta cgg ttc gtg 259
 Gly Leu Pro Asn Glu Asp Asp Phe Val Pro Tyr Ser Leu Arg Phe Val
 40 45 50

gcc ttt ttc cca ctg atg ctc tcc gca tcg atg gca gca tcc ttc ttc 307
 Ala Phe Phe Pro Leu Met Leu Ser Ala Ser Met Ala Ala Ser Phe Phe
 55 60 65

ggg gtg tgg gca gta cta atc att cct ttc ggt tac ttc cca tca ctg 355
 Gly Val Trp Ala Val Leu Ile Ile Pro Phe Gly Tyr Phe Pro Ser Leu
 70 75 80 85

atg atg gtt cat aag cac aac aag cag gta cag cga acc tgg gat tcc 403
 Met Met Val His Lys His Asn Lys Gln Val Gln Arg Thr Trp Asp Ser
 90 95 100

gtc acc gtt gct gac ttc tac gag gat tcc acc cct ctg gtc 445
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taatttcgat ttctaaatgt cat 468

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<211> 115

<212> PRT

<213> Corynebacterium glutamicum

<400> 2568

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 35 40 45

Ser Leu Arg Phe Val Ala Phe Phe Pro Leu Met Leu Ser Ala Ser Met
 50 55 60

Ala Ala Ser Phe Phe Gly Val Trp Ala Val Leu Ile Ile Pro Phe Gly
 65 70 75 80

Tyr Phe Pro Ser Leu Met Met Val His Lys His Asn Lys Gln Val Gln
 85 90 95

Arg Thr Trp Asp Ser Val Thr Val Ala Asp Phe Tyr Glu Asp Ser Thr
 100 105 110

Pro Leu Val
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<210> 2569

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(571)

<223> RXA02089

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ctctacactt cccactatga tcaaacaccg aaaccgccta atg tct tcc atc tac 115
 Met Ser Ser Ile Tyr
 1 5

tcc gca act cgc tac gcc gcc cac ttc aaa agc gtc ttc ccc acc gcc 163
 Ser Ala Thr Arg Tyr Ala Ala His Phe Lys Ser Val Phe Pro Thr Ala
 10 15 20

ctg gat gac att caa tcc atg atg cgc cac cct cga tca ctg gcc aga 211
 Leu Asp Asp Ile Gln Ser Met Met Arg His Pro Arg Ser Leu Ala Arg
 25 30 35

gcc ata ccc acg tgg cgc ccg ccg agc atc ccg cta ccg tca ctt ccc 259
 Ala Ile Pro Thr Trp Arg Pro Pro Ser Ile Pro Leu Pro Ser Leu Pro
 40 45 50

ggc gaa gat ccc ctc acc ctc acc ttg tca cgt cac cgc gca ggc ccc 307
 Gly Glu Asp Pro Leu Thr Leu Thr Leu Ser Arg His Arg Ala Gly Pro
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gcc gcc cgc caa atc atc cgc gag ttc ggt gag caa cgt gaa ccc gcc 355
 Ala Ala Arg Gln Ile Ile Arg Glu Phe Gly Glu Gln Arg Glu Pro Ala

70	75	80	85	
tat ctc atc acc atc cgc atc acc agc cca gag ggc ttc aaa gta tcc				403
Tyr Leu Ile Thr Ile Arg Ile Thr Ser Pro Glu Gly Phe Lys Val Ser				
	90	95	100	
acc cgc ctc gcc gaa ggc tgg atc cgc gca att ctc agc acc gcg cac				451
Thr Arg Leu Ala Glu Gly Trp Ile Arg Ala Ile Leu Ser Thr Ala His				
	105	110	115	
agc ggc act gtc cac cag ctc acc gat gag ccg gca ccg acg ttt tgc				499
Ser Gly Thr Val His Gln Leu Thr Asp Glu Pro Ala Pro Thr Phe Cys				
	120	125	130	
tgg ctt gtc gac gcc cac ttt gat ccg gtg cgt tcc cct tcc ttc ctt				547
Trp Leu Val Asp Ala His Phe Asp Pro Val Arg Ser Pro Ser Phe Leu				
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Phe Glu Tyr Ser Lys Ser Ala Ala				
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<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 2570

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Arg Ser Leu Ala Arg Ala Ile Pro Thr Trp Arg Pro Pro Ser Ile Pro				
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Leu Pro Ser Leu Pro Gly Glu Asp Pro Leu Thr Leu Thr Leu Ser Arg				
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His Arg Ala Gly Pro Ala Ala Arg Gln Ile Ile Arg Glu Phe Gly Glu				
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Gln Arg Glu Pro Ala Tyr Leu Ile Thr Ile Arg Ile Thr Ser Pro Glu				
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Gly Phe Lys Val Ser Thr Arg Leu Ala Glu Gly Trp Ile Arg Ala Ile				
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Leu Ser Thr Ala His Ser Gly Thr Val His Gln Leu Thr Asp Glu Pro				
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Met Phe Ala Asp Leu Thr Ser Glu Leu Glu Phe Val Thr Asp Glu Val
 185 190 195

ctc gac ttg ggt acc ttc act gat ttt gat cga ctt ttc gat atc ctt 739
 Leu Asp Leu Gly Thr Phe Thr Asp Phe Asp Arg Leu Phe Asp Ile Leu
 200 205 210

tcc ctc gcc gat gac cag gct gag gat tgg gaa gca cag ctc gtt cct 787
 Ser Leu Ala Asp Asp Gln Ala Glu Asp Trp Glu Ala Gln Leu Val Pro
 215 220 225

ttt gag gac gag gaa ttt gat gag ccg gat gtt tat gac ctt ttc gtc 835
 Phe Glu Asp Glu Glu Phe Asp Glu Pro Asp Val Tyr Asp Leu Phe Val
 230 235 240 245

gat gac tct gaa gaa gat gac gac gac ctc gat gat gac gag gac gat 883
 Asp Asp Ser Glu Glu Asp Asp Asp Asp Leu Asp Asp Asp Glu Asp Asp
 250 255 260

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 Glu Asp Asp Asp Glu Asp
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<210> 2572

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 2572

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 20 25 30

Leu Glu Ile Gln Phe Val Glu Ile Asp Ser Leu Leu Pro Ala Ala Asn
 35 40 45

Val Tyr Ile Ala Ala Ala Asn Val Asp Glu Asp Asp Asp Glu Phe Glu
 50 55 60

Ala Val Leu Val Ser Val Val Phe Ser Val Glu Asp Ala Val Ala Ala
 65 70 75 80

Val Ala Lys His Val Ala Thr Asp Gln Val Val Thr Val Leu Arg Asp
 85 90 95

Leu Leu Glu Gly Thr Asp Glu Arg Ile Gln Asp Leu Glu Phe Phe Gln
 100 105 110

Asp Ala Val Asn Ala Asn Leu Val Arg Ala Glu Val Gly Gln Asn Ser
 115 120 125

Glu Leu Gln Val Leu Val Glu Val Glu Asp Gly Val Pro Thr Ala Thr
 130 135 140

Val Asn Phe Ile Ala Ile Gly Glu Ser Phe Glu Asp Leu Ile Asp Gln
 145 150 155 160

Ala Ile Glu Glu Leu Trp Glu Ser Asp Gly Asp Ala Val Leu Ser Asp

165	170	175
Glu Asp Arg Gln Arg Met Phe Ala Asp Leu Thr Ser Glu Leu Glu Phe 180 185 190		
Val Thr Asp Glu Val Leu Asp Leu Gly Thr Phe Thr Asp Phe Asp Arg 195 200 205		
Leu Phe Asp Ile Leu Ser Leu Ala Asp Asp Gln Ala Glu Asp Trp Glu 210 215 220		
Ala Gln Leu Val Pro Phe Glu Asp Glu Glu Phe Asp Glu Pro Asp Val 225 230 235 240		
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 Met Ser Ile Trp Lys
 1 5
 cgt ctg tta gtg cag tac ccg cgc ttc gcc gac acc ctc aca gcc ggc 163
 Arg Leu Leu Val Gln Tyr Pro Arg Phe Ala Asp Thr Leu Thr Ala Gly
 10 15 20
 caa ccc atc acg ctc gag gaa tta gca acc ccg gaa gtg atc ttg gaa 211
 Gln Pro Ile Thr Leu Glu Glu Leu Ala Thr Pro Glu Val Ile Leu Glu
 25 30 35
 gct gtt gcc aaa ggc caa gaa att ttc ggc att gag cag cca aaa cat 259
 Ala Val Ala Lys Gly Gln Glu Ile Phe Gly Ile Glu Gln Pro Lys His
 40 45 50
 gca gca caa ctc tgg ttt cac tcc ctg tgc acc gca att gtc ggc ccc 307
 Ala Ala Gln Leu Trp Phe His Ser Leu Cys Thr Ala Ile Val Gly Pro
 55 60 65
 gcc gtc acc gcc atg gtg gaa ttc gat gtc atc ccc agc ctc gac ata 355
 Ala Val Thr Ala Met Val Glu Phe Asp Val Ile Pro Ser Leu Asp Ile
 70 75 80 85
 cgt cga ggt cag ctg cat aac atc gac ggt tac tgg ttc ggc ttc agg 403
 Arg Arg Gly Gln Leu His Asn Ile Asp Gly Tyr Trp Phe Gly Phe Arg
 90 95 100

ccg gag gag atg ctt gtc gac gcc tcc ctc cac ctg tcg ggc acc caa 451
 Pro Glu Glu Met Leu Val Asp Ala Ser Leu His Leu Ser Gly Thr Gln
 105 110 115

ttc ggc gag agt atc cgc gtg gtg att gat gca tta tgc gct gcc acg 499
 Phe Gly Glu Ser Ile Arg Val Val Ile Asp Ala Leu Cys Ala Ala Thr
 120 125 130

gat ctg cga ccg gca ccc ctg tgg gcg gtt gcc tca gat gcg ttg gga 547
 Asp Leu Arg Pro Ala Pro Leu Trp Ala Val Ala Ser Asp Ala Leu Gly
 135 140 145

atc gca gct agc ggc gca ggt gtc gag gcc ttt gaa gaa gaa cat gcc 595
 Ile Ala Ala Ser Gly Ala Gly Val Glu Ala Phe Glu Glu Glu His Ala
 150 155 160 165

cgc gag gtg gcg gaa gcc ctc att gaa gga atg aat agt gtg aac tca 643
 Arg Glu Val Ala Glu Ala Leu Ile Glu Gly Met Asn Ser Val Asn Ser
 170 175 180

gtt cca tcg ccg cgg ttt aac gac gac gat tat ttc att cga gct gga 691
 Val Pro Ser Pro Arg Phe Asn Asp Asp Asp Tyr Phe Ile Arg Ala Gly
 185 190 195

tgc tgc atg att ttc cac tca cca cga gct gat ttt tgc acg tcg tgc 739
 Cys Cys Met Ile Phe His Ser Pro Arg Ala Asp Phe Cys Thr Ser Cys
 200 205 210

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<211> 217

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<213> Corynebacterium glutamicum

<400> 2574

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Glu Val Ile Leu Glu Ala Val Ala Lys Gly Gln Glu Ile Phe Gly Ile
 35 40 45

Glu Gln Pro Lys His Ala Ala Gln Leu Trp Phe His Ser Leu Cys Thr
 50 55 60

Ala Ile Val Gly Pro Ala Val Thr Ala Met Val Glu Phe Asp Val Ile
 65 70 75 80

Pro Ser Leu Asp Ile Arg Arg Gly Gln Leu His Asn Ile Asp Gly Tyr
 85 90 95

Trp Phe Gly Phe Arg Pro Glu Glu Met Leu Val Asp Ala Ser Leu His
 100 105 110

Leu Ser Gly Thr Gln Phe Gly Glu Ser Ile Arg Val Val Ile Asp Ala
 115 120 125
 Leu Cys Ala Ala Thr Asp Leu Arg Pro Ala Pro Leu Trp Ala Val Ala
 130 135 140
 Ser Asp Ala Leu Gly Ile Ala Ala Ser Gly Ala Gly Val Glu Ala Phe
 145 150 155 160
 Glu Glu Glu His Ala Arg Glu Val Ala Glu Ala Leu Ile Glu Gly Met
 165 170 175
 Asn Ser Val Asn Ser Val Pro Ser Pro Arg Phe Asn Asp Asp Asp Tyr
 180 185 190
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<223> RXA02097

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 Met Pro Ala Gly Ile
 1 5
 gca gac atg aca gat tca ttg ctc gga tgg gca tca caa act gag ctg 163
 Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala Ser Gln Thr Glu Leu
 10 15 20
 gat ctg aac cag cgt ctt gca ggg gta gag tac ttt cca caa att cag 211
 Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln
 25 30 35
 ctg cga cac gat gag ctc gag cgc att cat cgg ttt tac ggc acc ttt 259
 Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe
 40 45 50
 ttg tcc cgc cag gta ggc gcg ggc gca agc ctt ggg gat ctt ttt gaa 307
 Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu
 55 60 65
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 Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val Ser Arg Ala Ser Arg
 70 75 80 85
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 Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr Ile Gly Gly Leu Gly

90	95	100	
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ttc gca cag gct ggc ctg ctc gtt cct gag gga att gca tct cca ttg Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly Ile Ala Ser Pro Leu 120 125 130			499
gag ttg tta tcc atc cac gca ggc att agt aac cac gaa gtg gcc gca Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn His Glu Val Ala Ala 135 140 145			547
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Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln	
360 365 370	
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Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala	
375 380 385	
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Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu Val Arg Cys Ile Asp	
390 395 400 405	
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Pro Arg Arg Arg Val Ala Phe His His Pro Ala Glu Leu Val Pro His	
410 415 420	
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Val Arg Ser Ile Ser Gly Leu Pro Val His Ala Gln Ser Leu Ile Ala	
425 430 435	
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Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser	
440 445 450	
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Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly Glu Glu Ile Ala Glu	
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cca gag cct ttg gaa gtc cct gcc gac ggt ggc ctt ttc gcc atc ttc	1555
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Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly Glu Tyr Leu Val Arg	
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Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro Glu Phe Ala Ile Val	
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Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser Leu Arg Val Arg Ser	
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Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu Val Thr Val Glu Ala	
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Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg Thr Val Cys Gly Pro	
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Val Gly Asp Pro Lys Val Ser Val Arg Asn His His Gly Ser Pro Leu	
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Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala	
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Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val Met Pro Arg Gly Ser	
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Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala Ala Gly Arg Gln Leu	
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745 750 755	
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Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala Val Thr Val Glu Gln	
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790 795 800 805	
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Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile Ser Asp Ala Val Val	
810 815 820	
ccc gca ctt tgg gat gtt tcc cat atc tgg acc gaa cag gga aac acc	2611

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			825					830					835					
gag	cat	ctt	cca	gta	gtc	cat	gcc	gcc	ctg	cgc	tcc	tca	cca	gcc	gca		2659	
Glu	His	Leu	Pro	Val	Val	His	Ala	Ala	Leu	Arg	Ser	Ser	Pro	Ala	Ala			
		840					845					850						
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Ala	Leu	Lys	Gly	Leu	Ser	Ala	Ser	Leu	Val	Pro	Ala	Gln	Ala	Leu	Pro			
		855				860				865								
gga	aaa	gtc	att	tcc	tcc	gga	ctg	gca	gcc	tca	ccg	ttc	acc	acg	gaa		2755	
Gly	Lys	Val	Ile	Ser	Ser	Gly	Leu	Ala	Ala	Ser	Pro	Phe	Thr	Thr	Glu			
		870				875				880					885			
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Ser	Pro	Ala	Thr	Glu	Val	His	Arg	Thr	Ala	Trp	Ile	Gly	Thr		Leu	Gln		
				890					895						900			
ctc	ctg	ggg	gca	ctg	cca	agc	gca	ttc	aag	gaa	gcc	gaa	gag	ctt	ggc		2851	
Leu	Leu	Gly	Ala	Leu	Pro	Ser	Ala	Phe	Lys	Glu	Ala	Glu	Glu	Leu	Gly			
			905					910						915				
aac	cgc	aca	cca	ctg	ctg	cca	atc	ctc	gga	caa	ctt	gag	gaa	gtc	gcc		2899	
Asn	Arg	Thr	Pro	Leu	Leu	Pro	Ile	Leu	Gly	Gln	Leu	Glu	Glu	Val	Ala			
		920					925					930						
ggc	aag	aac	atc	ctg	tcc	acc	ctt	gca	act	ggc	cgt	gac	tcc	act	ttg		2947	
Gly	Lys	Asn	Ile	Leu	Ser	Thr	Leu	Ala	Thr	Gly	Arg	Asp	Ser	Thr	Leu			
		935				940					945							
gac	acc	gca	tgc	atc	gac	caa	tcc	acc	gtt	gcg	att	gcc	ggc	atg	aac		2995	
Asp	Thr	Ala	Cys	Ile	Asp	Gln	Ser	Thr	Val	Ala	Ile	Ala	Gly	Met	Asn			
		950			955				960						965			
gaa	acc	cag	caa	aaa	gcc	ctg	ctg	gac	atg	ttc	ttc	agc	aac	gcc	gac		3043	
Glu	Thr	Gln	Gln	Lys	Ala	Leu	Leu	Asp	Met	Phe	Phe	Ser	Asn	Ala	Asp			
				970				975						980				
atc	gtt	cct	gga	cca	cta	atg	gaa	gac	aac	acc	cgc	ctc	atg	gca	gtg		3091	
Ile	Val	Pro	Gly	Pro	Leu	Met	Glu	Asp	Asn	Thr	Arg	Leu	Met	Ala	Val			
			985				990						995					
ttc	gaa	acc	ttc	aag	aag	cgc	gat	gca	ctc	cgt	gag	gtt	ctc	cag	act		3139	
Phe	Glu	Thr	Phe	Lys	Lys	Arg	Asp	Ala	Leu	Arg	Glu	Val	Leu	Gln	Thr			
		1000					1005					1010						
gaa	ggc	ttg	att	aag	acc	gct	gta	gaa	ctt	ctt	cgt	gcc	atg	cgt	gga		3187	
Glu	Gly	Leu	Ile	Lys	Thr	Ala	Val	Glu	Leu	Leu	Arg	Ala	Met	Arg	Gly			
		1015				1020					1025							
acc	cag	cgt	cag	ctg	tat	tcc	tcc	gca	cgt	att	cga	ttc	gac	aag	ctc		3235	
Thr	Gln	Arg	Gln	Leu	Tyr	Ser	Ser	Ala	Arg	Ile	Arg	Phe	Asp	Lys	Leu			
				1030		1035				1040					1045			
gat	ggg	gtc	aac	act	gac	aac	cca	gaa	aac	atg	tgg	gca	ctc	acc	cca		3283	
Asp	Gly	Val	Asn	Thr	Asp	Asn	Pro	Glu	Asn	Met	Trp	Ala	Leu	Thr	Pro			
			1050					1055						1060				
gtt	gtg	tca	ctg	gtg	ttc	gcg	ttg	tca	tcc	cgt	ttg	cat	gca	cac	gaa		3331	
Val	Val	Ser	Leu	Val	Phe	Ala	Leu	Ser	Ser	Arg	Leu	His	Ala	His	Glu			

1065	1070	1075	
ttg atc ggc aag acc cga act ctc gat cgt gca tct gcc ggt tgg ggt			3379
Leu Ile Gly Lys Thr Arg Thr	Leu Asp Arg Ala Ser	Ala Gly Trp Gly	
1080	1085	1090	
cga atc gct gat ctg gtg cca gac ctt gtc acc ggt gac ttg atc tcc			3427
Arg Ile Ala Asp Leu Val Pro	Asp Leu Val Thr	Gly Asp Leu Ile Ser	
1095	1100	1105	
gcg gag gca atg gtt ttg gga gct cga aac cca gga ctc gtc gat			3472
Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro	Gly Leu Val Asp		
1110	1115	1120	
tagtcctga tttcatcgga ggg			3495

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<211> 1124

<212> PRT

<213> Corynebacterium glutamicum

<400> 2576

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Ser	Gln	Thr	Glu	Leu	Asp	Leu	Asn	Gln	Arg	Leu	Ala	Gly	Val	Glu	Tyr
			20					25					30		
Phe	Pro	Gln	Ile	Gln	Leu	Arg	His	Asp	Glu	Leu	Glu	Arg	Ile	His	Arg
		35					40					45			
Phe	Tyr	Gly	Thr	Phe	Leu	Ser	Arg	Gln	Val	Gly	Ala	Gly	Ala	Ser	Leu
	50					55					60				
Gly	Asp	Leu	Phe	Glu	Met	Thr	Pro	Cys	Leu	Thr	Val	Thr	Thr	Leu	Val
65					70					75					80
Ser	Arg	Ala	Ser	Arg	Ile	Ser	Asp	Pro	Ala	Asp	Phe	Phe	Gly	Glu	Tyr
				85					90					95	
Ile	Gly	Gly	Leu	Gly	Leu	Ser	Ala	Glu	His	Ala	Ala	Val	Val	Glu	Gly
			100					105					110		
Leu	Thr	Glu	Lys	Leu	Phe	Ala	Gln	Ala	Gly	Leu	Leu	Val	Pro	Glu	Gly
		115					120					125			
Ile	Ala	Ser	Pro	Leu	Glu	Leu	Leu	Ser	Ile	His	Ala	Gly	Ile	Ser	Asn
		130				135					140				
His	Glu	Val	Ala	Ala	Val	Leu	Thr	Glu	Val	Glu	Asn	Gly	Thr	Thr	Glu
145					150					155					160
Tyr	Pro	Phe	Met	Phe	Asp	Ala	Val	Leu	Arg	Leu	Thr	Pro	Glu	Trp	Ala
			165						170					175	
Gln	Thr	Leu	Ile	Gly	Gly	Val	Gln	Glu	Leu	Ile	Glu	Phe	Ala	Thr	Thr
			180					185					190		
His	Arg	Thr	Ser	Trp	Ser	Asp	Arg	Gln	Arg	Glu	Ser	Ser	Leu	Pro	Ala
		195					200					205			

Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly
 210 215 220
 Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg
 225 230 235 240
 Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu
 245 250 255
 Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu
 260 265 270
 Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr
 275 280 285
 Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg
 290 295 300
 Glu Thr Thr Val Thr Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro
 305 310 315 320
 Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu
 325 330 335
 Asn Leu Thr Asp Lys Val Ser Leu His His Gln Glu Ile Tyr Val Leu
 340 345 350
 Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val
 355 360 365
 Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys
 370 375 380
 Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu
 385 390 395 400
 Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala
 405 410 415
 Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
 420 425 430
 Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu
 435 440 445
 Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly
 450 455 460
 Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly
 465 470 475 480
 Leu Phe Ala Ile Phe Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly
 485 490 495
 Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro
 500 505 510
 Glu Phe Ala Ile Val Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser
 515 520 525

Gly Ala Ser Phe Arg Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser
 530 535 540
 Leu Arg Val Arg Ser Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu
 545 550 555 560
 Val Thr Val Glu Ala Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr
 565 570 575
 Asp Glu Gly Asp Gln Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala
 580 585 590
 Ile Glu Leu Pro Leu Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg
 595 600 605
 Thr Val Cys Gly Pro Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile
 610 615 620
 Arg Thr Gly Val Asp Val Gly Asp Pro Lys Val Ser Val Arg Asn His
 625 630 635 640
 His Gly Ser Pro Leu Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly
 645 650 655
 Arg Thr Trp Ile Ala Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val
 660 665 670
 Met Pro Arg Gly Ser Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp
 675 680 685
 Arg Arg Val Ser Val Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe
 690 695 700
 Thr Gly Ile Thr Ile Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala
 705 710 715 720
 Ala Gly Arg Gln Leu Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp
 725 730 735
 Val Ser Ala Val Glu Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro
 740 745 750
 Glu Val Leu Val Gly Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala
 755 760 765
 Asp Pro Phe Thr Thr Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala
 770 775 780
 Val Thr Val Glu Gln Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr
 785 790 795 800
 Ala Gln Leu Ser Ala Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile
 805 810 815
 Ser Asp Ala Val Val Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr
 820 825 830
 Glu Gln Gly Asn Thr Glu His Leu Pro Val Val His Ala Ala Leu Arg
 835 840 845
 Ser Ser Pro Ala Ala Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro

850	855	860
Ala Gln Ala Leu Pro Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser		
865	870	875 880
Pro Phe Thr Thr Glu Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp		
	885	890 895
Ile Gly Thr Leu Gln Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu		
	900	905 910
Ala Glu Glu Leu Gly Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln		
	915	920 925
Leu Glu Glu Val Ala Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly		
	930	935 940
Arg Asp Ser Thr Leu Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala		
	945	950 955 960
Ile Ala Gly Met Asn Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe		
	965	970 975
Phe Ser Asn Ala Asp Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr		
	980	985 990
Arg Leu Met Ala Val Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg		
	995	1000 1005
Glu Val Leu Gln Thr Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu		
	1010	1015 1020
Arg Ala Met Arg Gly Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile		
	1025	1030 1035 1040
Arg Phe Asp Lys Leu Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met		
	1045	1050 1055
Trp Ala Leu Thr Pro Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg		
	1060	1065 1070
Leu His Ala His Glu Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala		
	1075	1080 1085
Ser Ala Gly Trp Gly Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr		
	1090	1095 1100
Gly Asp Leu Ile Ser Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro		
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Gly Leu Val Asp		

<210> 2577

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXA02102

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tcttcggcat	aacaccacag	tagacaatag	ccttggtggt	atg	act	agc	ccc	cat	115
				Met	Thr	Ser	Pro	His	
				1				5	

tct	ttt	tct	gtc	acc	ccc	att	cgc	acc	atg	gct	gac	ggc	acg	atc	aaa	163
Ser	Phe	Ser	Val	Thr	Pro	Ile	Arg	Thr	Met	Ala	Asp	Gly	Thr	Ile	Lys	
			10						15					20		

cag	att	cac	cct	ttc	aca	ggc	acc	gaa	gtg	tgg	acg	gtc	cct	ggg	cgt	211
Gln	Ile	His	Pro	Phe	Thr	Gly	Thr	Glu	Val	Trp	Thr	Val	Pro	Gly	Arg	
			25					30					35			

gga	aat	cga	cct	ctg	tca	cat	ccc	gct	tct	acg	atc	gtc	gaa	cta	tct	259
Gly	Asn	Arg	Pro	Leu	Ser	His	Pro	Ala	Ser	Thr	Ile	Val	Glu	Leu	Ser	
		40					45					50				

gca	cac	gat	cac	acc	tct	tac	tgt	gca	ttt	tgt	tcc	gac	aat	atg	ctc	307
Ala	His	Asp	His	Thr	Ser	Tyr	Cys	Ala	Phe	Cys	Ser	Asp	Asn	Met	Leu	
	55					60					65					

tcc	act	ccg	cct	gag	aaa	tcg	cgc	atc	atc	att	gat	agc	tcc	ggc	gac	355
Ser	Thr	Pro	Pro	Glu	Lys	Ser	Arg	Ile	Ile	Ile	Asp	Ser	Ser	Gly	Asp	
70					75					80					85	

ttt	gac	atc	ctt	ccc	gga	gca	ttg	cct	ggt	gag	ctt	tca	gaa	acc	act	403
Phe	Asp	Ile	Leu	Pro	Gly	Ala	Leu	Pro	Gly	Glu	Leu	Ser	Glu	Thr	Thr	
			90					95						100		

ccg	gaa	ttt	cga	cga	gtc	ccc	aat	ctg	ttt	gag	att	gtc	tct	ttt	gac	451
Pro	Glu	Phe	Arg	Arg	Val	Pro	Asn	Leu	Phe	Glu	Ile	Val	Ser	Phe	Asp	
			105					110					115			

tac	tgg	cac	cag	aat	ttt	ggt	ttc	gat	atg	gat	tca	gaa	acc	gcc	atg	499
Tyr	Trp	His	Gln	Asn	Phe	Gly	Phe	Asp	Met	Asp	Ser	Glu	Thr	Ala	Met	
		120				125						130				

cgc	atg	gcg	caa	tac	ttg	gcg	att	cca	gaa	ggt	cgc	gaa	cat	gtt	tta	547
Arg	Met	Ala	Gln	Tyr	Leu	Ala	Ile	Pro	Glu	Gly	Arg	Glu	His	Val	Leu	
	135				140					145						

gcc	att	gtg	cgc	acc	cga	ctt	tct	gcc	gct	ggt	gaa	gat	ccc	gcg	cac	595
Ala	Ile	Val	Arg	Thr	Arg	Leu	Ser	Ala	Ala	Gly	Glu	Asp	Pro	Ala	His	
150					155					160					165	

atg	acc	gat	ggc	gag	ttg	tta	gaa	aaa	gct	ccc	agc	tac	ttt	gct	ggt	643
Met	Thr	Asp	Gly	Glu	Leu	Leu	Glu	Lys	Ala	Pro	Ser	Tyr	Phe	Ala	Gly	
			170					175						180		

ggt	cat	gac	gtc	atc	atc	gga	cgc	cga	cac	ttt	gtc	gat	gac	gca	acc	691
Gly	His	Asp	Val	Ile	Ile	Gly	Arg	Arg	His	Phe	Val	Asp	Asp	Ala	Thr	
		185					190						195			

acc	agt	gat	caa	ttg	gcc	tca	tct	gga	aca	ctg	acc	gtt	aaa	gag	cat	739
Thr	Ser	Asp	Gln	Leu	Ala	Ser	Ser	Gly	Thr	Leu	Thr	Val	Lys	Glu	His	
		200				205						210				

gag gcg ttc atc cgc ctg act gtc gat ggc atc agg gat ttg tac cac 787
 Glu Ala Phe Ile Arg Leu Thr Val Asp Gly Ile Arg Asp Leu Tyr His
 215 220 225

cgc aac cgt tac gca ccg tat gta gtg gcg ttt caa aac tgg ttg aaa 835
 Arg Asn Arg Tyr Ala Pro Tyr Val Val Ala Phe Gln Asn Trp Leu Lys
 230 235 240 245

ccc gcc ggc gcg tct ttt gac cat ctt cat aaa cag ctc gtc gcc att 883
 Pro Ala Gly Ala Ser Phe Asp His Leu His Lys Gln Leu Val Ala Ile
 250 255 260

gat gaa cgc ggc cga ctt att gcc gat gaa ctg cat cat cta cgt ggc 931
 Asp Glu Arg Gly Arg Leu Ile Ala Asp Glu Leu His His Leu Arg Gly
 265 270 275

aat ccc aat atg tac aac gaa ctt gct gtt gat tac gcc gga tac cac 979
 Asn Pro Asn Met Tyr Asn Glu Leu Ala Val Asp Tyr Ala Gly Tyr His
 280 285 290

aac ctg atc atc gcg gaa aac gat cac gcc gtg gcc ttc gca ggt ttc 1027
 Asn Leu Ile Ile Ala Glu Asn Asp His Ala Val Ala Phe Ala Gly Phe
 295 300 305

ggt cac cgc tac ccc acc att gag att tac tct aag tcc gct att cct 1075
 Gly His Arg Tyr Pro Thr Ile Glu Ile Tyr Ser Lys Ser Ala Ile Pro
 310 315 320 325

gaa ccc tgg ctt caa agc gac gag gaa atc caa gcg atg agc aac ctc 1123
 Glu Pro Trp Leu Gln Ser Asp Glu Glu Ile Gln Ala Met Ser Asn Leu
 330 335 340

atc cat gca tgc cat gct gca acc ggc gca gat gta ccc tgc aat gag 1171
 Ile His Ala Cys His Ala Ala Thr Gly Ala Asp Val Pro Cys Asn Glu
 345 350 355

gga tgg gta cac aaa cca atc gat gtt gat atg cca atg ccc tgg cat 1219
 Gly Trp Val His Lys Pro Ile Asp Val Asp Met Pro Met Pro Trp His
 360 365 370

gtg atg atc aaa tgg cgt gtt tct acc ctg gca ggt ttt tgaaggtggc 1268
 Val Met Ile Lys Trp Arg Val Ser Thr Leu Ala Gly Phe
 375 380 385

accaaggtgt atc 1281

<210> 2578

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 2578

Met Thr Ser Pro His Ser Phe Ser Val Thr Pro Ile Arg Thr Met Ala
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Asp Gly Thr Ile Lys Gln Ile His Pro Phe Thr Gly Thr Glu Val Trp
 20 25 30

Thr Val Pro Gly Arg Gly Asn Arg Pro Leu Ser His Pro Ala Ser Thr

35	40	45
Ile Val Glu Leu Ser Ala His Asp His Thr Ser Tyr Cys Ala Phe Cys 50 55 60		
Ser Asp Asn Met Leu Ser Thr Pro Pro Glu Lys Ser Arg Ile Ile Ile 65 70 75 80		
Asp Ser Ser Gly Asp Phe Asp Ile Leu Pro Gly Ala Leu Pro Gly Glu 85 90 95		
Leu Ser Glu Thr Thr Pro Glu Phe Arg Arg Val Pro Asn Leu Phe Glu 100 105 110		
Ile Val Ser Phe Asp Tyr Trp His Gln Asn Phe Gly Phe Asp Met Asp 115 120 125		
Ser Glu Thr Ala Met Arg Met Ala Gln Tyr Leu Ala Ile Pro Glu Gly 130 135 140		
Arg Glu His Val Leu Ala Ile Val Arg Thr Arg Leu Ser Ala Ala Gly 145 150 155 160		
Glu Asp Pro Ala His Met Thr Asp Gly Glu Leu Leu Glu Lys Ala Pro 165 170 175		
Ser Tyr Phe Ala Gly Gly His Asp Val Ile Ile Gly Arg Arg His Phe 180 185 190		
Val Asp Asp Ala Thr Thr Ser Asp Gln Leu Ala Ser Ser Gly Thr Leu 195 200 205		
Thr Val Lys Glu His Glu Ala Phe Ile Arg Leu Thr Val Asp Gly Ile 210 215 220		
Arg Asp Leu Tyr His Arg Asn Arg Tyr Ala Pro Tyr Val Val Ala Phe 225 230 235 240		
Gln Asn Trp Leu Lys Pro Ala Gly Ala Ser Phe Asp His Leu His Lys 245 250 255		
Gln Leu Val Ala Ile Asp Glu Arg Gly Arg Leu Ile Ala Asp Glu Leu 260 265 270		
His His Leu Arg Gly Asn Pro Asn Met Tyr Asn Glu Leu Ala Val Asp 275 280 285		
Tyr Ala Gly Tyr His Asn Leu Ile Ile Ala Glu Asn Asp His Ala Val 290 295 300		
Ala Phe Ala Gly Phe Gly His Arg Tyr Pro Thr Ile Glu Ile Tyr Ser 305 310 315 320		
Lys Ser Ala Ile Pro Glu Pro Trp Leu Gln Ser Asp Glu Glu Ile Gln 325 330 335		
Ala Met Ser Asn Leu Ile His Ala Cys His Ala Ala Thr Gly Ala Asp 340 345 350		
Val Pro Cys Asn Glu Gly Trp Val His Lys Pro Ile Asp Val Asp Met 355 360 365		

Pro Met Pro Trp His Val Met Ile Lys Trp Arg Val Ser Thr Leu Ala
 370 375 380

Gly Phe
 385

<210> 2579
 <211> 519
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(496)
 <223> RXA02103

<400> 2579
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 Met Pro Lys Ile Gln
 1 5
 ttt gat gtt tta gtc ccc gac aca gat tcc atc gca cta gcg gga cgt 163
 Phe Asp Val Leu Val Pro Asp Thr Asp Ser Ile Ala Leu Ala Gly Arg
 10 15 20
 ttt acc gta gtc gcc aac ctt ttg atc gaa aaa ggc ctc atg gat cat 211
 Phe Thr Val Val Ala Asn Leu Leu Ile Glu Lys Gly Leu Met Asp His
 25 30 35
 ggc gtt gtt gtc cat gat cca gca gcg aaa atc gca gaa gct gtg gaa 259
 Gly Val Val Val His Asp Pro Ala Ala Lys Ile Ala Glu Ala Val Glu
 40 45 50
 gag cag ctt cgc cag act tac cgc gac gag cat gaa gat gca gac ttg 307
 Glu Gln Leu Arg Gln Thr Tyr Arg Asp Glu His Glu Asp Ala Asp Leu
 55 60 65
 gaa gaa tcc tcg gtc aac cgt tac ctc att gaa gtt gat gga gtt aaa 355
 Glu Glu Ser Ser Val Asn Arg Tyr Leu Ile Glu Val Asp Gly Val Lys
 70 75 80 85
 ggc tcc gtt aac caa gtg acc atg att ttt gcc cgt ttg ctc acc ccg 403
 Gly Ser Val Asn Gln Val Thr Met Ile Phe Ala Arg Leu Leu Thr Pro
 90 95 100
 cca gca gag ttg cca aag gac gct ttc ctc ctg gag cag gaa ctt gcc 451
 Pro Ala Glu Leu Pro Lys Asp Ala Phe Leu Leu Glu Gln Glu Leu Ala
 105 110 115
 tat gaa gtt cct gca gtc tac cca tgg act gtg gag atc ctt cgc 496
 Tyr Glu Val Pro Ala Val Tyr Pro Trp Thr Val Glu Ile Leu Arg
 120 125 130
 tagttttgag ctacgtattc ttg 519

<210> 2580

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 2580

Met Pro Lys Ile Gln Phe Asp Val Leu Val Pro Asp Thr Asp Ser Ile
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Ala Leu Ala Gly Arg Phe Thr Val Val Ala Asn Leu Leu Ile Glu Lys
 20 25 30

Gly Leu Met Asp His Gly Val Val Val His Asp Pro Ala Ala Lys Ile
 35 40 45

Ala Glu Ala Val Glu Glu Gln Leu Arg Gln Thr Tyr Arg Asp Glu His
 50 55 60

Glu Asp Ala Asp Leu Glu Glu Ser Ser Val Asn Arg Tyr Leu Ile Glu
 65 70 75 80

Val Asp Gly Val Lys Gly Ser Val Asn Gln Val Thr Met Ile Phe Ala
 85 90 95

Arg Leu Leu Thr Pro Pro Ala Glu Leu Pro Lys Asp Ala Phe Leu Leu
 100 105 110

Glu Gln Glu Leu Ala Tyr Glu Val Pro Ala Val Tyr Pro Trp Thr Val
 115 120 125

Glu Ile Leu Arg
 130

<210> 2581

<211> 1044

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1021)

<223> RXA02109

<400> 2581

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ttaagctctt atataacctg tataggaaag cgaaaacctc atg ctt gca gtg cta 115
 Met Leu Ala Val Leu
 1 5

ttc ggg gtg gtg gcc ggt gcc atc atg cct ttc caa act tcg gtg aat 163
 Phe Gly Val Val Ala Gly Ala Ile Met Pro Phe Gln Thr Ser Val Asn
 10 15 20

aat aga ttg cgt cag tcc gtg gga gca cca ctg ctg gcg tct ttt att 211
 Asn Arg Leu Arg Gln Ser Val Gly Ala Pro Leu Leu Ala Ser Phe Ile
 25 30 35

tcc ttt ttg gta gga act ttt tca ctc ctg gtt gca acg tgg atc acc 259
 Ser Phe Leu Val Gly Thr Phe Ser Leu Leu Val Ala Thr Trp Ile Thr
 40 45 50

agt ggg cac ccg tat cct gct cta gga aat aca act ggc caa ccg tgg	307
Ser Gly His Pro Tyr Pro Ala Leu Gly Asn Thr Thr Gly Gln Pro Trp	
55 60 65	
tgg att ttc acc ggt ggc atg ttg ggt gtt gtg ctg ctg acg gga aac	355
Trp Ile Phe Thr Gly Gly Met Leu Gly Val Val Leu Leu Thr Gly Asn	
70 75 80 85	
att ttg ctg ttt ccc cga gtc ggc agc gtg cag acc gtt att ttg ccc	403
Ile Leu Leu Phe Pro Arg Val Gly Ser Val Gln Thr Val Ile Leu Pro	
90 95 100	
atc tcc gga cag atc atc atg ggc cta att atc gat aca act ggc ctg	451
Ile Ser Gly Gln Ile Ile Met Gly Leu Ile Ile Asp Thr Thr Gly Leu	
105 110 115	
gca cat tcg cct caa gca ccg tta acc ctg ttc aga gta ttg ggt gct	499
Ala His Ser Pro Gln Ala Pro Leu Thr Leu Phe Arg Val Leu Gly Ala	
120 125 130	
gct gcg gta ctt gtt gga tcg ctg gcc gca gtg gga gtg ttc tct aag	547
Ala Ala Val Leu Val Gly Ser Leu Ala Ala Val Gly Val Phe Ser Lys	
135 140 145	
aaa aac atc gga cag acc caa tcc caa ggt gcc tcc att tgg ttg tgg	595
Lys Asn Ile Gly Gln Thr Gln Ser Gln Gly Ala Ser Ile Trp Leu Trp	
150 155 160 165	
cgc ctc ttc gga gtg gtg atg ggc atg tgc caa gca acc cag gtt gca	643
Arg Leu Phe Gly Val Val Met Gly Met Cys Gln Ala Thr Gln Val Ala	
170 175 180	
gtc aat ggt tac ttg gga act gtc cta gga tcc ccc att gag tca gca	691
Val Asn Gly Tyr Leu Gly Thr Val Leu Gly Ser Pro Ile Glu Ser Ala	
185 190 195	
ctg gtg tct ttc gct gtt ggc acc acc gcg ctg ttt att ctg ctg ttg	739
Leu Val Ser Phe Ala Val Gly Thr Thr Ala Leu Phe Ile Leu Leu Leu	
200 205 210	
gtc acc cga acc aag tgg cgt gga atc aac ggc gct ggg aag aaa aac	787
Val Thr Arg Thr Lys Trp Arg Gly Ile Asn Gly Ala Gly Lys Lys Asn	
215 220 225	
cca tgg tgg atg tgg atc ggt ggc gtc atc ggc gcg act gtt att ttc	835
Pro Trp Trp Met Trp Ile Gly Gly Val Ile Gly Ala Thr Val Ile Phe	
230 235 240 245	
agt act gct tac ctg gga ccg atc att ggc act ggt gtt acc gtg gtg	883
Ser Thr Ala Tyr Leu Gly Pro Ile Ile Gly Thr Gly Val Thr Val Val	
250 255 260	
gtt atg ttg ctg ggc atg atg ttg gcc agc ctg atg atc gac gct ttt	931
Val Met Leu Leu Gly Met Met Leu Ala Ser Leu Met Ile Asp Ala Phe	
265 270 275	
gga atc ctt ggc agc ccg cgc cgc cac att cac atc gcg cag ctt ctc	979
Gly Ile Leu Gly Ser Pro Arg Arg His Ile His Ile Ala Gln Leu Leu	
280 285 290	

ggg ctc gtg gtg atc atc ctc ggc gta aca atg atc aga atc
 Gly Leu Val Val Ile Ile Leu Gly Val Thr Met Ile Arg Ile
 295 300 305

1021

taaaccaaga atctaaacca aga

1044

<210> 2582

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 2582

Met Leu Ala Val Leu Phe Gly Val Val Ala Gly Ala Ile Met Pro Phe
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Gln Thr Ser Val Asn Asn Arg Leu Arg Gln Ser Val Gly Ala Pro Leu
 20 25 30

Leu Ala Ser Phe Ile Ser Phe Leu Val Gly Thr Phe Ser Leu Leu Val
 35 40 45

Ala Thr Trp Ile Thr Ser Gly His Pro Tyr Pro Ala Leu Gly Asn Thr
 50 55 60

Thr Gly Gln Pro Trp Trp Ile Phe Thr Gly Gly Met Leu Gly Val Val
 65 70 75 80

Leu Leu Thr Gly Asn Ile Leu Leu Phe Pro Arg Val Gly Ser Val Gln
 85 90 95

Thr Val Ile Leu Pro Ile Ser Gly Gln Ile Ile Met Gly Leu Ile Ile
 100 105 110

Asp Thr Thr Gly Leu Ala His Ser Pro Gln Ala Pro Leu Thr Leu Phe
 115 120 125

Arg Val Leu Gly Ala Ala Ala Val Leu Val Gly Ser Leu Ala Ala Val
 130 135 140

Gly Val Phe Ser Lys Lys Asn Ile Gly Gln Thr Gln Ser Gln Gly Ala
 145 150 155 160

Ser Ile Trp Leu Trp Arg Leu Phe Gly Val Val Met Gly Met Cys Gln
 165 170 175

Ala Thr Gln Val Ala Val Asn Gly Tyr Leu Gly Thr Val Leu Gly Ser
 180 185 190

Pro Ile Glu Ser Ala Leu Val Ser Phe Ala Val Gly Thr Thr Ala Leu
 195 200 205

Phe Ile Leu Leu Leu Val Thr Arg Thr Lys Trp Arg Gly Ile Asn Gly
 210 215 220

Ala Gly Lys Lys Asn Pro Trp Trp Met Trp Ile Gly Gly Val Ile Gly
 225 230 235 240

Ala Thr Val Ile Phe Ser Thr Ala Tyr Leu Gly Pro Ile Ile Gly Thr
 245 250 255

cag cag gat ctc acc cgc att ctt cat gat tgg gat gag gaa gac att 499
Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp Asp Glu Glu Asp Ile
120 125 130

aaa acg cat gcc aag cta ttg cgg aag cac aat gaa agc ttg gaa gaa 547
Lys Thr His Ala Lys Leu Leu Arg Lys His Asn Glu Ser Leu Glu Glu
135 140 145

tac ctc gat atg aag tgg ccc cgc ccc taagtgccca taaacgcacc 594
Tyr Leu Asp Met Lys Trp Pro Arg Pro
150 155

tct 597

<210> 2584

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 2584

Val Ser Thr Asp Pro Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln
1 5 10 15

Leu Ala Tyr Glu Ile Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr
20 25 30

Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu
35 40 45

Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala
50 55 60

Glu Ser Phe Gly Leu Asn Val Ser Thr Val His Arg Gln Leu Lys Ala
65 70 75 80

Ala Ile Ala Asn Gly Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro
85 90 95

Ala Lys Leu His Arg Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln
100 105 110

Glu Leu Leu Ala Arg Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp
115 120 125

Asp Glu Glu Asp Ile Lys Thr His Ala Lys Leu Leu Arg Lys His Asn
130 135 140

Glu Ser Leu Glu Glu Tyr Leu Asp Met Lys Trp Pro Arg Pro
145 150 155

<210> 2585

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXA02123

<400> 2585

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gcgaaaaatt cctgaccgcc cacttaaaaa aagggtctagg	gtg tgg ggt gtg agt	115
	Val Trp Gly Val Ser	
	1 5	
ctt cca cca aat gta caa act gtc ggt gag ctg aag gcc gcc ggc cac	163	
Leu Pro Pro Asn Val Gln Thr Val Gly Glu Leu Lys Ala Ala Gly His		
	10 15 20	
atc tac cga cct ttg cgc gta gaa atc cgc gac aac ctc cta gcc aaa	211	
Ile Tyr Arg Pro Leu Arg Val Glu Ile Arg Asp Asn Leu Leu Ala Lys		
	25 30 35	
ctt cgc agc ggc gaa gat ccg tgg cca ggc ctg cac ggc ctg aac tac	259	
Leu Arg Ser Gly Glu Asp Pro Trp Pro Gly Leu His Gly Leu Asn Tyr		
	40 45 50	
acg gtc atc cgg cag ctt gaa cgc gcg ctc atc gcc ggc cac gac atc	307	
Thr Val Ile Arg Gln Leu Glu Arg Ala Leu Ile Ala Gly His Asp Ile		
	55 60 65	
gtg ctg ctc ggc gaa cgc ggc cag ggt aaa acc cgc ctg ctc cgc acg	355	
Val Leu Leu Gly Glu Arg Gly Gln Gly Lys Thr Arg Leu Leu Arg Thr		
	70 75 80 85	
tta ata acg ctt ctc gac gag tgg tcc ccg atc att ccc ggg cgc gac	403	
Leu Ile Thr Leu Leu Asp Glu Trp Ser Pro Ile Ile Pro Gly Arg Asp		
	90 95 100	
gtt cca gaa cac cct ctt gcg cca aac gta gag atc tcc gat gat cag	451	
Val Pro Glu His Pro Leu Ala Pro Asn Val Glu Ile Ser Asp Asp Gln		
	105 110 115	
ccc att gaa tgg gta cac cgc gat gcg cgc tat acc gag aaa ctt gcc	499	
Pro Ile Glu Trp Val His Arg Asp Ala Arg Tyr Thr Glu Lys Leu Ala		
	120 125 130	
acc cca gat act tcc gtg gct gat ctt atc ggt gat gtt gac cca atg	547	
Thr Pro Asp Thr Ser Val Ala Asp Leu Ile Gly Asp Val Asp Pro Met		
	135 140 145	
cgt gtt gct gaa ggc cgc agc ctc ggt gat cta gaa acc att cac tac	595	
Arg Val Ala Glu Gly Arg Ser Leu Gly Asp Leu Glu Thr Ile His Tyr		
	150 155 160 165	
ggt ctg att cct cgc gcc aac cgt ggc atc gtg gcg atc aac gag ctt	643	
Gly Leu Ile Pro Arg Ala Asn Arg Gly Ile Val Ala Ile Asn Glu Leu		
	170 175 180	
cct gac ctc gct gaa cgc atc cag gtt gcc atg ctc aac gtc atg gag	691	
Pro Asp Leu Ala Glu Arg Ile Gln Val Ala Met Leu Asn Val Met Glu		
	185 190 195	
gaa cgt gat gtg cag att cgt ggc tac aac att cgt ttg gac ttg gat	739	
Glu Arg Asp Val Gln Ile Arg Gly Tyr Asn Ile Arg Leu Asp Leu Asp		
	200 205 210	
gtg ctg gtt gtt gcc tca gcc aac cct gag gat tac acc aac cgt ggc	787	
Val Leu Val Val Ala Ser Ala Asn Pro Glu Asp Tyr Thr Asn Arg Gly		
	215 220 225	

cga att atc act ccg ctc aaa gac cgc ttc ggt gca gaa atc cgc acc Arg Ile Ile Thr Pro Leu Lys Asp Arg Phe Gly Ala Glu Ile Arg Thr 230 235 240 245	835
cac tac cca ctt gag ttg gac gat gaa gtg gca att atc cgc cag gaa His Tyr Pro Leu Glu Leu Asp Asp Glu Val Ala Ile Ile Arg Gln Glu 250 255 260	883
gca gag ctt gtt gcg caa gtc cct gat atc ttg gtt gaa att ctt gcc Ala Glu Leu Val Ala Gln Val Pro Asp Ile Leu Val Glu Ile Leu Ala 265 270 275	931
cgc tac acc cga gcg ctt cgt gaa tcc tca tcg gtg aat cag cgt tct Arg Tyr Thr Arg Ala Leu Arg Glu Ser Ser Ser Val Asn Gln Arg Ser 280 285 290	979
ggt gtg tct gct cgt ttc tcc att gca ggt gca gaa act gtg gcc gca Gly Val Ser Ala Arg Phe Ser Ile Ala Gly Ala Glu Thr Val Ala Ala 295 300 305	1027
gca gct ctt cga cgc gca gca gtg ttc ggc gaa gat gag gcc gtt gcc Ala Ala Leu Arg Arg Ala Ala Val Phe Gly Glu Asp Glu Ala Val Ala 310 315 320 325	1075
cgc ctg gtt gat ttg gaa gca gcc gtg gaa gtc ctc ggc ggc aag att Arg Leu Val Asp Leu Glu Ala Ala Val Glu Val Leu Gly Gly Lys Ile 330 335 340	1123
gaa ttt gaa tcc ggc gaa gaa gga cgc gaa tgg gaa atc ctt gat tat Glu Phe Glu Ser Gly Glu Glu Gly Arg Glu Trp Glu Ile Leu Asp Tyr 345 350 355	1171
ctc ctg cgc acc gca acc gca gaa gcg ctg cgt tcc act ctg cgc tcg Leu Leu Arg Thr Ala Thr Ala Glu Ala Leu Arg Ser Thr Leu Arg Ser 360 365 370	1219
ctg gat ctc acc ccg ctc atc gca gca tta gac ggc agc atc acc gtt Leu Asp Leu Thr Pro Leu Ile Ala Ala Leu Asp Gly Ser Ile Thr Val 375 380 385	1267
tcc act ggc acg aac atc acc gcg tca gaa ttt ttg gct tcg ctc ccc Ser Thr Gly Thr Asn Ile Thr Ala Ser Glu Phe Leu Ala Ser Leu Pro 390 395 400 405	1315
gaa ctc ggc gaa agc acg cta tat gac gac atc gct caa gct ttt ggt Glu Leu Gly Glu Ser Thr Leu Tyr Asp Asp Ile Ala Gln Ala Phe Gly 410 415 420	1363
gcc acc aca cca agt act cgc gcg atg gcc att gag ctt gct ttg gaa Ala Thr Thr Pro Ser Thr Arg Ala Met Ala Ile Glu Leu Ala Leu Glu 425 430 435	1411
ggt ctt tac ctt tcc cga aaa att gcc aag gat tct ggc gaa ggt gaa Gly Leu Tyr Leu Ser Arg Lys Ile Ala Lys Asp Ser Gly Glu Gly Glu 440 445 450	1459
acc att tac ggt taactgggttt taaggagcac cac Thr Ile Tyr Gly 455	1494

<210> 2586

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 2586

Val Trp Gly Val Ser Leu Pro Pro Asn Val Gln Thr Val Gly Glu Leu
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Lys Ala Ala Gly His Ile Tyr Arg Pro Leu Arg Val Glu Ile Arg Asp
20 25 30

Asn Leu Leu Ala Lys Leu Arg Ser Gly Glu Asp Pro Trp Pro Gly Leu
35 40 45

His Gly Leu Asn Tyr Thr Val Ile Arg Gln Leu Glu Arg Ala Leu Ile
50 55 60

Ala Gly His Asp Ile Val Leu Leu Gly Glu Arg Gly Gln Gly Lys Thr
65 70 75 80

Arg Leu Leu Arg Thr Leu Ile Thr Leu Leu Asp Glu Trp Ser Pro Ile
85 90 95

Ile Pro Gly Arg Asp Val Pro Glu His Pro Leu Ala Pro Asn Val Glu
100 105 110

Ile Ser Asp Asp Gln Pro Ile Glu Trp Val His Arg Asp Ala Arg Tyr
115 120 125

Thr Glu Lys Leu Ala Thr Pro Asp Thr Ser Val Ala Asp Leu Ile Gly
130 135 140

Asp Val Asp Pro Met Arg Val Ala Glu Gly Arg Ser Leu Gly Asp Leu
145 150 155 160

Glu Thr Ile His Tyr Gly Leu Ile Pro Arg Ala Asn Arg Gly Ile Val
165 170 175

Ala Ile Asn Glu Leu Pro Asp Leu Ala Glu Arg Ile Gln Val Ala Met
180 185 190

Leu Asn Val Met Glu Glu Arg Asp Val Gln Ile Arg Gly Tyr Asn Ile
195 200 205

Arg Leu Asp Leu Asp Val Leu Val Val Ala Ser Ala Asn Pro Glu Asp
210 215 220

Tyr Thr Asn Arg Gly Arg Ile Ile Thr Pro Leu Lys Asp Arg Phe Gly
225 230 235 240

Ala Glu Ile Arg Thr His Tyr Pro Leu Glu Leu Asp Asp Glu Val Ala
245 250 255

Ile Ile Arg Gln Glu Ala Glu Leu Val Ala Gln Val Pro Asp Ile Leu
260 265 270

Val Glu Ile Leu Ala Arg Tyr Thr Arg Ala Leu Arg Glu Ser Ser Ser
275 280 285

Val Asn Gln Arg Ser Gly Val Ser Ala Arg Phe Ser Ile Ala Gly Ala

290	295	300
Glu Thr Val Ala Ala Ala Ala Leu Arg Arg Ala Ala Val Phe Gly Glu 305 310 315 320		
Asp Glu Ala Val Ala Arg Leu Val Asp Leu Glu Ala Ala Val Glu Val 325 330 335		
Leu Gly Gly Lys Ile Glu Phe Glu Ser Gly Glu Glu Gly Arg Glu Trp 340 345 350		
Glu Ile Leu Asp Tyr Leu Leu Arg Thr Ala Thr Ala Glu Ala Leu Arg 355 360 365		
Ser Thr Leu Arg Ser Leu Asp Leu Thr Pro Leu Ile Ala Ala Leu Asp 370 375 380		
Gly Ser Ile Thr Val Ser Thr Gly Thr Asn Ile Thr Ala Ser Glu Phe 385 390 395 400		
Leu Ala Ser Leu Pro Glu Leu Gly Glu Ser Thr Leu Tyr Asp Asp Ile 405 410 415		
Ala Gln Ala Phe Gly Ala Thr Thr Pro Ser Thr Arg Ala Met Ala Ile 420 425 430		
Glu Leu Ala Leu Glu Gly Leu Tyr Leu Ser Arg Lys Ile Ala Lys Asp 435 440 445		
Ser Gly Glu Gly Glu Thr Ile Tyr Gly 450 455		

<210> 2587
 <211> 2079
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2056)
 <223> RXA02124

<400> 2587
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 aaccatttac ggtaactgg ttttaaggag caccacagcc atg gcc act tca cat 115
 Met Ala Thr Ser His
 1 5
 tca cga ccc cgc cgc agc cgt tac gga cgc tac acc gga ggc cca gat 163
 Ser Arg Pro Arg Arg Ser Arg Tyr Gly Arg Tyr Thr Gly Gly Pro Asp
 10 15 20
 ccg ctg gca cct cca gtg gat ctg agc gat gcc ctg cgc gat att gct 211
 Pro Leu Ala Pro Pro Val Asp Leu Ser Asp Ala Leu Arg Asp Ile Ala
 25 30 35
 gat gat gtc atg gct ggt tat tcc cct gag cag gca cta cgt gaa tac 259
 Asp Asp Val Met Ala Gly Tyr Ser Pro Glu Gln Ala Leu Arg Glu Tyr
 40 45 50

ctg cgc aga ggc gcc cga gga cag gaa ggc ctc gat gat cta gcc tgg	307
Leu Arg Arg Gly Ala Arg Gly Gln Glu Gly Leu Asp Asp Leu Ala Trp	
55 60 65	
cgt gca gcc gaa cgc cgc cga gaa tta ctt agc cga aac aac ctc ggt	355
Arg Ala Ala Glu Arg Arg Arg Glu Leu Leu Ser Arg Asn Asn Leu Gly	
70 75 80 85	
ggc aca ctc gct gag gtt cgc aag ctt ctc gat gaa ggc ctc aag ctg	403
Gly Thr Leu Ala Glu Val Arg Lys Leu Leu Asp Glu Gly Leu Lys Leu	
90 95 100	
gaa cgc gct caa ctg gcc cgc gat atc gat atg gat gac acc gat cga	451
Glu Arg Ala Gln Leu Ala Arg Asp Ile Asp Met Asp Asp Thr Asp Arg	
105 110 115	
gca ttc cgc gaa atg cag atc agc aac ctc cct gaa tcc acc gcc gct	499
Ala Phe Arg Glu Met Gln Ile Ser Asn Leu Pro Glu Ser Thr Ala Ala	
120 125 130	
gcc gtt tcc gag cta aat tcc tac gat tgg caa tcc caa gaa gca cgc	547
Ala Val Ser Glu Leu Asn Ser Tyr Asp Trp Gln Ser Gln Glu Ala Arg	
135 140 145	
caa aag ttt gaa caa atc cgt gac ctg ctt ggc cgt gaa atg tta gat	595
Gln Lys Phe Glu Gln Ile Arg Asp Leu Leu Gly Arg Glu Met Leu Asp	
150 155 160 165	
cag caa ttc tcc ggc atg aaa caa gcc atg gaa ggt gcc tcc gac gag	643
Gln Gln Phe Ser Gly Met Lys Gln Ala Met Glu Gly Ala Ser Asp Glu	
170 175 180	
gac aaa gca gcc atc gcc gaa atg ctg cgc gat ctc aac gac ctg ctc	691
Asp Lys Ala Ala Ile Ala Glu Met Leu Arg Asp Leu Asn Asp Leu Leu	
185 190 195	
tcc aaa cac cgc gag gga acg gac act ccc acc gat ttc gcc aat ttt	739
Ser Lys His Arg Glu Gly Thr Asp Thr Pro Thr Asp Phe Ala Asn Phe	
200 205 210	
atg gcc aaa cac ggc gag cac ttc ccc gag cag ccg cgc gac atc aat	787
Met Ala Lys His Gly Glu His Phe Pro Glu Gln Pro Arg Asp Ile Asn	
215 220 225	
gag ctc atc gat gcc ctc gca gcc cgt tcc gcc gca gcc agt cgc atg	835
Glu Leu Ile Asp Ala Leu Ala Ala Arg Ser Ala Ala Ala Ser Arg Met	
230 235 240 245	
ttc aac tcc ata tca gag gaa caa cgc cgc gaa ctc atg aaa cta tct	883
Phe Asn Ser Ile Ser Glu Glu Gln Arg Glu Leu Met Lys Leu Ser	
250 255 260	
gcc caa gct ttc gga tcc cca gag ctg cag gaa ttg ctc ggt gac ctg	931
Ala Gln Ala Phe Gly Ser Pro Glu Leu Gln Glu Leu Leu Gly Asp Leu	
265 270 275	
gct gga aac ctc caa ggt ctg cgc ccc gac ctc aac tgg gat ggc tcc	979
Ala Gly Asn Leu Gln Gly Leu Arg Pro Asp Leu Asn Trp Asp Gly Ser	
280 285 290	

gaa caa ttc tcc ggc gac gaa ggc atg gga ctt ggt gat ggc acc ggc Glu Gln Phe Ser Gly Asp Glu Gly Met Gly Leu Gly Asp Gly Thr Gly 295 300 305	1027
gcc atg cag gac ctc gcc gaa ctc gac aac ctt gct gaa caa ctg agc Ala Met Gln Asp Leu Ala Glu Leu Asp Asn Leu Ala Glu Gln Leu Ser 310 315 320 325	1075
aac tcc cac acc gac ctc gac att gat gcg att cgc cgc caa ctc ggc Asn Ser His Thr Asp Leu Asp Ile Asp Ala Ile Arg Arg Gln Leu Gly 330 335 340	1123
gat gac gcc gct gtc tct gcc gaa act ttg gcc aaa ctg gag cgc gcg Asp Asp Ala Ala Val Ser Ala Glu Thr Leu Ala Lys Leu Glu Arg Ala 345 350 355	1171
ctc cgc gac agc ggc ctt ctt cgc cgc aac ccc gat ggc tca ttg aag Leu Arg Asp Ser Gly Leu Leu Arg Arg Asn Pro Asp Gly Ser Leu Lys 360 365 370	1219
ctc agc ccc cag gcc atg cgc cgt cta ggg aaa gcg ctt ctc gac gcc Leu Ser Pro Gln Ala Met Arg Arg Leu Gly Lys Ala Leu Leu Asp Ala 375 380 385	1267
gcc agc gaa caa tta tcg tcc cgc cca ggc tcg cga gac tcc cgg ttg Ala Ser Glu Gln Leu Ser Ser Arg Pro Gly Ser Arg Asp Ser Arg Leu 390 395 400 405	1315
gca gga gca aac ggt gaa gcg acg gga gca tcc cga cct tat gtt ttc Ala Gly Ala Asn Gly Glu Ala Thr Gly Ala Ser Arg Pro Tyr Val Phe 410 415 420	1363
gga gac acc caa cca tgg gat gtc acc cgc acc atc acc aat gct ctg Gly Asp Thr Gln Pro Trp Asp Val Thr Arg Thr Ile Thr Asn Ala Leu 425 430 435	1411
cag cga aca gcc gga aca gat acg gaa ggt ccg ctg cgc atc aac tta Gln Arg Thr Ala Gly Thr Asp Thr Glu Gly Pro Leu Arg Ile Asn Leu 440 445 450	1459
gat gat gtg gaa gtc att gaa act gaa gcc cgc acc ctc aac gcc gtg Asp Asp Val Glu Val Ile Glu Thr Glu Ala Arg Thr Leu Asn Ala Val 455 460 465	1507
gca ctg cta gta gac acc agt tat tcc atg gct gcc gaa ggc cgc tgg Ala Leu Leu Val Asp Thr Ser Tyr Ser Met Ala Ala Glu Gly Arg Trp 470 475 480 485	1555
gtg ccc atg aag caa aca gcg ctt gcc ctc cac cac ctg gta tcc acc Val Pro Met Lys Gln Thr Ala Leu Ala Leu His His Leu Val Ser Thr 490 495 500	1603
cgg ttt aga gga gat gaa cta gca cta atc act ttt ggt cga cat gcc Arg Phe Arg Gly Asp Glu Leu Ala Leu Ile Thr Phe Gly Arg His Ala 505 510 515	1651
caa aac atg gac atc gag gaa ctg act gca ctg cca ccg gtt cac gaa Gln Asn Met Asp Ile Glu Glu Leu Thr Ala Leu Pro Pro Val His Glu 520 525 530	1699
caa gga act aat ctc cac cac gca tta ctg ctg gca gaa cgg ttc ttt	1747

Gln Gly Thr Asn Leu His His Ala Leu Leu Leu Ala Glu Arg Phe Phe
 535 540 545

gct cgc cat ccc tcc atg aaa gca agc ctg ctc att gtc aca gat ggc 1795
 Ala Arg His Pro Ser Met Lys Ala Ser Leu Leu Ile Val Thr Asp Gly
 550 555 560 565

gaa ccc aca gct cac ctc gaa gcc gat gga cac gcc tgg ttc aac tgg 1843
 Glu Pro Thr Ala His Leu Glu Ala Asp Gly His Ala Trp Phe Asn Trp
 570 575 580

ccc act gac cca gaa acc atg ttc aag acc gtc acc caa cta gat aaa 1891
 Pro Thr Asp Pro Glu Thr Met Phe Lys Thr Val Thr Gln Leu Asp Lys
 585 590 595

gta acc aag cga gga acc cac acc aca ctc ttc cga ctg gga cat gat 1939
 Val Thr Lys Arg Gly Thr His Thr Thr Leu Phe Arg Leu Gly His Asp
 600 605 610

caa gga tta gag cac ttt ctc aac caa cta gcc gac cgt gtt ggc ggc 1987
 Gln Gly Leu Glu His Phe Leu Asn Gln Leu Ala Asp Arg Val Gly Gly
 615 620 625

acc gtg gtg gct ccc gat ctg gac gga ctc ggc gcc gca gtc gtg ggc 2035
 Thr Val Val Ala Pro Asp Leu Asp Gly Leu Gly Ala Ala Val Val Gly
 630 635 640 645

gag tat tta cga cac cgc tac tgagcattgg acgttttcgc ctt 2079
 Glu Tyr Leu Arg His Arg Tyr
 650

<210> 2588

<211> 652

<212> PRT

<213> Corynebacterium glutamicum

<400> 2588

Met Ala Thr Ser His Ser Arg Pro Arg Arg Ser Arg Tyr Gly Arg Tyr
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Leu Arg Asp Ile Ala Asp Asp Val Met Ala Gly Tyr Ser Pro Glu Gln
 35 40 45

Ala Leu Arg Glu Tyr Leu Arg Arg Gly Ala Arg Gly Gln Glu Gly Leu
 50 55 60

Asp Asp Leu Ala Trp Arg Ala Ala Glu Arg Arg Arg Glu Leu Leu Ser
 65 70 75 80

Arg Asn Asn Leu Gly Gly Thr Leu Ala Glu Val Arg Lys Leu Leu Asp
 85 90 95

Glu Gly Leu Lys Leu Glu Arg Ala Gln Leu Ala Arg Asp Ile Asp Met
 100 105 110

Asp Asp Thr Asp Arg Ala Phe Arg Glu Met Gln Ile Ser Asn Leu Pro
 115 120 125

Glu Ser Thr Ala Ala Ala Val Ser Glu Leu Asn Ser Tyr Asp Trp Gln
130 135 140

Ser Gln Glu Ala Arg Gln Lys Phe Glu Gln Ile Arg Asp Leu Leu Gly
145 150 155 160

Arg Glu Met Leu Asp Gln Gln Phe Ser Gly Met Lys Gln Ala Met Glu
165 170 175

Gly Ala Ser Asp Glu Asp Lys Ala Ala Ile Ala Glu Met Leu Arg Asp
180 185 190

Leu Asn Asp Leu Leu Ser Lys His Arg Glu Gly Thr Asp Thr Pro Thr
195 200 205

Asp Phe Ala Asn Phe Met Ala Lys His Gly Glu His Phe Pro Glu Gln
210 215 220

Pro Arg Asp Ile Asn Glu Leu Ile Asp Ala Leu Ala Ala Arg Ser Ala
225 230 235 240

Ala Ala Ser Arg Met Phe Asn Ser Ile Ser Glu Glu Gln Arg Arg Glu
245 250 255

Leu Met Lys Leu Ser Ala Gln Ala Phe Gly Ser Pro Glu Leu Gln Glu
260 265 270

Leu Leu Gly Asp Leu Ala Gly Asn Leu Gln Gly Leu Arg Pro Asp Leu
275 280 285

Asn Trp Asp Gly Ser Glu Gln Phe Ser Gly Asp Glu Gly Met Gly Leu
290 295 300

Gly Asp Gly Thr Gly Ala Met Gln Asp Leu Ala Glu Leu Asp Asn Leu
305 310 315 320

Ala Glu Gln Leu Ser Asn Ser His Thr Asp Leu Asp Ile Asp Ala Ile
325 330 335

Arg Arg Gln Leu Gly Asp Asp Ala Ala Val Ser Ala Glu Thr Leu Ala
340 345 350

Lys Leu Glu Arg Ala Leu Arg Asp Ser Gly Leu Leu Arg Arg Asn Pro
355 360 365

Asp Gly Ser Leu Lys Leu Ser Pro Gln Ala Met Arg Arg Leu Gly Lys
370 375 380

Ala Leu Leu Asp Ala Ala Ser Glu Gln Leu Ser Ser Arg Pro Gly Ser
385 390 395 400

Arg Asp Ser Arg Leu Ala Gly Ala Asn Gly Glu Ala Thr Gly Ala Ser
405 410 415

Arg Pro Tyr Val Phe Gly Asp Thr Gln Pro Trp Asp Val Thr Arg Thr
420 425 430

Ile Thr Asn Ala Leu Gln Arg Thr Ala Gly Thr Asp Thr Glu Gly Pro
435 440 445

Leu Arg Ile Asn Leu Asp Asp Val Glu Val Ile Glu Thr Glu Ala Arg
 450 455 460
 Thr Leu Asn Ala Val Ala Leu Leu Val Asp Thr Ser Tyr Ser Met Ala
 465 470 475 480
 Ala Glu Gly Arg Trp Val Pro Met Lys Gln Thr Ala Leu Ala Leu His
 485 490 495
 His Leu Val Ser Thr Arg Phe Arg Gly Asp Glu Leu Ala Leu Ile Thr
 500 505 510
 Phe Gly Arg His Ala Gln Asn Met Asp Ile Glu Glu Leu Thr Ala Leu
 515 520 525
 Pro Pro Val His Glu Gln Gly Thr Asn Leu His His Ala Leu Leu Leu
 530 535 540
 Ala Glu Arg Phe Phe Ala Arg His Pro Ser Met Lys Ala Ser Leu Leu
 545 550 555 560
 Ile Val Thr Asp Gly Glu Pro Thr Ala His Leu Glu Ala Asp Gly His
 565 570 575
 Ala Trp Phe Asn Trp Pro Thr Asp Pro Glu Thr Met Phe Lys Thr Val
 580 585 590
 Thr Gln Leu Asp Lys Val Thr Lys Arg Gly Thr His Thr Thr Leu Phe
 595 600 605
 Arg Leu Gly His Asp Gln Gly Leu Glu His Phe Leu Asn Gln Leu Ala
 610 615 620
 Asp Arg Val Gly Gly Thr Val Val Ala Pro Asp Leu Asp Gly Leu Gly
 625 630 635 640
 Ala Ala Val Val Gly Glu Tyr Leu Arg His Arg Tyr
 645 650

<210> 2589

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXA02125

<400> 2589

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gaatatccat ttatgctgct gtagtcggct atgtggacgc atg gtg gca acc tct 115
 Met Val Ala Thr Ser
 1 5

cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att 163
 Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile
 10 15 20

gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag 211
 Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu
 25 30 35

cgc ggc gtt ggc gaa ggc att cgc acc gct gga gtg ccc cgc gag gag 259
 Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu
 40 45 50

ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga 307
 Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly
 55 60 65

gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat 355
 Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr
 70 75 80 85

gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt 403
 Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg
 90 95 100

ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa 451
 Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu
 105 110 115

gat gcc tac aaa gcc gga aag att cga tcc att ggt gtc tcg aac ttc 499
 Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile Gly Val Ser Asn Phe
 120 125 130

ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct 547
 Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro
 135 140 145

cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta 595
 His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu
 150 155 160 165

atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc 643
 Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro
 170 175 180

atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct 691
 Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala
 185 190 195

gac aag tac aac gtg agc att ccg cag cta tgc att cgg tac aca att 739
 Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile
 200 205 210

caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg 787
 Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met
 215 220 225

agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg 835
 Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala
 230 235 240 245

gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt 883
 Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe
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cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac 924

Pro Val Tyr Ser Gly Lys
265

<210> 2590

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 2590

Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala
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Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu
20 25 30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
35 40 45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile
50 55 60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
65 70 75 80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
85 90 95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
100 105 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
115 120 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
130 135 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
145 150 155 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
165 170 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
180 185 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
195 200 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
210 215 220

Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
225 230 235 240

Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly
245 250 255

Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
260 265

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<400> 2592
Met Lys Ile Ile Phe Lys Met Ala Ser Asn Lys Phe Ile Asp Asn Lys
  1             5             10             15

Lys Gly Leu Ala Met Leu Val Phe Ala Glu Leu Val Met Glu Met Leu
      20             25             30

Asp Gln Pro Glu Glu Gln Leu His Asn Val Arg Gly Val Ala Ile Glu
      35             40             45

Lys Arg Glu Phe Leu Lys Ala Leu Thr Ala Asp Phe Thr Ser Arg Leu
      50             55             60

Lys Gln Ala Gln Thr Asp Lys Ile Leu Val Trp Asp Phe Ala
      65             70             75

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<210> 2593
 <211> 739
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(739)
 <223> RXA02132

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 gagcacatcc tcttccact acccaagaaa gagctataac gtg cac aac ttc tcc 115
 Val His Asn Phe Ser
 1 5
 ttc gac gtg gac gaa tcc tac gcc aag aag aac aac gaa atc ctc cgc 163
 Phe Asp Val Asp Glu Ser Tyr Ala Lys Lys Asn Asn Glu Ile Leu Arg
 10 15 20
 gac gca aag cga ctc cag atc tca gca ctg tgc ctt gga ctc atc ctc 211
 Asp Ala Lys Arg Leu Gln Ile Ser Ala Leu Cys Leu Gly Leu Ile Leu
 25 30 35
 ggc ggc gga gcc gta gcc gtc tac ctg ttt tct aac gga gca gtg tgg 259
 Gly Gly Gly Ala Val Ala Val Tyr Leu Phe Ser Asn Gly Ala Val Trp
 40 45 50
 atg tgg atg atc gcc atc gtc atg gtc ttc ctc gcc ctg ttg agc ttc 307
 Met Trp Met Ile Ala Ile Val Met Val Phe Leu Ala Leu Leu Ser Phe
 55 60 65
 atc atg att cct gtg atc ccc cgc caa atg ggc aac gca caa acg ctc 355
 Ile Met Ile Pro Val Ile Pro Arg Gln Met Gly Asn Ala Gln Thr Leu
 70 75 80 85
 tac gat gac tac gaa cta gcc ccc gcc atc atc gca gaa gta aac ccc 403
 Tyr Asp Asp Tyr Glu Leu Ala Pro Ala Ile Ile Ala Glu Val Asn Pro
 90 95 100
 cgc gat gtg gtc ctc ctg gca ctc gtc aac cgc aat gtg aac ccc gaa 451
 Arg Asp Val Val Leu Leu Ala Leu Val Asn Arg Asn Val Asn Pro Glu
 105 110 115
 gcc aaa cca gag tgg gca ttg gcc acc cgc acg atc gtt cgc gtc gga 499
 Ala Lys Pro Glu Trp Ala Leu Ala Thr Arg Thr Ile Val Arg Val Gly
 120 125 130
 gca cac gaa cgt cgc ctc ggc gaa cgt atc cca tcc gtc gca atc acc 547
 Ala His Glu Arg Arg Leu Gly Glu Arg Ile Pro Ser Val Ala Ile Thr
 135 140 145
 ggc cga cgc acc gtc aaa gac caa gac cac tgg gat gaa atc agc ccc 595
 Gly Arg Arg Thr Val Lys Asp Gln Asp His Trp Asp Glu Ile Ser Pro
 150 155 160 165
 atg cca att acc tgg ggc acc acg gac aaa gac atc atc cgt gaa gcc 643
 Met Pro Ile Thr Trp Gly Thr Thr Asp Lys Asp Ile Ile Arg Glu Ala

170										175					180					
gag	aaa	act	atc	ccc	cac	gaa	ctc	tgg	gcc	aaa	cta	gaa	aag	aac	cgc	691				
Glu	Lys	Thr	Ile	Pro	His	Glu	Leu	Trp	Ala	Lys	Leu	Glu	Lys	Asn	Arg					
			185					190					195							
ggc	aag	ttg	gag	gac	gtt	aaa	aag	acc	ccc	aac	aac	ctg	ttc	aaa	cta	739				
Gly	Lys	Leu	Glu	Asp	Val	Lys	Lys	Thr	Pro	Asn	Asn	Leu	Phe	Lys	Leu					
		200					205					210								

<210> 2594

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 2594

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Asn	Glu	Ile	Leu	Arg	Asp	Ala	Lys	Arg	Leu	Gln	Ile	Ser	Ala	Leu	Cys
			20					25						30	

Leu	Gly	Leu	Ile	Leu	Gly	Gly	Gly	Ala	Val	Ala	Val	Tyr	Leu	Phe	Ser
		35					40					45			

Asn	Gly	Ala	Val	Trp	Met	Trp	Met	Ile	Ala	Ile	Val	Met	Val	Phe	Leu
	50					55					60				

Ala	Leu	Leu	Ser	Phe	Ile	Met	Ile	Pro	Val	Ile	Pro	Arg	Gln	Met	Gly
65					70					75					80

Asn	Ala	Gln	Thr	Leu	Tyr	Asp	Asp	Tyr	Glu	Leu	Ala	Pro	Ala	Ile	Ile
				85					90					95	

Ala	Glu	Val	Asn	Pro	Arg	Asp	Val	Val	Leu	Leu	Ala	Leu	Val	Asn	Arg
			100					105					110		

Asn	Val	Asn	Pro	Glu	Ala	Lys	Pro	Glu	Trp	Ala	Leu	Ala	Thr	Arg	Thr
		115					120					125			

Ile	Val	Arg	Val	Gly	Ala	His	Glu	Arg	Arg	Leu	Gly	Glu	Arg	Ile	Pro
	130					135					140				

Ser	Val	Ala	Ile	Thr	Gly	Arg	Arg	Thr	Val	Lys	Asp	Gln	Asp	His	Trp
145					150					155					160

Asp	Glu	Ile	Ser	Pro	Met	Pro	Ile	Thr	Trp	Gly	Thr	Thr	Asp	Lys	Asp
				165					170					175	

Ile	Ile	Arg	Glu	Ala	Glu	Lys	Thr	Ile	Pro	His	Glu	Leu	Trp	Ala	Lys
			180					185					190		

Leu	Glu	Lys	Asn	Arg	Gly	Lys	Leu	Glu	Asp	Val	Lys	Lys	Thr	Pro	Asn
		195					200					205			

Asn	Leu	Phe	Lys	Leu
	210			

<210> 2595

<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(898)
<223> RXA02137

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acctgcgtgg gctgaaagtc ttcaactttta atccttacag atg gtc gtt ctg att 115
Met Val Val Leu Ile
1 5
cct ttc aac gat gaa gtg tgc acc cct att ccc gat ttg gga ggt ttt 163
Pro Phe Asn Asp Glu Val Cys Thr Pro Ile Pro Asp Leu Gly Gly Phe
10 15 20
cct tgt agc cta ttg agt gtg aaa ctt cct tgg gat aaa aat aag aac 211
Pro Cys Ser Leu Leu Ser Val Lys Leu Pro Trp Asp Lys Asn Lys Asn
25 30 35
aac gaa ggg gct gac gct gca ggc caa gac gcc agc tcc acc cct gag 259
Asn Glu Gly Ala Asp Ala Ala Gly Gln Asp Ala Ser Ser Thr Pro Glu
40 45 50
acc gct acg cct gac gct act gag cag aaa ttg cca aag ggg cac acg 307
Thr Ala Thr Pro Asp Ala Thr Glu Gln Lys Leu Pro Lys Gly His Thr
55 60 65
gca ccg aag ggc cgt ccc act ccg aag cgt cgt gaa gtt gag tta gag 355
Ala Pro Lys Gly Arg Pro Thr Pro Lys Arg Arg Glu Val Glu Leu Glu
70 75 80 85
cga ggt gtc gtt ggc ggc cag tct ttg gcg cct act gat act tat gcg 403
Arg Gly Val Val Gly Gly Gln Ser Leu Ala Pro Thr Asp Thr Tyr Ala
90 95 100
cag cag cgc cag aag cgt aaa gaa ttt aaa gct tct atg acc aag gaa 451
Gln Gln Arg Gln Lys Arg Lys Glu Phe Lys Ala Ser Met Thr Lys Glu
105 110 115
gaa ttc aag gca tac aag cag aaa gag cgc gat gcc cga gtt aag cgt 499
Glu Phe Lys Ala Tyr Lys Gln Lys Glu Arg Asp Ala Arg Val Lys Arg
120 125 130
cag cgc gaa acc caa gct gca atg gat cgc ggc gaa gat gct tat ttg 547
Gln Arg Glu Thr Gln Ala Ala Met Asp Arg Gly Glu Asp Ala Tyr Leu
135 140 145
atg gat cgc gat aag ggc gag gtt cgc cgt ttt gcg cgt gac tgg gtg 595
Met Asp Arg Asp Lys Gly Glu Val Arg Arg Phe Ala Arg Asp Trp Val
150 155 160 165
gat tcc cgc agg ttc ttg tct aac ttt gtg atg cca gta gct att gct 643
Asp Ser Arg Arg Phe Leu Ser Asn Phe Val Met Pro Val Ala Ile Ala
170 175 180
ttg ctg gtt gtc atg ctg atc ggt aac ttc aac cca tca ttc gct gcg 691

Leu Leu Val Val Met Leu Ile Gly Asn Phe Asn Pro Ser Phe Ala Ala
 185 190 195
 act tct tcc atg gtt gcc atg gtt ttg atg ttg ggc ttc ctg att gag 739
 Thr Ser Ser Met Val Ala Met Val Leu Met Leu Gly Phe Leu Ile Glu
 200 205 210
 ggc atc acc act ggt cgt cgt gtg aac aag gct gct cgc acg agg ttc 787
 Gly Ile Thr Thr Gly Arg Arg Val Asn Lys Ala Ala Arg Thr Arg Phe
 215 220 225
 cct ggt acc acc gag act ggt ttt ggt ctg ggt tac tac gcg tat tcc 835
 Pro Gly Thr Thr Glu Thr Gly Phe Gly Leu Gly Tyr Tyr Ala Tyr Ser
 230 235 240 245
 cgc acc att cag cct cgt aag tgg cgt acc cct cgt gca cgc gtt gaa 883
 Arg Thr Ile Gln Pro Arg Lys Trp Arg Thr Pro Arg Ala Arg Val Glu
 250 255 260
 att ggt gct gaa gtc tagcgcacatgc gcacgtagt tct 921
 Ile Gly Ala Glu Val
 265

<210> 2596

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 2596

Met Val Val Leu Ile Pro Phe Asn Asp Glu Val Cys Thr Pro Ile Pro
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 Asp Lys Asn Lys Asn Asn Glu Gly Ala Asp Ala Ala Gly Gln Asp Ala
 35 40 45
 Ser Ser Thr Pro Glu Thr Ala Thr Pro Asp Ala Thr Glu Gln Lys Leu
 50 55 60
 Pro Lys Gly His Thr Ala Pro Lys Gly Arg Pro Thr Pro Lys Arg Arg
 65 70 75 80
 Glu Val Glu Leu Glu Arg Gly Val Val Gly Gly Gln Ser Leu Ala Pro
 85 90 95
 Thr Asp Thr Tyr Ala Gln Gln Arg Gln Lys Arg Lys Glu Phe Lys Ala
 100 105 110
 Ser Met Thr Lys Glu Glu Phe Lys Ala Tyr Lys Gln Lys Glu Arg Asp
 115 120 125
 Ala Arg Val Lys Arg Gln Arg Glu Thr Gln Ala Ala Met Asp Arg Gly
 130 135 140
 Glu Asp Ala Tyr Leu Met Asp Arg Asp Lys Gly Glu Val Arg Arg Phe
 145 150 155 160
 Ala Arg Asp Trp Val Asp Ser Arg Arg Phe Leu Ser Asn Phe Val Met

165	170	175
Pro Val Ala Ile Ala Leu Leu Val Val Met Leu Ile Gly Asn Phe Asn		
180	185	190
Pro Ser Phe Ala Ala Thr Ser Ser Met Val Ala Met Val Leu Met Leu		
195	200	205
Gly Phe Leu Ile Glu Gly Ile Thr Thr Gly Arg Arg Val Asn Lys Ala		
210	215	220
Ala Arg Thr Arg Phe Pro Gly Thr Thr Glu Thr Gly Phe Gly Leu Gly		
225	230	235
Tyr Tyr Ala Tyr Ser Arg Thr Ile Gln Pro Arg Lys Trp Arg Thr Pro		
245	250	255
Arg Ala Arg Val Glu Ile Gly Ala Glu Val		
260	265	

<210> 2597
 <211> 531
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(508)
 <223> RXA02141

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 Met Tyr Gly Pro Thr
 1 5
 gta ttc atg gcc gca atg gct gtc atc tac atc ttc gca aca atg cac 163
 Val Phe Met Ala Ala Met Ala Val Ile Tyr Ile Phe Ala Thr Met His
 10 15 20
 gtt agt gat ggc ggc agc gtt aaa ggt gtt gag tgg gtc ggt tct gtg 211
 Val Ser Asp Gly Gly Ser Val Lys Gly Val Glu Trp Val Gly Ser Val
 25 30 35
 gcc ctg gtc ctg tca gca ggt ctg acg ctt atg ctc ggt gtc tac ctt 259
 Ala Leu Val Leu Ser Ala Gly Leu Thr Leu Met Leu Gly Val Tyr Leu
 40 45 50
 cac ttc act gaa gtc cgc gta gat gtt ctt cca gag gac tgg gaa gag 307
 His Phe Thr Glu Val Arg Val Asp Val Leu Pro Glu Asp Trp Glu Glu
 55 60 65
 gct gag gtt gcc gac aag gca gga acc ctc ggg ttc ttc agc cca agc 355
 Ala Glu Val Ala Asp Lys Ala Gly Thr Leu Gly Phe Phe Ser Pro Ser
 70 75 80 85
 tcc att tgg ccg gca gct atg tcc ggt gcg gtt gga ttc ctt gca ttc 403
 Ser Ile Trp Pro Ala Ala Met Ser Gly Ala Val Gly Phe Leu Ala Phe
 90 95 100

ggc gtt gtg tac ttc cac tac tgg atg atc gca gtt ggt ctg atg ctc 451
 Gly Val Val Tyr Phe His Tyr Trp Met Ile Ala Val Gly Leu Met Leu
 105 110 115

 ctg atc ttc acg atc acc aag ctc aac ctt cag tac ggc gtg cca aaa 499
 Leu Ile Phe Thr Ile Thr Lys Leu Asn Leu Gln Tyr Gly Val Pro Lys
 120 125 130

 gaa aag cac tagtactaaa accacatatg ctc 531
 Glu Lys His
 135

<210> 2598
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2598
 Met Tyr Gly Pro Thr Val Phe Met Ala Ala Met Ala Val Ile Tyr Ile
 1 5 10 15

 Phe Ala Thr Met His Val Ser Asp Gly Gly Ser Val Lys Gly Val Glu
 20 25 30

 Trp Val Gly Ser Val Ala Leu Val Leu Ser Ala Gly Leu Thr Leu Met
 35 40 45

 Leu Gly Val Tyr Leu His Phe Thr Glu Val Arg Val Asp Val Leu Pro
 50 55 60

 Glu Asp Trp Glu Glu Ala Glu Val Ala Asp Lys Ala Gly Thr Leu Gly
 65 70 75 80

 Phe Phe Ser Pro Ser Ser Ile Trp Pro Ala Ala Met Ser Gly Ala Val
 85 90 95

 Gly Phe Leu Ala Phe Gly Val Val Tyr Phe His Tyr Trp Met Ile Ala
 100 105 110

 Val Gly Leu Met Leu Leu Ile Phe Thr Ile Thr Lys Leu Asn Leu Gln
 115 120 125

 Tyr Gly Val Pro Lys Glu Lys His
 130 135

<210> 2599
 <211> 750
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(727)
 <223> RXA02146

<400> 2599
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	Val Gly Lys His Arg	
	1 5	
cgc aac aat tca aac gca act cgc aag gct gta gca gca tct gca gtt	163	
Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val Ala Ala Ser Ala Val		
10 15 20		
gcg ctt gga gca acc gca gct atc gcc tcc cca gca cag gca gct gag	211	
Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro Ala Gln Ala Ala Glu		
25 30 35		
gtt gtt gtt cct ggc acc gga atc agc gtt gac atc gct ggc atc gag	259	
Val Val Val Pro Gly Thr Gly Ile Ser Val Asp Ile Ala Gly Ile Glu		
40 45 50		
acc act cca ggt ctt aac aac gtt cca gga atc gat cag tgg atc cct	307	
Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile Asp Gln Trp Ile Pro		
55 60 65		
tcc ctt agc agc cag gca gct cct act gct tac gca gcc gtc att gat	355	
Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr Ala Ala Val Ile Asp		
70 75 80 85		
gca cct gca gca cag gct gca cct gca gca agc acc ggt cag gca atc	403	
Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser Thr Gly Gln Ala Ile		
90 95 100		
gtt gat gca gcg cgc acc aag att ggt tcc cca tac ggt tgg ggt gct	451	
Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro Tyr Gly Trp Gly Ala		
105 110 115		
acc ggt cct aac gct ttc gac tgc tcc ggc ctt acc tca tgg gca tac	499	
Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu Thr Ser Trp Ala Tyr		
120 125 130		
agc cag gtt ggc aag tcc atc cca cgt acc tcc cag gct cag gct gca	547	
Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser Gln Ala Gln Ala Ala		
135 140 145		
cag ggc acc cct gtt gct tac tct gac ctt cag gct ggc gac atc gtt	595	
Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln Ala Gly Asp Ile Val		
150 155 160 165		
gcg ttc tac tcc ggc gct acc cac gtt ggt atc tac tcc ggc cac ggc	643	
Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile Tyr Ser Gly His Gly		
170 175 180		
acc gtt atc cac gca ctg aac agc agc acc cct ctg tct gag cac tcc	691	
Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro Leu Ser Glu His Ser		
185 190 195		
ttg gat tac atg cca ttc cac tct gca gtt cgt ttc taatctgcat	737	
Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg Phe		
200 205		
aaagtcttaa gct	750	

<210> 2600

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 2600

Val Gly Lys His Arg Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val
1 5 10 15

Ala Ala Ser Ala Val Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro
20 25 30

Ala Gln Ala Ala Glu Val Val Val Pro Gly Thr Gly Ile Ser Val Asp
35 40 45

Ile Ala Gly Ile Glu Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile
50 55 60

Asp Gln Trp Ile Pro Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr
65 70 75 80

Ala Ala Val Ile Asp Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser
85 90 95

Thr Gly Gln Ala Ile Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro
100 105 110

Tyr Gly Trp Gly Ala Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu
115 120 125

Thr Ser Trp Ala Tyr Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser
130 135 140

Gln Ala Gln Ala Ala Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln
145 150 155 160

Ala Gly Asp Ile Val Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile
165 170 175

Tyr Ser Gly His Gly Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro
180 185 190

Leu Ser Glu His Ser Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg
195 200 205

Phe

<210> 2601

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA02152

<400> 2601

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aaggtagcta ccggaatcaa atcttaggga aggaaaacat atg gct att tac cgt 115

Met Ala Ile Tyr Arg
1 5

aag ctt gcg gct tcc gct gca gca ctg gcc ctg tcc gca tca ctg gtc 163
Lys Leu Ala Ala Ser Ala Ala Ala Leu Ala Leu Ser Ala Ser Leu Val
10 15 20

gct tgt ggc gac tct gag gac acc acc gaa gaa acc tca acc acc tct 211
Ala Cys Gly Asp Ser Glu Asp Thr Thr Glu Glu Thr Ser Thr Thr Ser
25 30 35

tct tcg acc act tcc agc tcc tcc agc agc tct agc tcc agc acc gcg 259
Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ala
40 45 50

gct act tcc gag gaa tct tcc gca gtt gaa gag cca gca gtg gaa gct 307
Ala Thr Ser Glu Glu Ser Ser Ala Val Glu Glu Pro Ala Val Glu Ala
55 60 65

cct gtg gaa gag gct cca gtc gag gca cct gtt gag cag gca cct gtc 355
Pro Val Glu Glu Ala Pro Val Glu Ala Pro Val Glu Gln Ala Pro Val
70 75 80 85

gtg gag caa gct cca gtt gag cag gct ccg gca ccg gtt cag gaa gca 403
Val Glu Gln Ala Pro Val Glu Gln Ala Pro Ala Pro Val Gln Glu Ala
90 95 100

cct gca cca gtc gag cag gct cca gct cca gtt cag gaa gca cct gca 451
Pro Ala Pro Val Glu Gln Ala Pro Ala Pro Val Gln Glu Ala Pro Ala
105 110 115

gct gac gcg cca cct gca ctt cca ggt ggt ggc ggc gga cac gct ggc 499
Ala Asp Ala Pro Pro Ala Leu Pro Gly Gly Gly Gly Gly His Ala Gly
120 125 130

tac taataattca tgcttttacc cac 525
Tyr

<210> 2602

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 2602

Met Ala Ile Tyr Arg Lys Leu Ala Ala Ser Ala Ala Ala Leu Ala Leu
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20 25 30

Thr Ser Thr Thr Ser Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser
35 40 45

Ser Ser Ser Thr Ala Ala Thr Ser Glu Glu Ser Ser Ala Val Glu Glu
50 55 60

Pro Ala Val Glu Ala Pro Val Glu Glu Ala Pro Val Glu Ala Pro Val
65 70 75 80

<400> 2603																
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Met Ala Val Ala Thr 5																
ttc gga acc atc acc gac atg ttg gaa acc aag ggg atc gtg agc aat 163																
Phe Gly Thr Ile Thr Asp Met Leu Glu Thr Lys Gly Ile Val Ser Asn 20																
gta ggc ggc acc gac acc atc gat ttg ggc gcg ttg ttg aat gaa acc 211																
Val Gly Gly Thr Asp Thr Ile Asp Leu Gly Ala Leu Leu Asn Glu Thr 35																
caa gcc gga acc cgc tgg agc gaa ctt agc ccc aac tat cag tcc aac 259																
Gln Ala Gly Thr Arg Trp Ser Glu Leu Ser Pro Asn Tyr Gln Ser Asn 50																
cgc gtc gtg cag att tct acc acc gat gtg cgc acc tct aac tcg gcg 307																
Arg Val Val Gln Ile Ser Thr Thr Asp Val Arg Thr Ser Asn Ser Ala 65																
gcc atg tac cta tca atg atg tcc tgg gtg aaa aat ggc gga aaa acg 355																
Ala Met Tyr Leu Ser Met Met Ser Trp Val Lys Asn Gly Gly Lys Thr 85																
gtg agc agc act gcg gaa gcc gat gcc atc atc cca gag ctt agc caa 403																
Val Ser Ser Thr Ala Glu Ala Asp Ala Ile Ile Pro Glu Leu Ser Gln 100																
ctg ttc gtg ggc cag ggc tat acc gaa agc acc tcc gcc ggc ccg ttt 451																
Leu Phe Val Gly Gln Gly Tyr Thr Glu Ser Thr Ser Ala Gly Pro Phe 115																
gat gaa tac ctc tcc caa gga atg ggt tct aaa cca atg gtg atg atc 499																
Asp Glu Tyr Leu Ser Gln Gly Met Gly Ser Lys Pro Met Val Met Ile 125																

tac gaa gcc cag ttc ctc gcg gaa caa aac aag gaa aac tca cgg att 547
 Tyr Glu Ala Gln Phe Leu Ala Glu Gln Asn Lys Glu Asn Ser Arg Ile
 135 140 145
 tcc ggc gat atg gaa cta gtg tat cca agc ccc acc gtg tac agc acg 595
 Ser Gly Asp Met Glu Leu Val Tyr Pro Ser Pro Thr Val Tyr Ser Thr
 150 155 160 165
 cat acg gtg gtt agc ttg agt gac gtc ggc gcg gag atc ggc gaa ctc 643
 His Thr Val Val Ser Leu Ser Asp Val Gly Ala Glu Ile Gly Glu Leu
 170 175 180
 cta gaa acc gac gaa acc ctg cag cag ttg gca gtc aaa cac ggt ttt 691
 Leu Glu Thr Asp Glu Thr Leu Gln Gln Leu Ala Val Lys His Gly Phe
 185 190 195
 agg cca aag aac tcc gca atg atc gcc gat gct ggc atg acc gac cgc 739
 Arg Pro Lys Asn Ser Ala Met Ile Ala Asp Ala Gly Met Thr Asp Arg
 200 205 210
 atg ccc aac aac ctc aat gtc att gat ccg ccg gac tat gac ttc cta 787
 Met Pro Asn Asn Leu Asn Val Ile Asp Pro Pro Asp Tyr Asp Phe Leu
 215 220 225
 gaa cga ctc att gat ggc gtg ggc gca tcg tac agt gcc acc cca gca 835
 Glu Arg Leu Ile Asp Gly Val Gly Ala Ser Tyr Ser Ala Thr Pro Ala
 230 235 240 245
 gaa gag gac aca gat cta tgaaaaatct tgtaaaaggt aca 876
 Glu Glu Asp Thr Asp Leu
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<210> 2604

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2604

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 20 25 30
 Leu Leu Asn Glu Thr Gln Ala Gly Thr Arg Trp Ser Glu Leu Ser Pro
 35 40 45
 Asn Tyr Gln Ser Asn Arg Val Val Gln Ile Ser Thr Thr Asp Val Arg
 50 55 60
 Thr Ser Asn Ser Ala Ala Met Tyr Leu Ser Met Met Ser Trp Val Lys
 65 70 75 80
 Asn Gly Gly Lys Thr Val Ser Ser Thr Ala Glu Ala Asp Ala Ile Ile
 85 90 95
 Pro Glu Leu Ser Gln Leu Phe Val Gly Gln Gly Tyr Thr Glu Ser Thr
 100 105 110

Ser Ala Gly Pro Phe Asp Glu Tyr Leu Ser Gln Gly Met Gly Ser Lys
 115 120 125

Pro Met Val Met Ile Tyr Glu Ala Gln Phe Leu Ala Glu Gln Asn Lys
 130 135 140

Glu Asn Ser Arg Ile Ser Gly Asp Met Glu Leu Val Tyr Pro Ser Pro
 145 150 155 160

Thr Val Tyr Ser Thr His Thr Val Val Ser Leu Ser Asp Val Gly Ala
 165 170 175

Glu Ile Gly Glu Leu Leu Glu Thr Asp Glu Thr Leu Gln Gln Leu Ala
 180 185 190

Val Lys His Gly Phe Arg Pro Lys Asn Ser Ala Met Ile Ala Asp Ala
 195 200 205

Gly Met Thr Asp Arg Met Pro Asn Asn Leu Asn Val Ile Asp Pro Pro
 210 215 220

Asp Tyr Asp Phe Leu Glu Arg Leu Ile Asp Gly Val Gly Ala Ser Tyr
 225 230 235 240

Ser Ala Thr Pro Ala Glu Glu Asp Thr Asp Leu
 245 250

<210> 2605

<211> 1698

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1675)

<223> RXA02164

<400> 2605

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catcgtacag tgccacccca gcagaagagg acacagatct atg aaa aat ctt gta 115
 Met Lys Asn Leu Val
 1 5

aaa ggt aca gcg ctg ggc ttg agc ttg gtg ctt ctg gca ggt tgt tca 163
 Lys Gly Thr Ala Leu Gly Leu Ser Leu Val Leu Leu Ala Gly Cys Ser
 10 15 20

act gtt tcg gat tct atc gat agc ctc ggc ggg ggc ctg ggt ggt tcc 211
 Thr Val Ser Asp Ser Ile Asp Ser Leu Gly Gly Gly Leu Gly Gly Ser
 25 30 35

tct gag act ttg aag att gtg gcc gcc aca gag ctg gaa gat ctg cag 259
 Ser Glu Thr Leu Lys Ile Val Ala Ala Thr Glu Leu Glu Asp Leu Gln
 40 45 50

ccc gcg atc gag caa gcc tcc gac gac ttg ggt ttt gat att gaa ctg 307
 Pro Ala Ile Glu Gln Ala Ser Asp Asp Leu Gly Phe Asp Ile Glu Leu
 55 60 65

agc ttt cca ggc ggc aca ctc agc aac agc caa gcc ctc atg gat ggc	355
Ser Phe Pro Gly Gly Thr Leu Ser Asn Ser Gln Ala Leu Met Asp Gly	
70 75 80 85	
gct ttt gac cag gac tat gat gcc acc tgg ttt gcc acc aac cgt tac	403
Ala Phe Asp Gln Asp Tyr Asp Ala Thr Trp Phe Ala Thr Asn Arg Tyr	
90 95 100	
gtc gat ctg atc ggc gct tcc aac aag ctg ggg gag acc acc aaa atc	451
Val Asp Leu Ile Gly Ala Ser Asn Lys Leu Gly Glu Thr Thr Lys Ile	
105 110 115	
gcg acc tct ccc gtg gcg ttc ggt gtg aaa act tcc atg gcc cag gag	499
Ala Thr Ser Pro Val Ala Phe Gly Val Lys Thr Ser Met Ala Gln Glu	
120 125 130	
ctc ggc tgg gat cag cgc cag cca acc tgg gaa gag ctg ggc cag gcc	547
Leu Gly Trp Asp Gln Arg Gln Pro Thr Trp Glu Glu Leu Gly Gln Ala	
135 140 145	
tcg cag acc caa gat ttc acc ttc ggt atg acc gat ccg gcc act tcc	595
Ser Gln Thr Gln Asp Phe Thr Phe Gly Met Thr Asp Pro Ala Thr Ser	
150 155 160 165	
aac tcc gga ttt tcc gcg ctc gtt gcc atg gcc acg gca tat gct gat	643
Asn Ser Gly Phe Ser Ala Leu Val Ala Met Ala Thr Ala Tyr Ala Asp	
170 175 180	
acc ggc cag gcc tta aca acc aac gac atc ccc gcg atc gcc gag ccg	691
Thr Gly Gln Ala Leu Thr Thr Asn Asp Ile Pro Ala Ile Ala Glu Pro	
185 190 195	
atg tcc aca tcc ctt tcc ggc caa acc atc acc tcc ggt tcc tct ggc	739
Met Ser Thr Ser Leu Ser Gly Gln Thr Ile Thr Ser Gly Ser Ser Gly	
200 205 210	
tgg ctc aaa gac act ttc ctg gaa cag cct gac cgc gcg aat gcg atc	787
Trp Leu Lys Asp Thr Phe Leu Glu Gln Pro Asp Arg Ala Asn Ala Ile	
215 220 225	
atc aac tac gag tcc gtc ctg cac acc atg atc agc gaa gac ggc gcc	835
Ile Asn Tyr Glu Ser Val Leu His Thr Met Ile Ser Glu Asp Gly Ala	
230 235 240 245	
gat atc acc gtc gtg gtg ccc gcc gat ggc gtg gtc agc gcc gat tac	883
Asp Ile Thr Val Val Val Pro Ala Asp Gly Val Val Ser Ala Asp Tyr	
250 255 260	
ccg ctc tct acg atc acg ggc tcc gac cag ggc gag cat gta gca gag	931
Pro Leu Ser Thr Ile Thr Gly Ser Asp Gln Gly Glu His Val Ala Glu	
265 270 275	
ctg gcc ggc tgg ttc gct gag cac ccc gac gct tta aca gat act tat	979
Leu Ala Gly Trp Phe Ala Glu His Pro Asp Ala Leu Thr Asp Thr Tyr	
280 285 290	
cga cgt ccg acc acc gcg aac gca acg ctc cca gcg gag ctt agc tcg	1027
Arg Arg Pro Thr Thr Ala Asn Ala Thr Leu Pro Ala Glu Leu Ser Ser	
295 300 305	
cag acc atc atc gaa gct ccc ttc cca ggg agc aag acg gtc acc gac	1075

Gln Thr Ile Ile Glu Ala Pro Phe Pro Gly Ser Lys Thr Val Thr Asp
 310 315 320 325
 gcg ctt atc gac gcc tac acc aat caa ttc cgc gtc cca ggc gaa acc 1123
 Ala Leu Ile Asp Ala Tyr Thr Asn Gln Phe Arg Val Pro Gly Glu Thr
 330 335 340
 acc ttt gtg ctc gac gtt tcc gga tcc atg ctg ggc cag cgc atc acc 1171
 Thr Phe Val Leu Asp Val Ser Gly Ser Met Leu Gly Gln Arg Ile Thr
 345 350 355
 ttg ctc aaa gac acc atg tca gac ctg atc agc ggc ggc gcg acc act 1219
 Leu Leu Lys Asp Thr Met Ser Asp Leu Ile Ser Gly Gly Ala Thr Thr
 360 365 370
 gac ctt gcc aac gtg tcc ctg cgc gac cgc gaa aaa gta tcg atc att 1267
 Asp Leu Ala Asn Val Ser Leu Arg Asp Arg Glu Lys Val Ser Ile Ile
 375 380 385
 cct ttc agc ttc ggg cca cac gaa gta atc agc gaa acc ctc ggt gcg 1315
 Pro Phe Ser Phe Gly Pro His Glu Val Ile Ser Glu Thr Leu Gly Ala
 390 395 400 405
 gtg ggc agc cca agc cgc acc gat ctg cag cag cgc gtt gaa gcc ttg 1363
 Val Gly Ser Pro Ser Arg Thr Asp Leu Gln Gln Arg Val Glu Ala Leu
 410 415 420
 caa gca gac ggc gga acc gga att tac gac gca gtg ctc gcc gcc tac 1411
 Gln Ala Asp Gly Gly Thr Gly Ile Tyr Asp Ala Val Leu Ala Ala Tyr
 425 430 435
 gca gag tcc gct ggt ggc gac tac atc cca tcc atc gtg ctc atg acc 1459
 Ala Glu Ser Ala Gly Gly Asp Tyr Ile Pro Ser Ile Val Leu Met Thr
 440 445 450
 gac ggc gaa ctc acc gca gga cga acc tac gat caa ttc ctc acc gaa 1507
 Asp Gly Glu Leu Thr Ala Gly Arg Thr Tyr Asp Gln Phe Leu Thr Glu
 455 460 465
 tgg aac gcg ctt cct agc aat atc cga tca att cca gtg ttt gtc atc 1555
 Trp Asn Ala Leu Pro Ser Asn Ile Arg Ser Ile Pro Val Phe Val Ile
 470 475 480 485
 ctt tac ggt gaa gcc aat gtt gcg gat atg gaa caa ttg gca gca aca 1603
 Leu Tyr Gly Glu Ala Asn Val Ala Asp Met Glu Gln Leu Ala Ala Thr
 490 495 500
 acc ggc ggt gag acc ttt gac gcc atc aac ggt gac cta gac gaa gca 1651
 Thr Gly Gly Glu Thr Phe Asp Ala Ile Asn Gly Asp Leu Asp Glu Ala
 505 510 515
 ttt aag gag att cgt gcc tac caa taatggagga tccttctttt tct 1698
 Phe Lys Glu Ile Arg Ala Tyr Gln
 520 525

<210> 2606

<211> 525

<212> PRT

<213> Corynebacterium glutamicum

<400> 2606

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 Leu Ala Gly Cys Ser Thr Val Ser Asp Ser Ile Asp Ser Leu Gly Gly
 20 25 30
 Gly Leu Gly Gly Ser Ser Glu Thr Leu Lys Ile Val Ala Ala Thr Glu
 35 40 45
 Leu Glu Asp Leu Gln Pro Ala Ile Glu Gln Ala Ser Asp Asp Leu Gly
 50 55 60
 Phe Asp Ile Glu Leu Ser Phe Pro Gly Gly Thr Leu Ser Asn Ser Gln
 65 70 75 80
 Ala Leu Met Asp Gly Ala Phe Asp Gln Asp Tyr Asp Ala Thr Trp Phe
 85 90 95
 Ala Thr Asn Arg Tyr Val Asp Leu Ile Gly Ala Ser Asn Lys Leu Gly
 100 105 110
 Glu Thr Thr Lys Ile Ala Thr Ser Pro Val Ala Phe Gly Val Lys Thr
 115 120 125
 Ser Met Ala Gln Glu Leu Gly Trp Asp Gln Arg Gln Pro Thr Trp Glu
 130 135 140
 Glu Leu Gly Gln Ala Ser Gln Thr Gln Asp Phe Thr Phe Gly Met Thr
 145 150 155 160
 Asp Pro Ala Thr Ser Asn Ser Gly Phe Ser Ala Leu Val Ala Met Ala
 165 170 175
 Thr Ala Tyr Ala Asp Thr Gly Gln Ala Leu Thr Thr Asn Asp Ile Pro
 180 185 190
 Ala Ile Ala Glu Pro Met Ser Thr Ser Leu Ser Gly Gln Thr Ile Thr
 195 200 205
 Ser Gly Ser Ser Gly Trp Leu Lys Asp Thr Phe Leu Glu Gln Pro Asp
 210 215 220
 Arg Ala Asn Ala Ile Ile Asn Tyr Glu Ser Val Leu His Thr Met Ile
 225 230 235 240
 Ser Glu Asp Gly Ala Asp Ile Thr Val Val Val Pro Ala Asp Gly Val
 245 250 255
 Val Ser Ala Asp Tyr Pro Leu Ser Thr Ile Thr Gly Ser Asp Gln Gly
 260 265 270
 Glu His Val Ala Glu Leu Ala Gly Trp Phe Ala Glu His Pro Asp Ala
 275 280 285
 Leu Thr Asp Thr Tyr Arg Arg Pro Thr Thr Ala Asn Ala Thr Leu Pro
 290 295 300
 Ala Glu Leu Ser Ser Gln Thr Ile Ile Glu Ala Pro Phe Pro Gly Ser
 305 310 315 320


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gca acg ctg att atc gcg ctg cac tta gtg atc gga ctc gga gca ttt 211
Ala Thr Leu Ile Ile Ala Leu His Leu Val Ile Gly Leu Gly Ala Phe
      25                      30                      35

tgg cct gtt gtc gcc atc gcc gga tac ggc gct gcg gtg gca ctt aca 259
Trp Pro Val Val Ala Ile Ala Gly Tyr Gly Ala Ala Val Ala Leu Thr
      40                      45                      50

cct aaa aac cct ccg aag aag gaa ctc cct ccg gtt cag gca act ccc 307
Pro Lys Asn Pro Pro Lys Lys Glu Leu Pro Pro Val Gln Ala Thr Pro
      55                      60                      65

gaa tta gat agc ccg ggt ctg ctt gca gcc agg tct caa gaa ctc gtg 355
Glu Leu Asp Ser Pro Gly Leu Leu Ala Ala Arg Ser Gln Glu Leu Val
      70                      75                      80                      85

aga act atg tat agc cac ggt gct gca gca cca gtg atc gaa gcg att 403
Arg Thr Met Tyr Ser His Gly Ala Ala Ala Pro Val Ile Glu Ala Ile
      90                      95                      100

aag agg cta gac agc tca ctg caa ttg gtc att ggt aac tgg aca agc 451
Lys Arg Leu Asp Ser Ser Leu Gln Leu Val Ile Gly Asn Trp Thr Ser
      105                      110                      115

ctg acc aat ttt ccc gag cac caa gtc acc att cgc tca att atc aac 499
Leu Thr Asn Phe Pro Glu His Gln Val Thr Ile Arg Ser Ile Ile Asn
      120                      125                      130

cag tac atc cca ggc att atc gac gct tac ctg aag atc ccc acc cgc 547
Gln Tyr Ile Pro Gly Ile Ile Asp Ala Tyr Leu Lys Ile Pro Thr Arg
      135                      140                      145

aac gat cct cgg gca gtc gaa gac ctc att gaa tcc ttc gac ctc ctg 595
Asn Asp Pro Arg Ala Val Glu Asp Leu Ile Glu Ser Phe Asp Leu Leu
      150                      155                      160                      165

aac tcc gag acg atg aag atc ttc aat gcg atc caa gaa caa ggc ctt 643
Asn Ser Glu Thr Met Lys Ile Phe Asn Ala Ile Gln Glu Gln Gly Leu
      170                      175                      180

aat aac ctt gaa gat cac ggt cgc gca ctg cgc atg caa ttt ggt caa 691
Asn Asn Leu Glu Asp His Gly Arg Ala Leu Arg Met Gln Phe Gly Gln
      185                      190                      195

ctg cca gaa gaa ttc cgg gaa tagccactca atgcagttaa gtt 735
Leu Pro Glu Glu Phe Arg Glu
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<210> 2608

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 2608

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Val Pro Thr Asn Asn Gly Gly Ser Phe Phe Phe Ser Arg Lys Asn Leu
  1                      5                      10                      15

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Ala Gly Ile Ala Ile Ala Thr Leu Ile Ile Ala Leu His Leu Val Ile
  20                      25                      30

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<210> 2609
<211> 300
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(277)  
<223> RXA02166
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caatgcagtt aagtttttcc tgcccggtag gatgggtccgt atg agt ctt gat cca 115
Met Ser Leu Asp Pro
1 5
cag ctt ctt gaa gtc ctg gcc tgc cca aag gac aag ggc cca ctt cga 163
Gln Leu Leu Glu Val Leu Ala Cys Pro Lys Asp Lys Gly Pro Leu Arg
10 15 20
tat ctg gag agc gaa cag ctc ttg gtc aac gaa cgc ctc aac ctg gcc 211
Tyr Leu Glu Ser Glu Gln Leu Leu Val Asn Glu Arg Leu Asn Leu Ala
25 30 35
tat cgc att gac gac gga att ccg gtg ctt ctc atc gac gaa gcc acc 259
Tyr Arg Ile Asp Asp Gly Ile Pro Val Leu Leu Ile Asp Glu Ala Thr

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40 45 50

gag tgg acc ccc aac aac tagaagtaca tcaaggacat ttt 300
 Glu Trp Thr Pro Asn Asn
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<210> 2610
 <211> 59
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2610
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 1 5 10 15
 Lys Gly Pro Leu Arg Tyr Leu Glu Ser Glu Gln Leu Leu Val Asn Glu
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 Arg Leu Asn Leu Ala Tyr Arg Ile Asp Asp Gly Ile Pro Val Leu Leu
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 Ile Asp Glu Ala Thr Glu Trp Thr Pro Asn Asn
 50 55

<210> 2611
 <211> 2937
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2914)
 <223> RXA02168

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 Val Ser Ile Ser Ser
 1 5
 ctg aca ccg ctg cac tct ttc aaa gag cca gca att ctg tac gcc ggt 163
 Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala Ile Leu Tyr Ala Gly
 10 15 20
 cag gct tct gcc tgg cag cag gtg atc gct gat tcc agc gaa gac cac 211
 Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp Ser Ser Glu Asp His
 25 30 35
 atc acc gca acg cac ctg cgc gag ctc ctg tct cgc tcc cgt gca aag 259
 Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser Arg Ser Arg Ala Lys
 40 45 50
 act gca cct ttc gct cgc caa atc acc gcc atc gtg cct ggc tca ctt 307
 Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile Val Pro Gly Ser Leu
 55 60 65
 gct cgt ctt gag gaa ctg acc cgc gaa gac gca caa atc ggt gca gac 355
 Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala Gln Ile Gly Ala Asp

70	75	80	85	
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atc gct gca acc cgt cag ctg cgt gac ctc gga ctc gat gtc gca gca Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly Leu Asp Val Ala Ala 105 110 115				451
gct tcc cgc ctt gga cac tcc cag ggc att ttg ggc gtt gaa gca gta Ala Ser Arg Leu Gly His Ser Gln Gly Ile Leu Gly Val Glu Ala Val 120 125 130				499
gac aat gaa gaa gac gtt tta gct ttc gcc atc ctg ctg ggc gca gca Asp Asn Glu Glu Asp Val Leu Ala Phe Ala Ile Leu Leu Gly Ala Ala 135 140 145				547
gct tcc cag ttc gct ggc aag ggc gca cat atg ctc tct gtt cgc ggc Ala Ser Gln Phe Ala Gly Lys Gly Ala His Met Leu Ser Val Arg Gly 150 155 160 165				595
ctg tcc cgt gag atc atc cag gac acc atc gct ggt gtc gat ggg gta Leu Ser Arg Glu Ile Ile Gln Asp Thr Ile Ala Gly Val Asp Gly Val 170 175 180				643
gag gtc tcc ctg cgc aac gct cgt gca cac ttt gtt gtc tct ggt aag Glu Val Ser Leu Arg Asn Ala Arg Ala His Phe Val Val Ser Gly Lys 185 190 195				691
cca gag gca ctg aag aag gct gct gct gct cta cag cgc gca gct gat Pro Glu Ala Leu Lys Lys Ala Ala Ala Leu Gln Arg Ala Ala Asp 200 205 210				739
gtt tac aac gaa gac atc aac gaa aag cgc aag ggt gga tcc ctg gca Val Tyr Asn Glu Asp Ile Asn Glu Lys Arg Lys Gly Gly Ser Leu Ala 215 220 225				787
gag cct aag ttt gac tac ttg gat gtg gcc att cct ttc cac cac tcc Glu Pro Lys Phe Asp Tyr Leu Asp Val Ala Ile Pro Phe His His Ser 230 235 240 245				835
tcc atg cag gac gca gcc gac ttg gct gtc gag tgg gca acc acc tgt Ser Met Gln Asp Ala Ala Asp Leu Ala Val Glu Trp Ala Thr Thr Cys 250 255 260				883
ggc cta aac gtc aac gcg cgc gcg ttg gca gaa gca att cta gtt aac Gly Leu Asn Val Asn Ala Arg Ala Leu Ala Glu Ala Ile Leu Val Asn 265 270 275				931
cca gct gac tgg gtt gag cag atc gca aac ctc aag gct gat tac gtt Pro Ala Asp Trp Val Glu Gln Ile Ala Asn Leu Lys Ala Asp Tyr Val 280 285 290				979
ctt tcc ctc gat gca ggc gtc agc cgt ttc acc gct cca ttg cta gac Leu Ser Leu Asp Ala Gly Val Ser Arg Phe Thr Ala Pro Leu Leu Asp 295 300 305				1027
ggt cgc gga atc tct ttg gtt cct gcg ttc tcc gct gca gag cgc gac Gly Arg Gly Ile Ser Leu Val Pro Ala Phe Ser Ala Ala Glu Arg Asp 310 315 320 325				1075

aac ttg gct cgc cct ggc ttc cac gtt cct acc gct gag gat tgg tcc	1123
Asn Leu Ala Arg Pro Gly Phe His Val Pro Thr Ala Glu Asp Trp Ser	
330 335 340	
gag ttc gct cca aag ctg gtt aag ctt cca aac ggt gag cac aag gtt	1171
Glu Phe Ala Pro Lys Leu Val Lys Leu Pro Asn Gly Glu His Lys Val	
345 350 355	
ctc acc ggg ttc tcc cgc ctg act ggt tat tcc cca atc gtc ctg gct	1219
Leu Thr Gly Phe Ser Arg Leu Thr Gly Tyr Ser Pro Ile Val Leu Ala	
360 365 370	
ggc atg acc cca acc acc gtt gat cct gag atc gtt gca gct gca gcg	1267
Gly Met Thr Pro Thr Thr Val Asp Pro Glu Ile Val Ala Ala Ala Ala	
375 380 385	
aac gct gga cac tgg gcc gaa atg gcc ggt ggc gga cag tac tct gaa	1315
Asn Ala Gly His Trp Ala Glu Met Ala Gly Gly Gly Gln Tyr Ser Glu	
390 395 400 405	
gaa gtc ttc acc aag aac aag gaa aag ctc gtt tcc ctg ctg aag gtt	1363
Glu Val Phe Thr Lys Asn Lys Glu Lys Leu Val Ser Leu Leu Lys Val	
410 415 420	
gga cgc tcc gca cag ttc aac tcc atg ttc ttc gac cgc tac atg tgg	1411
Gly Arg Ser Ala Gln Phe Asn Ser Met Phe Phe Asp Arg Tyr Met Trp	
425 430 435	
aac ctg cag ttc ggt gca cag cgc atc gtt tcc aag gca cgt gca acc	1459
Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser Lys Ala Arg Ala Thr	
440 445 450	
ggt acc tcc atc aac ggt gtt gtt gtc tcc gct ggt atc cca gag gtt	1507
Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala Gly Ile Pro Glu Val	
455 460 465	
gag gaa gca act gag ctg atc aac gat ctg aac gct gat ggc ttc cca	1555
Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn Ala Asp Gly Phe Pro	
470 475 480 485	
tac gtt gca ttc aag cca ggc acc gtg gat cag atc cgc gca acc ctg	1603
Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln Ile Arg Ala Thr Leu	
490 495 500	
aag att gct gat gca aac cca gag acc aag atc atc atc cag atc gag	1651
Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile Ile Ile Gln Ile Glu	
505 510 515	
gac gga cac gct ggt ggc cac cac tcc tgg gtc aac ttg gac gat ctg	1699
Asp Gly His Ala Gly Gly His His Ser Trp Val Asn Leu Asp Asp Leu	
520 525 530	
ctc ctg acc acc tac gca gag ctg cgt tcc cgc aag aac gtt gtc gtc	1747
Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg Lys Asn Val Val Val	
535 540 545	
atg atc ggt ggc ggc atc gga acc cct gca aag gct gct tac tac ctg	1795
Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys Ala Ala Tyr Tyr Leu	
550 555 560 565	

acc ggt gaa tgg tcc acc gat ttg ggc ttc cca gca atg cca gtg gac	1843
Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro Ala Met Pro Val Asp	
570 575 580	
ggc atc ctc gtg ggt acc gct gcc atg gca acc aag gaa gca acc act	1891
Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr Thr	
585 590 595	
tct cct cag gtc aag cag gca ctg gtc gac acc cca ggt gtt gat cca	1939
Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr Pro Gly Val Asp Pro	
600 605 610	
cac gac gct ggc ggc tgg gtt ggc cgt ggc gat gct cgt ggt ggc gtg	1987
His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp Ala Arg Gly Gly Val	
615 620 625	
acc tct ggt ctg tca cac ctg cac gct gac atg tac gag ctg gac aac	2035
Thr Ser Gly Leu Ser His Leu His Ala Asp Met Tyr Glu Leu Asp Asn	
630 635 640 645	
gat tct gct gca gct tcc cgc ctg atc tct tcc atc gat tct gat gat	2083
Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser Ile Asp Ser Asp Asp	
650 655 660	
tac gca gat cac cgc gaa gag ctc atc gag gct atc aac aag acc gct	2131
Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala Ile Asn Lys Thr Ala	
665 670 675	
aag cct ttc ttc ggc gag gtc gaa gag atg act tac gca gag tgg atc	2179
Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr Tyr Ala Glu Trp Ile	
680 685 690	
cag cgt tgg gtt gag ctt gct tac cca act cag gac cca acc tgg gat	2227
Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln Asp Pro Thr Trp Asp	
695 700 705	
gat cgt ttc ctc gat ttg gtt cac cgc att gaa gct cgt ctc aac gag	2275
Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu Ala Arg Leu Asn Glu	
710 715 720 725	
gca gag cac ggc gcc atc acc aca ctg ttc cca gac cat gcg tct gtg	2323
Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro Asp His Ala Ser Val	
730 735 740	
gaa aat gag gaa gag gcc gtc gaa aag ctt ctt gct gct tac ccg cag	2371
Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu Ala Ala Tyr Pro Gln	
745 750 755	
gcc cgc gag atc cag gtc tct gcg cgc gac gcc gcg tgg ttt att ggt	2419
Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala Ala Trp Phe Ile Gly	
760 765 770	
ctg tgc cgc aag cac cac aag cct atg cct tgg gtt cca gca atc gat	2467
Leu Cys Arg Lys His His Lys Pro Met Pro Trp Val Pro Ala Ile Asp	
775 780 785	
gct gac cta gca cgc tgg tgg ggc ctt gac acc ctg tgg cag tcc cag	2515
Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr Leu Trp Gln Ser Gln	
790 795 800 805	
aac gag cgc tac ggc gcg aac tca gtc cgc gtt atc cca gga cca gtc	2563

Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val Ile Pro Gly Pro Val
 810 815 820
 tcc gtc gcc ggc atc gac cgt gtt gac gag cca gtt gca gag ctg ctc 2611
 Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro Val Ala Glu Leu Leu
 825 830 835
 ggc cgc ttc gaa gct gcc tgc gtt gac gct ctc gac ggc gag cca gaa 2659
 Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu Asp Gly Glu Pro Glu
 840 845 850
 gag atc ttc gct cgc ctc aat gag tcc aag aac gag cgc gaa ttc ctg 2707
 Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn Glu Arg Glu Phe Leu
 855 860 865
 ctg gct acc cca cac atc gtg tgg cac ggc aac ctg atc gac aac cca 2755
 Leu Ala Thr Pro His Ile Val Trp His Gly Asn Leu Ile Asp Asn Pro
 870 875 880 885
 gct cac gtc ctc aac gag ggt gct ttc gag ctc atc gag gag gat ggc 2803
 Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu Ile Glu Glu Asp Gly
 890 895 900
 tac tgg gtc atc cgt atc ctg gct gat tcc tac ttc gac gat ctg cca 2851
 Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr Phe Asp Asp Leu Pro
 905 910 915
 gtt gag cag cgc cca tac ctg gtt cag cat gtt gac atc cca gtt gag 2899
 Val Glu Gln Arg Pro Tyr Leu Val Gln His Val Asp Ile Pro Val Glu
 920 925 930
 ctg ggt gac gct ggt tgaaccggtg gtttcccaat tgg 2937
 Leu Gly Asp Ala Gly
 935

<210> 2612

<211> 938

<212> PRT

<213> Corynebacterium glutamicum

<400> 2612

Val Ser Ile Ser Ser Leu Thr Pro Leu His Ser Phe Lys Glu Pro Ala
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 20 25 30
 Ser Ser Glu Asp His Ile Thr Ala Thr His Leu Arg Glu Leu Leu Ser
 35 40 45
 Arg Ser Arg Ala Lys Thr Ala Pro Phe Ala Arg Gln Ile Thr Ala Ile
 50 55 60
 Val Pro Gly Ser Leu Ala Arg Leu Glu Glu Leu Thr Arg Glu Asp Ala
 65 70 75 80
 Gln Ile Gly Ala Asp Ile Asp Ala Gln Pro Ala Val Ser Ile Pro Gly
 85 90 95
 Ile Leu Leu Gly Gln Ile Ala Ala Thr Arg Gln Leu Arg Asp Leu Gly

100					105					110					
Leu	Asp	Val	Ala	Ala	Ala	Ser	Arg	Leu	Gly	His	Ser	Gln	Gly	Ile	Leu
	115						120					125			
Gly	Val	Glu	Ala	Val	Asp	Asn	Glu	Glu	Asp	Val	Leu	Ala	Phe	Ala	Ile
	130					135					140				
Leu	Leu	Gly	Ala	Ala	Ala	Ser	Gln	Phe	Ala	Gly	Lys	Gly	Ala	His	Met
145					150					155					160
Leu	Ser	Val	Arg	Gly	Leu	Ser	Arg	Glu	Ile	Ile	Gln	Asp	Thr	Ile	Ala
				165					170					175	
Gly	Val	Asp	Gly	Val	Glu	Val	Ser	Leu	Arg	Asn	Ala	Arg	Ala	His	Phe
			180					185					190		
Val	Val	Ser	Gly	Lys	Pro	Glu	Ala	Leu	Lys	Lys	Ala	Ala	Ala	Ala	Leu
		195					200					205			
Gln	Arg	Ala	Ala	Asp	Val	Tyr	Asn	Glu	Asp	Ile	Asn	Glu	Lys	Arg	Lys
	210					215					220				
Gly	Gly	Ser	Leu	Ala	Glu	Pro	Lys	Phe	Asp	Tyr	Leu	Asp	Val	Ala	Ile
225					230					235					240
Pro	Phe	His	His	Ser	Ser	Met	Gln	Asp	Ala	Ala	Asp	Leu	Ala	Val	Glu
				245					250					255	
Trp	Ala	Thr	Thr	Cys	Gly	Leu	Asn	Val	Asn	Ala	Arg	Ala	Leu	Ala	Glu
			260					265					270		
Ala	Ile	Leu	Val	Asn	Pro	Ala	Asp	Trp	Val	Glu	Gln	Ile	Ala	Asn	Leu
	275						280					285			
Lys	Ala	Asp	Tyr	Val	Leu	Ser	Leu	Asp	Ala	Gly	Val	Ser	Arg	Phe	Thr
	290					295					300				
Ala	Pro	Leu	Leu	Asp	Gly	Arg	Gly	Ile	Ser	Leu	Val	Pro	Ala	Phe	Ser
305					310					315					320
Ala	Ala	Glu	Arg	Asp	Asn	Leu	Ala	Arg	Pro	Gly	Phe	His	Val	Pro	Thr
				325					330					335	
Ala	Glu	Asp	Trp	Ser	Glu	Phe	Ala	Pro	Lys	Leu	Val	Lys	Leu	Pro	Asn
			340					345					350		
Gly	Glu	His	Lys	Val	Leu	Thr	Gly	Phe	Ser	Arg	Leu	Thr	Gly	Tyr	Ser
		355					360					365			
Pro	Ile	Val	Leu	Ala	Gly	Met	Thr	Pro	Thr	Thr	Val	Asp	Pro	Glu	Ile
	370					375					380				
Val	Ala	Ala	Ala	Ala	Asn	Ala	Gly	His	Trp	Ala	Glu	Met	Ala	Gly	Gly
385					390					395					400
Gly	Gln	Tyr	Ser	Glu	Glu	Val	Phe	Thr	Lys	Asn	Lys	Glu	Lys	Leu	Val
				405					410					415	
Ser	Leu	Leu	Lys	Val	Gly	Arg	Ser	Ala	Gln	Phe	Asn	Ser	Met	Phe	Phe
			420					425					430		

Asp Arg Tyr Met Trp Asn Leu Gln Phe Gly Ala Gln Arg Ile Val Ser
435 440 445

Lys Ala Arg Ala Thr Gly Thr Ser Ile Asn Gly Val Val Val Ser Ala
450 455 460

Gly Ile Pro Glu Val Glu Glu Ala Thr Glu Leu Ile Asn Asp Leu Asn
465 470 475 480

Ala Asp Gly Phe Pro Tyr Val Ala Phe Lys Pro Gly Thr Val Asp Gln
485 490 495

Ile Arg Ala Thr Leu Lys Ile Ala Asp Ala Asn Pro Glu Thr Lys Ile
500 505 510

Ile Ile Gln Ile Glu Asp Gly His Ala Gly Gly His His Ser Trp Val
515 520 525

Asn Leu Asp Asp Leu Leu Leu Thr Thr Tyr Ala Glu Leu Arg Ser Arg
530 535 540

Lys Asn Val Val Val Met Ile Gly Gly Gly Ile Gly Thr Pro Ala Lys
545 550 555 560

Ala Ala Tyr Tyr Leu Thr Gly Glu Trp Ser Thr Asp Leu Gly Phe Pro
565 570 575

Ala Met Pro Val Asp Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr
580 585 590

Lys Glu Ala Thr Thr Ser Pro Gln Val Lys Gln Ala Leu Val Asp Thr
595 600 605

Pro Gly Val Asp Pro His Asp Ala Gly Gly Trp Val Gly Arg Gly Asp
610 615 620

Ala Arg Gly Gly Val Thr Ser Gly Leu Ser His Leu His Ala Asp Met
625 630 635 640

Tyr Glu Leu Asp Asn Asp Ser Ala Ala Ala Ser Arg Leu Ile Ser Ser
645 650 655

Ile Asp Ser Asp Asp Tyr Ala Asp His Arg Glu Glu Leu Ile Glu Ala
660 665 670

Ile Asn Lys Thr Ala Lys Pro Phe Phe Gly Glu Val Glu Glu Met Thr
675 680 685

Tyr Ala Glu Trp Ile Gln Arg Trp Val Glu Leu Ala Tyr Pro Thr Gln
690 695 700

Asp Pro Thr Trp Asp Asp Arg Phe Leu Asp Leu Val His Arg Ile Glu
705 710 715 720

Ala Arg Leu Asn Glu Ala Glu His Gly Ala Ile Thr Thr Leu Phe Pro
725 730 735

Asp His Ala Ser Val Glu Asn Glu Glu Glu Ala Val Glu Lys Leu Leu
740 745 750

Ala Ala Tyr Pro Gln Ala Arg Glu Ile Gln Val Ser Ala Arg Asp Ala
 755 760 765

Ala Trp Phe Ile Gly Leu Cys Arg Lys His His Lys Pro Met Pro Trp
 770 775 780

Val Pro Ala Ile Asp Ala Asp Leu Ala Arg Trp Trp Gly Leu Asp Thr
 785 790 795 800

Leu Trp Gln Ser Gln Asn Glu Arg Tyr Gly Ala Asn Ser Val Arg Val
 805 810 815

Ile Pro Gly Pro Val Ser Val Ala Gly Ile Asp Arg Val Asp Glu Pro
 820 825 830

Val Ala Glu Leu Leu Gly Arg Phe Glu Ala Ala Cys Val Asp Ala Leu
 835 840 845

Asp Gly Glu Pro Glu Glu Ile Phe Ala Arg Leu Asn Glu Ser Lys Asn
 850 855 860

Glu Arg Glu Phe Leu Leu Ala Thr Pro His Ile Val Trp His Gly Asn
 865 870 875 880

Leu Ile Asp Asn Pro Ala His Val Leu Asn Glu Gly Ala Phe Glu Leu
 885 890 895

Ile Glu Glu Asp Gly Tyr Trp Val Ile Arg Ile Leu Ala Asp Ser Tyr
 900 905 910

Phe Asp Asp Leu Pro Val Glu Gln Arg Pro Tyr Leu Val Gln His Val
 915 920 925

Asp Ile Pro Val Glu Leu Gly Asp Ala Gly
 930 935

<210> 2613

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA02170

<400> 2613

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ggacgtgtca agaacttcta aggttcaccc gggatggcgg gtg tct act gtc ctt 115
 Val Ser Thr Val Leu
 1 5

tta gca gga gta gtt att att ggc gga att ttt act ctc cct cag aag 163
 Leu Ala Gly Val Val Ile Ile Gly Gly Ile Phe Thr Leu Pro Gln Lys
 10 15 20

gag gaa gta aag gtt tcc gaa ttg cag cca cag gcc agc gct gca tcc 211
 Glu Glu Val Lys Val Ser Glu Leu Gln Pro Gln Ala Ser Ala Ala Ser
 25 30 35

atc ccg tct tca tct tcc aca gct ggg aaa gca gtg gaa gaa agc cct 259
 Ile Pro Ser Ser Ser Ser Thr Ala Gly Lys Ala Val Glu Glu Ser Pro
 40 45 50

cta acg cag ttt gtg gaa aac tcg aca ggc tcc caa att acg tac atg 307
 Leu Thr Gln Phe Val Glu Asn Ser Thr Gly Ser Gln Ile Thr Tyr Met
 55 60 65

agc ctg aaa gac gat ttc cat act ggc acg tct acg gaa cgt ttt gcg 355
 Ser Leu Lys Asp Asp Phe His Thr Gly Thr Ser Thr Glu Arg Phe Ala
 70 75 80 85

cgc cca gcg tta agt ttg tct aag ctc tac atc gct gaa tat gtg ctc 403
 Arg Pro Ala Leu Ser Leu Ser Lys Leu Tyr Ile Ala Glu Tyr Val Leu
 90 95 100

gag cac ggc acg aat aat gag aag tct ttg gcg atg gaa atg atc aaa 451
 Glu His Gly Thr Asn Asn Glu Lys Ser Leu Ala Met Glu Met Ile Lys
 105 110 115

gat tcc tcc gac gta tcc gcc gaa atc ttg tat gag gcg tac cca gaa 499
 Asp Ser Ser Asp Val Ser Ala Glu Ile Leu Tyr Glu Ala Tyr Pro Glu
 120 125 130

tca att gag gag att gcg gat caa tac gga ttg ctc tcc aca agg gga 547
 Ser Ile Glu Glu Ile Ala Asp Gln Tyr Gly Leu Leu Ser Thr Arg Gly
 135 140 145

gac gcg cac tgg gga tac tcg gtg aca tcc act tac gat ttg gtg aaa 595
 Asp Ala His Trp Gly Tyr Ser Val Thr Ser Thr Tyr Asp Leu Val Lys
 150 155 160 165

ttt gtc agc gct ctc att atc gat gat cca gat tca ccg atc ctt gaa 643
 Phe Val Ser Ala Leu Ile Ile Asp Asp Pro Asp Ser Pro Ile Leu Glu
 170 175 180

gcg atg cgt aat gcc agc gca gtc gcg gct gac ggt tat ccg caa gac 691
 Ala Met Arg Asn Ala Ser Ala Val Ala Ala Asp Gly Tyr Pro Gln Asp
 185 190 195

tgg ggg aca gcg gtg ctt gat gag gca gaa gga tcc aaa tgg gga tgg 739
 Trp Gly Thr Ala Val Leu Asp Glu Ala Glu Gly Ser Lys Trp Gly Trp
 200 205 210

tct gat gat ctc atg ctg cac tcc tct gtg acc ttt ggc gaa gac tat 787
 Ser Asp Asp Leu Met Leu His Ser Ser Val Thr Phe Gly Glu Asp Tyr
 215 220 225

gtt gtg gca gct gct gtg act gga tca aaa gaa gac ctc acc caa ttg 835
 Val Val Ala Ala Ala Val Thr Gly Ser Lys Glu Asp Leu Thr Gln Leu
 230 235 240 245

gtg gaa aac caa ttg ggt gag gtt gtg agt cag cac ggc tagtttagct 884
 Val Glu Asn Gln Leu Gly Glu Val Val Ser Gln His Gly
 250 255

agatagggtg cca 897

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 2614

Val Ser Thr Val Leu Leu Ala Gly Val Val Ile Ile Gly Gly Ile Phe
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Thr Leu Pro Gln Lys Glu Glu Val Lys Val Ser Glu Leu Gln Pro Gln
20 25 30
Ala Ser Ala Ala Ser Ile Pro Ser Ser Ser Ser Thr Ala Gly Lys Ala
35 40 45
Val Glu Glu Ser Pro Leu Thr Gln Phe Val Glu Asn Ser Thr Gly Ser
50 55 60
Gln Ile Thr Tyr Met Ser Leu Lys Asp Asp Phe His Thr Gly Thr Ser
65 70 75 80
Thr Glu Arg Phe Ala Arg Pro Ala Leu Ser Leu Ser Lys Leu Tyr Ile
85 90 95
Ala Glu Tyr Val Leu Glu His Gly Thr Asn Asn Glu Lys Ser Leu Ala
100 105 110
Met Glu Met Ile Lys Asp Ser Ser Asp Val Ser Ala Glu Ile Leu Tyr
115 120 125
Glu Ala Tyr Pro Glu Ser Ile Glu Glu Ile Ala Asp Gln Tyr Gly Leu
130 135 140
Leu Ser Thr Arg Gly Asp Ala His Trp Gly Tyr Ser Val Thr Ser Thr
145 150 155 160
Tyr Asp Leu Val Lys Phe Val Ser Ala Leu Ile Ile Asp Asp Pro Asp
165 170 175
Ser Pro Ile Leu Glu Ala Met Arg Asn Ala Ser Ala Val Ala Ala Asp
180 185 190
Gly Tyr Pro Gln Asp Trp Gly Thr Ala Val Leu Asp Glu Ala Glu Gly
195 200 205
Ser Lys Trp Gly Trp Ser Asp Asp Leu Met Leu His Ser Ser Val Thr
210 215 220
Phe Gly Glu Asp Tyr Val Val Ala Ala Ala Val Thr Gly Ser Lys Glu
225 230 235 240
Asp Leu Thr Gln Leu Val Glu Asn Gln Leu Gly Glu Val Val Ser Gln
245 250 255
His Gly

<210> 2615

<211> 462

<212> DNA

<213> Corynebacterium glutamicum

Thr Pro Val Phe Gly Ala Ile Asn Ile Gly Leu Ile Phe Gly Phe Leu
65 70 75 80

Gln Phe Val Thr Thr Phe Val Ile Thr Tyr Ile Tyr Val Met Phe Ala
85 90 95

Asn Lys Asn Leu Glu Pro Arg Gln Ala Ala Ile Arg Gln Lys Met Glu
100 105 110

Gly

<210> 2617

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA02177

<400> 2617

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aagccttgggt gatcacttaa cccagctaga aggagtcaac atg cgg gaa ata ttc 115
Met Arg Glu Ile Phe
1 5
ctg atc agc ggt gat tcc acc gaa tca tcc ttg gtt ttc aag acc tcc 163
Leu Ile Ser Gly Asp Ser Thr Glu Ser Ser Leu Val Phe Lys Thr Ser
10 15 20
gaa gag gac ggc gct gag gaa ttt ttc att gct gta aca gat gaa ctc 211
Glu Glu Asp Gly Ala Glu Glu Phe Phe Ile Ala Val Thr Asp Glu Leu
25 30 35
cac gcc att ctt gca ggt cat agc gag att aag agc gcc cca gaa ccc 259
His Ala Ile Leu Ala Gly His Ser Glu Ile Lys Ser Ala Pro Glu Pro
40 45 50
gaa gaa cac aaa gag gtc cca cct cct gtt cta gag ccg gtc gct gcg 307
Glu Glu His Lys Glu Val Pro Pro Pro Val Leu Glu Pro Val Ala Ala
55 60 65
gta gaa gag ccc cgt gag gaa aaa gaa att gac cct cgt atc agc gct 355
Val Glu Glu Pro Arg Glu Glu Lys Glu Ile Asp Pro Arg Ile Ser Ala
70 75 80 85
ccc ctg acg atg tca ccc cgc gaa att cag att cgg gtt cgc tca ggc 403
Pro Leu Thr Met Ser Pro Arg Glu Ile Gln Ile Arg Val Arg Ser Gly
90 95 100
gcc acc atc gaa gaa tta gcc gaa gaa atc ggc gtc acc gaa gcc cgc 451
Ala Thr Ile Glu Glu Leu Ala Glu Glu Ile Gly Val Thr Glu Ala Arg
105 110 115
gtt gag ccc tat gcc cac ccc gtt ttg ctg gaa cgt gcc cgc att gcc 499
Val Glu Pro Tyr Ala His Pro Val Leu Leu Glu Arg Ala Arg Ile Ala

120	125	130	
gac ttg gct aag caa tca cac ccc atc agg gaa aat ggt cct gca aaa			547
Asp Leu Ala Lys Gln Ser His Pro Ile Arg Glu Asn Gly Pro Ala Lys			
135	140	145	
ctg act ctc tgg gaa att ctt gca acg gcg ttt gcc act cgc ggc cac			595
Leu Thr Leu Trp Glu Ile Leu Ala Thr Ala Phe Ala Thr Arg Gly His			
150	155	160	165
gat ctc acc aca gca cgc tgg gac gcc tac aaa gac gcc acc aac cag			643
Asp Leu Thr Thr Ala Arg Trp Asp Ala Tyr Lys Asp Ala Thr Asn Gln			
170	175	180	
tgg atc gtg cga gtt gat tgg aaa gca gga ctc agc gac aac tac gcg			691
Trp Ile Val Arg Val Asp Trp Lys Ala Gly Leu Ser Asp Asn Tyr Ala			
185	190	195	
gag tgg acg tta aac ctg cac aac acc agc aat ccc acc gct gat ccg			739
Glu Trp Thr Leu Asn Leu His Asn Thr Ser Asn Pro Thr Ala Asp Pro			
200	205	210	
cgg acc cca gtc gca gcc gat ttg atc gat cct gaa ttc att cag ccg			787
Arg Thr Pro Val Ala Ala Asp Leu Ile Asp Pro Glu Phe Ile Gln Pro			
215	220	225	
gta cgt acc ttg acg tcc gta aac tcc acc cag gaa cag tac gac gac			835
Val Arg Thr Leu Thr Ser Val Asn Ser Thr Gln Glu Gln Tyr Asp Asp			
230	235	240	245
gaa acc gat gtt ttc gac acc gta cca agc cct gac gac gca cca gac			883
Glu Thr Asp Val Phe Asp Thr Val Pro Ser Pro Asp Asp Ala Pro Asp			
250	255	260	
tca gaa tcc gat gcc gtt gct gaa atc acc aac gac aac gaa cct gaa			931
Ser Glu Ser Asp Ala Val Ala Glu Ile Thr Asn Asp Asn Glu Pro Glu			
265	270	275	
gtc gat gcg gaa ggc cca cgc aac agg cgt cga aaa gca gta acc cca			979
Val Asp Ala Glu Gly Pro Arg Asn Arg Arg Arg Lys Ala Val Thr Pro			
280	285	290	
cac tgg gaa gat gtt ctt tta gga gtt cgc gca aac aca aag cgc ccg			1027
His Trp Glu Asp Val Leu Gly Val Arg Ala Asn Thr Lys Arg Pro			
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aag aaa taggatgtgc tgatgccaag tca			1056
Lys Lys			
310			

<210> 2618

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 2618

Met	Arg	Glu	Ile	Phe	Leu	Ile	Ser	Gly	Asp	Ser	Thr	Glu	Ser	Ser	Leu
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Val Phe Lys Thr Ser Glu Glu Asp Gly Ala Glu Glu Phe Phe Ile Ala

20	25	30
Val Thr Asp Glu Leu His Ala Ile	Leu Ala Gly His Ser Glu Ile Lys	
35	40	45
Ser Ala Pro Glu Pro Glu Glu His Lys Glu Val Pro Pro Pro Val Leu		
50	55	60
Glu Pro Val Ala Ala Val Glu Glu Pro Arg Glu Glu Lys Glu Ile Asp		
65	70	75
Pro Arg Ile Ser Ala Pro Leu Thr Met Ser Pro Arg Glu Ile Gln Ile		
85	90	95
Arg Val Arg Ser Gly Ala Thr Ile Glu Glu Leu Ala Glu Glu Ile Gly		
100	105	110
Val Thr Glu Ala Arg Val Glu Pro Tyr Ala His Pro Val Leu Leu Glu		
115	120	125
Arg Ala Arg Ile Ala Asp Leu Ala Lys Gln Ser His Pro Ile Arg Glu		
130	135	140
Asn Gly Pro Ala Lys Leu Thr Leu Trp Glu Ile Leu Ala Thr Ala Phe		
145	150	155
Ala Thr Arg Gly His Asp Leu Thr Thr Ala Arg Trp Asp Ala Tyr Lys		
165	170	175
Asp Ala Thr Asn Gln Trp Ile Val Arg Val Asp Trp Lys Ala Gly Leu		
180	185	190
Ser Asp Asn Tyr Ala Glu Trp Thr Leu Asn Leu His Asn Thr Ser Asn		
195	200	205
Pro Thr Ala Asp Pro Arg Thr Pro Val Ala Ala Asp Leu Ile Asp Pro		
210	215	220
Glu Phe Ile Gln Pro Val Arg Thr Leu Thr Ser Val Asn Ser Thr Gln		
225	230	235
Glu Gln Tyr Asp Asp Glu Thr Asp Val Phe Asp Thr Val Pro Ser Pro		
245	250	255
Asp Asp Ala Pro Asp Ser Glu Ser Asp Ala Val Ala Glu Ile Thr Asn		
260	265	270
Asp Asn Glu Pro Glu Val Asp Ala Glu Gly Pro Arg Asn Arg Arg Arg		
275	280	285
Lys Ala Val Thr Pro His Trp Glu Asp Val Leu Leu Gly Val Arg Ala		
290	295	300
Asn Thr Lys Arg Pro Lys Lys		
305	310	

<210> 2619

<211> 993

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(970)

<223> RXA02178

<400> 2619

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                                         Met Pro Ser Gln Leu
                                         1 5

gga gaa aac gcg gcg atc gtc acc ctc tgg ttt gtt agc gca tcc gat 163
Gly Glu Asn Ala Ala Ile Val Thr Leu Trp Phe Val Ser Ala Ser Asp
                        10 15 20

ccc caa tcc atc atc cgc tgc gaa cct cgg gcg gat cgt gga tat ggc 211
Pro Gln Ser Ile Ile Arg Ser Glu Pro Arg Ala Asp Arg Gly Tyr Gly
                        25 30 35

cga aaa ctg ttg gca cag ctc aac cca acg tgg cca att acc ccc atc 259
Arg Lys Leu Leu Ala Gln Leu Asn Pro Thr Trp Pro Ile Thr Pro Ile
                        40 45 50

ggg cag ttc gcc ctc aac aga tcc gtt cct gct agt gcc aac gag ttc 307
Gly Gln Phe Ala Leu Asn Arg Ser Val Pro Ala Ser Ala Asn Glu Phe
                        55 60 65

tac atc gct ggt ttt ccc ggc atc acc atc att caa acc gtg ttg gaa 355
Tyr Ile Ala Gly Phe Pro Gly Ile Thr Ile Ile Gln Thr Val Leu Glu
                        70 75 80 85

gat gtc acc tct tta tcc aag ctg aat cct cgg tta ctg cgc agc gtc 403
Asp Val Thr Ser Leu Ser Lys Leu Asn Pro Arg Leu Leu Arg Ser Val
                        90 95 100

ccg gca aca gat gtc tac att ttc gcc gtc aat gaa gaa acc acc ctt 451
Pro Ala Thr Asp Val Tyr Ile Phe Ala Val Asn Glu Glu Thr Thr Leu
                        105 110 115

ggt ggc ttc gca cac atc tac aac ggt gag atc aaa cga tcc ttc atc 499
Gly Gly Phe Ala His Ile Tyr Asn Gly Glu Ile Lys Arg Ser Phe Ile
                        120 125 130

gcc tat gaa gag cgc gtc ttc gaa gac aac ggc atc ccc ggc ggc ttt 547
Ala Tyr Glu Glu Arg Val Phe Glu Asp Asn Gly Ile Pro Gly Gly Phe
                        135 140 145

gaa acc ccc tac tgg gca ggc aaa aaa ggc acc cgg aaa act gcg ctg 595
Glu Thr Pro Tyr Trp Ala Gly Lys Lys Gly Thr Arg Lys Thr Ala Leu
                        150 155 160 165

tcg ttg ccc ttc aac ccc atc gaa cta gtc cac gaa gca caa cgt gca 643
Ser Leu Pro Phe Asn Pro Ile Glu Leu Val His Glu Ala Gln Arg Ala
                        170 175 180

tgg ctc gga ttc gac gcc acc acc tcc cct gac atc aac gtc gtt gcc 691
Trp Leu Gly Phe Asp Ala Thr Thr Ser Pro Asp Ile Asn Val Val Ala
                        185 190 195

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tat gcc acc gat ggt cgc ccc gag ccg cgc atc gct gca ccc cgc ata 739
 Tyr Ala Thr Asp Gly Arg Pro Glu Pro Arg Ile Ala Ala Pro Arg Ile
 200 205 210

att aac agc gag gaa gtg aca agg tcc gcc gtc gaa aag cta gga ctg 787
 Ile Asn Ser Glu Glu Val Thr Arg Ser Ala Val Glu Lys Leu Gly Leu
 215 220 225

cgc gaa tcc gcc ttc tac gac gac tac gaa gaa tac gag gca ccc gat 835
 Arg Glu Ser Ala Phe Tyr Asp Asp Tyr Glu Glu Tyr Glu Ala Pro Asp
 230 235 240 245

cga gtg gtg tcc aag cgc att acc tca aac gcg aaa aaa gcg gcc agc 883
 Arg Val Val Ser Lys Arg Ile Thr Ser Asn Ala Lys Lys Ala Ala Ser
 250 255 260

tca gca cag aaa ttt ggt aaa tct ctg tgg cga gcc agc cgc gaa ttc 931
 Ser Ala Gln Lys Phe Gly Lys Ser Leu Trp Arg Ala Ser Arg Glu Phe
 265 270 275

ggg tca aac atg gcg gaa aga ctc cgc cac act gac cgc tagcgctact 980
 Gly Ser Asn Met Ala Glu Arg Leu Arg His Thr Asp Arg
 280 285 290

acttagcgct gtt 993

<210> 2620
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 <213> Corynebacterium glutamicum

<400> 2620
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 20 25 30
 Asp Arg Gly Tyr Gly Arg Lys Leu Leu Ala Gln Leu Asn Pro Thr Trp
 35 40 45
 Pro Ile Thr Pro Ile Gly Gln Phe Ala Leu Asn Arg Ser Val Pro Ala
 50 55 60
 Ser Ala Asn Glu Phe Tyr Ile Ala Gly Phe Pro Gly Ile Thr Ile Ile
 65 70 75 80
 Gln Thr Val Leu Glu Asp Val Thr Ser Leu Ser Lys Leu Asn Pro Arg
 85 90 95
 Leu Leu Arg Ser Val Pro Ala Thr Asp Val Tyr Ile Phe Ala Val Asn
 100 105 110
 Glu Glu Thr Thr Leu Gly Gly Phe Ala His Ile Tyr Asn Gly Glu Ile
 115 120 125
 Lys Arg Ser Phe Ile Ala Tyr Glu Glu Arg Val Phe Glu Asp Asn Gly
 130 135 140
 Ile Pro Gly Gly Phe Glu Thr Pro Tyr Trp Ala Gly Lys Lys Gly Thr

55	60	65	
acc cac ggc cac cgc gat gag cgc cta cat cca aag att aaa ggc cac			355
Thr His Gly His Arg Asp Glu Arg Leu His Pro Lys Ile Lys Gly His			
70	75	80	85
gat atc gcg tgg cag aac acg gcc acc gca aac agc cgc cgc cag ggc			403
Asp Ile Ala Trp Gln Asn Thr Ala Thr Ala Asn Ser Arg Arg Gln Gly			
	90	95	100
gcc gat gat gga ttg ctt gtc gac gag tcc ggc cag gtg atc atg gct			451
Ala Asp Asp Gly Leu Leu Val Asp Glu Ser Gly Gln Val Ile Met Ala			
	105	110	115
atc aat gcc tct ctc ttg gcg att aag ggc gac acc gtg ttt cat tcc			499
Ile Asn Ala Ser Leu Leu Ala Ile Lys Gly Asp Thr Val Phe His Ser			
	120	125	130
acg cac ccc agg tcg ctg ccg tct gtt ctg gaa tca acg gtc att gcc			547
Thr His Pro Arg Ser Leu Pro Ser Val Leu Glu Ser Thr Val Ile Ala			
	135	140	145
tac ctg cag gaa caa ggc tgt aat gca aag cct cga gag caa ggc ttc			595
Tyr Leu Gln Glu Gln Gly Cys Asn Ala Lys Pro Arg Glu Gln Gly Phe			
	150	155	160
aac atc aat gat ttg cgc tct tcg gaa gtg tgg ctg gtg gat tct ttg			643
Asn Ile Asn Asp Leu Arg Ser Ser Glu Val Trp Leu Val Asp Ser Leu			
	170	175	180
tcc ggc atc cgt cgc gtc gct gca tgg ctc gaa tac ggt tcc aaa ttc			691
Ser Gly Ile Arg Arg Val Ala Ala Trp Leu Glu Tyr Gly Ser Lys Phe			
	185	190	195
cca gtc tca gaa acg cga cct gtg gca gct ttc gtg ccg acg ttt tct			739
Pro Val Ser Glu Thr Arg Pro Val Ala Ala Phe Val Pro Thr Phe Ser			
	200	205	210
gaa gtc aat gac tac cta tgg agc act gca cag caa gtg taggtcgctc			788
Glu Val Asn Asp Tyr Leu Trp Ser Thr Ala Gln Gln Val			
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gactgttatt ctc			801

<210> 2622

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 2622

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Glu Ala Ala Ala Pro Thr Ala Ser Gln Phe His Asp Arg Ile Ile Thr
20 25 30

Gln Leu Arg Glu Ala Pro Gly Ser Val Gln Ala Ala Val Thr Ile Glu
35 40 45

Asn Asn His Tyr Asn Val Glu Leu Arg Pro Pro Arg Lys Leu Asn Ser

cgc cca gag cca ctc ccc caa gag atc tct atc tca gca tct tct ccc 259
 Arg Pro Glu Pro Leu Pro Gln Glu Ile Ser Ile Ser Ala Ser Ser Pro
 40 45 50

gct ggt gaa atc gag gta ttc cca ttc agc atg tgt gaa cca ggt gtt 307
 Ala Gly Glu Ile Glu Val Phe Pro Phe Ser Met Cys Glu Pro Gly Val
 55 60 65

gaa tgc gaa gag aac gag gtg cca acg ctg gaa gtt ggt gct gat gaa 355
 Glu Cys Glu Glu Asn Glu Val Pro Thr Leu Glu Val Gly Ala Asp Glu
 70 75 80 85

gag ttg cac ctg acg att cca gag gca att cat gat cat gac tgg tac 403
 Glu Leu His Leu Thr Ile Pro Glu Ala Ile His Asp His Asp Trp Tyr
 90 95 100

ttg ttg acc att tat gat gat ccg gct gca aat gac gag ttc tac cac 451
 Leu Leu Thr Ile Tyr Asp Asp Pro Ala Ala Asn Asp Glu Phe Tyr His
 105 110 115

acc agt tac gac gcc acc gag gca acc gtt cct ggt tct gtg gat cca 499
 Thr Ser Tyr Asp Ala Thr Glu Ala Thr Val Pro Gly Ser Val Asp Pro
 120 125 130

acc gaa gag ggt gcg gag cgc cca cgt ctg gtc gta gtg gaa gtg tcc 547
 Thr Glu Glu Gly Ala Glu Arg Pro Arg Leu Val Val Val Glu Val Ser
 135 140 145

gct gtg atg atc ggt gag gat gaa aat ggt gag gaa agc cct tac acc 595
 Ala Val Met Ile Gly Glu Asp Glu Asn Gly Glu Glu Ser Pro Tyr Thr
 150 155 160 165

gtc acg tgg tcg cta tcc acg atg aac gag taactcactc acaaacaata 645
 Val Thr Trp Ser Leu Ser Thr Met Asn Glu
 170 175

agg 648

<210> 2624

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 2624

Met Ala Ser Arg Lys Thr Lys Arg Lys Asn Leu Ile Gln Ile Leu Ser
 1 5 10 15

Leu Ile Val Ala Val Leu Leu Val Val Ile Leu Ser Val Val Phe Gln
 20 25 30

Gln Trp Trp Asn Asn Arg Pro Glu Pro Leu Pro Gln Glu Ile Ser Ile
 35 40 45

Ser Ala Ser Ser Pro Ala Gly Glu Ile Glu Val Phe Pro Phe Ser Met
 50 55 60

Cys Glu Pro Gly Val Glu Cys Glu Glu Asn Glu Val Pro Thr Leu Glu
 65 70 75 80

Val Gly Ala Asp Glu Glu Leu His Leu Thr Ile Pro Glu Ala Ile His

85	90	95
Asp His Asp Trp Tyr Leu Leu Thr Ile Tyr Asp Asp Pro Ala Ala Asn		
100	105	110
Asp Glu Phe Tyr His Thr Ser Tyr Asp Ala Thr Glu Ala Thr Val Pro		
115	120	125
Gly Ser Val Asp Pro Thr Glu Glu Gly Ala Glu Arg Pro Arg Leu Val		
130	135	140
Val Val Glu Val Ser Ala Val Met Ile Gly Glu Asp Glu Asn Gly Glu		
145	150	155
Glu Ser Pro Tyr Thr Val Thr Trp Ser Leu Ser Thr Met Asn Glu		
165	170	175

<210> 2625

<211> 2322

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2299)

<223> RXA02187

<400> 2625

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aacaaaagtc acctcaacaa ggcttaaact taacaacatc atg aaa aaa gac tcc 115
                                     Met Lys Lys Asp Ser
                                     1           5
ccc atc ccc acc ctc aag ggg tgg ttg gat act caa agt gat gat cag 163
Pro Ile Pro Thr Leu Lys Gly Trp Leu Asp Thr Gln Ser Asp Asp Gln
                10                15                20
ctc tcc aca atc ctt aga aat cga ccc gat acg gtt ctc cct tta cca 211
Leu Ser Thr Ile Leu Arg Asn Arg Pro Asp Thr Val Leu Pro Leu Pro
                25                30                35
cct aat ttg gcc tct ctt gct gcg cgt tta cag ctg agg gcg tct gcg 259
Pro Asn Leu Ala Ser Leu Ala Ala Arg Leu Gln Leu Arg Ala Ser Ala
                40                45                50
att cgc gcg gtg ttg aaa ctc aat gcg ttg gaa ctt ggt gtg ttg gag 307
Ile Arg Ala Val Leu Lys Leu Asn Ala Leu Glu Leu Gly Val Leu Glu
                55                60                65
gcc gtg gcc aac ctt ggt ggt gaa ctc cac ccg gtt act gcc ccc gaa 355
Ala Val Ala Asn Leu Gly Gly Glu Leu His Pro Val Thr Ala Pro Glu
                70                75                80                85
gtg gtg gaa tat ttg cat gtg gcg ttg gca gag gat ctt cca gcg caa 403
Val Val Glu Tyr Leu His Val Ala Leu Ala Glu Asp Leu Pro Ala Gln
                90                95                100
gac acg att ggt gcg gct ctt gcc acg ctg aaa aat ttc gcg ttg gtt 451
Asp Thr Ile Gly Ala Ala Leu Ala Thr Leu Lys Asn Phe Ala Leu Val

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105	110	115	
tat ggc gat gac cag ttg atg att gct cag gag acg atg gct gcg ttg Tyr Gly Asp Asp Gln Leu Met Ile Ala Gln Glu Thr Met Ala Ala Leu 120			499
	125	130	
cct gtt cat tgg cgg ttg ctt ccg gag gta agt gat cgc ggg cag agt Pro Val His Trp Arg Leu Leu Pro Glu Val Ser Asp Arg Gly Gln Ser 135	140	145	547
gag gaa cag gtg agg gaa agc gtc gat aag ctt tct gat agg cac cgc Glu Glu Gln Val Arg Glu Ser Val Asp Lys Leu Ser Asp Arg His Arg 150	155	160	595
		165	
aaa ctt ttg cac acg ctt gcg gcc tcg ggt ggc ttc ggt ctg acg cgc Lys Leu Leu His Thr Leu Ala Ala Ser Gly Gly Phe Gly Leu Thr Arg 170	175	180	643
gat gcg gcg cct gat gcg gat ccg tcg cgg ccg att ccg cag ttg ctg Asp Ala Ala Pro Asp Ala Asp Pro Ser Arg Pro Ile Pro Gln Leu Leu 185	190	195	691
gcg tcg ggg ttg ttg gcg cgc gtg gat gag cag acc gtg cgc ctg ccg Ala Ser Gly Leu Leu Ala Arg Val Asp Glu Gln Thr Val Arg Leu Pro 200	205	210	739
gcg atg gtg cgg cgt gtg att gag ggc cgc gag cag ctg ccc gct cag Ala Met Val Arg Arg Val Ile Glu Gly Arg Glu Gln Leu Pro Ala Gln 215	220	225	787
gtg cgc cca att ccg cgc acg gcg gcg cca ggt tcg aat gat ggc ggc Val Arg Pro Ile Pro Arg Thr Ala Ala Pro Gly Ser Asn Asp Gly Gly 230	235	240	835
		245	
att gca gcc ggc ctt gag gtg gtg cgg cac atg cga ttg ctt atc gac Ile Ala Ala Gly Leu Glu Val Val Arg His Met Arg Leu Leu Ile Asp 250	255	260	883
gcc ctc agc cac gtt ccc gcc ccc acg ctg aaa gtc gga gcc ctc ggt Ala Leu Ser His Val Pro Ala Pro Thr Leu Lys Val Gly Ala Leu Gly 265	270	275	931
gtg cgc gtg gtg act cgc ctg agc aag gaa tta gac ctt gat gag acc Val Arg Val Val Thr Arg Leu Ser Lys Glu Leu Asp Leu Asp Glu Thr 280	285	290	979
gag ctg gca cgt cta ctg agt ttg ggt atg gcc agc ggt cta atc cgt Glu Leu Ala Arg Leu Leu Ser Leu Gly Met Ala Ser Gly Leu Ile Arg 295	300	305	1027
aaa ggc gtg ccc gat cca ttg ccc atg gat gat gat ggc ggc gat tac Lys Gly Val Pro Asp Pro Leu Pro Met Asp Asp Asp Gly Gly Asp Tyr 310	315	320	1075
		325	
gtc gct ccc acc ccg ctg gct gac gaa tgg atg gaa tat gat ctg gcg Val Ala Pro Thr Pro Leu Ala Asp Glu Trp Met Glu Tyr Asp Leu Ala 330	335	340	1123
cac caa ttg ggc acg ttg atg tct ggt tgg tgg aag caa act tac gcg His Gln Leu Gly Thr Leu Met Ser Gly Trp Trp Lys Gln Thr Tyr Ala 345	350	355	1171

ccg tgg ttg gtg ggt cgg gct gat gat aag gac aag ccg atc cat gtt Pro Trp Leu Val Gly Arg Ala Asp Asp Lys Asp Lys Pro Ile His Val 360 365 370	1219
ctc agt aaa aca agc atc att gat tgc ctt cct gat gct cgt gcg aag Leu Ser Lys Thr Ser Ile Ile Asp Ser Leu Pro Asp Ala Arg Ala Lys 375 380 385	1267
atc ctg tcc tct tta tct agg gtt tta gtg gac aat ctg cac gcg gat Ile Leu Ser Ser Leu Ser Arg Val Leu Val Asp Asn Leu His Ala Asp 390 395 400 405	1315
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acc atg gat tgc atc gca tgc ttg gaa tca cct ggt ttg gcc tgc gtg Thr Met Asp Ser Ile Ala Ser Leu Glu Ser Pro Gly Leu Ala Ser Val 490 495 500	1603
tat cga ctc agc gag aaa tcc atc agg cat gct ctg gat ctt ggg ctc Tyr Arg Leu Ser Glu Lys Ser Ile Arg His Ala Leu Asp Leu Gly Leu 505 510 515	1651
acc acc ccg gaa atc ttg gag ttt ctc aaa gaa cat tcc atg aca gat Thr Thr Pro Glu Ile Leu Glu Phe Leu Lys Glu His Ser Met Thr Asp 520 525 530	1699
ctg ccc caa tct gtg ggc tat ttg ctc agc gat atc gcc aga aag cac Leu Pro Gln Ser Val Gly Tyr Leu Leu Ser Asp Ile Ala Arg Lys His 535 540 545	1747
ggc acc ctc cga ggc ggc cct gca ctg tcc tat atc cgt agc gac gat Gly Thr Leu Arg Gly Gly Pro Ala Leu Ser Tyr Ile Arg Ser Asp Asp 550 555 560 565	1795
ccc gct ttg ctg cat tcc gca gtg gag gcg ggc gcc gat gtg gcg ctt Pro Ala Leu Leu His Ser Ala Val Glu Ala Gly Ala Asp Val Ala Leu 570 575 580	1843
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gtg atc act gtg ctg cgt gct gcc ggg ttc caa cct gtg gca gaa gac 1939
Val Ile Thr Val Leu Arg Ala Ala Gly Phe Gln Pro Val Ala Glu Asp
600 605 610

ggc gaa ggc gca agt ctg aat atc tcg cca tcc cct gca cgt gtg ccc 1987
Gly Glu Gly Ala Ser Leu Asn Ile Ser Pro Ser Pro Ala Arg Val Pro
615 620 625

gca gct tcc cca cca cca gtt gtt ccg gca ctg gat gaa agc cgg gta 2035
Ala Ala Ser Pro Pro Pro Val Val Pro Ala Leu Asp Glu Ser Arg Val
630 635 640 645

cag gca gca gtc aaa gca atc cga cgg gaa aat tca gca tct caa gga 2083
Gln Ala Ala Val Lys Ala Ile Arg Arg Glu Asn Ser Ala Ser Gln Gly
650 655 660

act gtt tcc aca cag cca act ctt tcg gtg ctg cag gct gca gtg cga 2131
Thr Val Ser Thr Gln Pro Thr Leu Ser Val Leu Gln Ala Ala Val Arg
665 670 675

ggg cag cgc acg gtg acg ttg ggg ttc gtc gat aag caa ggc gtg gcc 2179
Gly Gln Arg Thr Val Thr Leu Gly Phe Val Asp Lys Gln Gly Val Ala
680 685 690

gtg cac cgc gtc gtc aag cct tta acc gtc aac gcc ggg cag gtg gac 2227
Val His Arg Val Val Lys Pro Leu Thr Val Asn Ala Gly Gln Val Asp
695 700 705

gct gtg gat gaa gcc aca ggt gcg gtg cat cgt ttc atg ttg cac agg 2275
Ala Val Asp Glu Ala Thr Gly Ala Val His Arg Phe Met Leu His Arg
710 715 720 725

atc aca gaa gta ata gtg gat aac tagcctagaa gtgacataat gga 2322
Ile Thr Glu Val Ile Val Asp Asn
730

<210> 2626

<211> 733

<212> PRT

<213> Corynebacterium glutamicum

<400> 2626

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20 25 30

Val Leu Pro Leu Pro Pro Asn Leu Ala Ser Leu Ala Ala Arg Leu Gln
35 40 45

Leu Arg Ala Ser Ala Ile Arg Ala Val Leu Lys Leu Asn Ala Leu Glu
50 55 60

Leu Gly Val Leu Glu Ala Val Ala Asn Leu Gly Gly Glu Leu His Pro
65 70 75 80

Val Thr Ala Pro Glu Val Val Glu Tyr Leu His Val Ala Leu Ala Glu
85 90 95

Asp Leu Pro Ala Gln Asp Thr Ile Gly Ala Ala Leu Ala Thr Leu Lys
100 105 110

Asn Phe Ala Leu Val Tyr Gly Asp Asp Gln Leu Met Ile Ala Gln Glu
115 120 125

Thr Met Ala Ala Leu Pro Val His Trp Arg Leu Leu Pro Glu Val Ser
130 135 140

Asp Arg Gly Gln Ser Glu Glu Gln Val Arg Glu Ser Val Asp Lys Leu
145 150 155 160

Ser Asp Arg His Arg Lys Leu Leu His Thr Leu Ala Ala Ser Gly Gly
165 170 175

Phe Gly Leu Thr Arg Asp Ala Ala Pro Asp Ala Asp Pro Ser Arg Pro
180 185 190

Ile Pro Gln Leu Leu Ala Ser Gly Leu Leu Ala Arg Val Asp Glu Gln
195 200 205

Thr Val Arg Leu Pro Ala Met Val Arg Arg Val Ile Glu Gly Arg Glu
210 215 220

Gln Leu Pro Ala Gln Val Arg Pro Ile Pro Arg Thr Ala Ala Pro Gly
225 230 235 240

Ser Asn Asp Gly Gly Ile Ala Ala Gly Leu Glu Val Val Arg His Met
245 250 255

Arg Leu Leu Ile Asp Ala Leu Ser His Val Pro Ala Pro Thr Leu Lys
260 265 270

Val Gly Ala Leu Gly Val Arg Val Val Thr Arg Leu Ser Lys Glu Leu
275 280 285

Asp Leu Asp Glu Thr Glu Leu Ala Arg Leu Leu Ser Leu Gly Met Ala
290 295 300

Ser Gly Leu Ile Arg Lys Gly Val Pro Asp Pro Leu Pro Met Asp Asp
305 310 315 320

Asp Gly Gly Asp Tyr Val Ala Pro Thr Pro Leu Ala Asp Glu Trp Met
325 330 335

Glu Tyr Asp Leu Ala His Gln Leu Gly Thr Leu Met Ser Gly Trp Trp
340 345 350

Lys Gln Thr Tyr Ala Pro Trp Leu Val Gly Arg Ala Asp Asp Lys Asp
355 360 365

Lys Pro Ile His Val Leu Ser Lys Thr Ser Ile Ile Asp Ser Leu Pro
370 375 380

Asp Ala Arg Ala Lys Ile Leu Ser Ser Leu Ser Arg Val Leu Val Asp
385 390 395 400

Asn Leu His Ala Asp Leu Ala Phe His Tyr Pro Leu Ala Ala Ser Arg
405 410 415

Met Asn Pro Asp Thr Ile Thr Gln Leu Val Gln Glu Ala Gln Trp Ile

420	425	430
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Gly Glu Asn Pro Thr Glu Val Ile Lys Ala Pro Ala Pro Val Glu Asn 450 455 460		
Phe Ile Val Gln Gly Asp Phe Thr Ile Met Val Pro Gly Pro Leu Thr 465 470 475 480		
Pro Ala Met Gln Lys Thr Met Asp Ser Ile Ala Ser Leu Glu Ser Pro 485 490 495		
Gly Leu Ala Ser Val Tyr Arg Leu Ser Glu Lys Ser Ile Arg His Ala 500 505 510		
Leu Asp Leu Gly Leu Thr Thr Pro Glu Ile Leu Glu Phe Leu Lys Glu 515 520 525		
His Ser Met Thr Asp Leu Pro Gln Ser Val Gly Tyr Leu Leu Ser Asp 530 535 540		
Ile Ala Arg Lys His Gly Thr Leu Arg Gly Gly Pro Ala Leu Ser Tyr 545 550 555 560		
Ile Arg Ser Asp Asp Pro Ala Leu Leu His Ser Ala Val Glu Ala Gly 565 570 575		
Ala Asp Val Ala Leu Arg Gln Ile Ala Pro Thr Val Ala Ile Ala Gln 580 585 590		
Ala Pro Leu Leu Gln Val Ile Thr Val Leu Arg Ala Ala Gly Phe Gln 595 600 605		
Pro Val Ala Glu Asp Gly Glu Gly Ala Ser Leu Asn Ile Ser Pro Ser 610 615 620		
Pro Ala Arg Val Pro Ala Ala Ser Pro Pro Pro Val Val Pro Ala Leu 625 630 635 640		
Asp Glu Ser Arg Val Gln Ala Ala Val Lys Ala Ile Arg Arg Glu Asn 645 650 655		
Ser Ala Ser Gln Gly Thr Val Ser Thr Gln Pro Thr Leu Ser Val Leu 660 665 670		
Gln Ala Ala Val Arg Gly Gln Arg Thr Val Thr Leu Gly Phe Val Asp 675 680 685		
Lys Gln Gly Val Ala Val His Arg Val Val Lys Pro Leu Thr Val Asn 690 695 700		
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<211> 693
 <212> DNA
 <213> Corynebacterium glutamicum

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 <221> CDS
 <222> (101)..(670)
 <223> RXA02199

<400> 2627

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                                   Met Thr Asp Ser Thr
                                   1      5

ccg caa ggc tca aca cca ggc atg tcc cct gaa gct atc ctc aac ggc 163
Pro Gln Gly Ser Thr Pro Gly Met Ser Pro Glu Ala Ile Leu Asn Gly
      10      15      20

acc gga aag ccg tgg gaa gag tgg cta aaa ttg ctt gac gac gta aaa 211
Thr Gly Lys Pro Trp Glu Glu Trp Leu Lys Leu Leu Asp Asp Val Lys
      25      30      35

gcc acc tct tgg act cac acc cac atc gca aag cac atc gtg gac aac 259
Ala Thr Ser Trp Thr His Thr His Ile Ala Lys His Ile Val Asp Asn
      40      45      50

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Phe Asp Val Ser Gly Trp Trp Ala Gln Gly Ile Ala Ile Gly Tyr Glu
      55      60      65

tac gaa cgt ggc atg cgc aaa ccc ggg atg acc agc gat ggg ttc gcg 355
Tyr Glu Arg Gly Met Arg Lys Pro Gly Met Thr Ser Asp Gly Phe Ala
      70      75      80      85

gcc aat gcc tcc aaa acc ctt aac ctg ccg gtc gaa aaa gtg tgg aag 403
Ala Asn Ala Ser Lys Thr Leu Asn Leu Pro Val Glu Lys Val Trp Lys
      90      95      100

ctc ttc gga gac gat gac ctg cgg gcg cag tgg ctc gat ccc gca cta 451
Leu Phe Gly Asp Asp Asp Leu Arg Ala Gln Trp Leu Asp Pro Ala Leu
      105      110      115

att gag aaa acc tcc gcc tcc gaa cct aga aca ttc aat gcc aaa tgg 499
Ile Glu Lys Thr Ser Ala Ser Glu Pro Arg Thr Phe Asn Ala Lys Trp
      120      125      130

ttg gcc gat gat tct cga gtg agc gtc aac ttc acc tcc aaa ggc gac 547
Leu Ala Asp Asp Ser Arg Val Ser Val Asn Phe Thr Ser Lys Gly Asp
      135      140      145

aat aaa tcc agc ttc ggc atc cag cac aga cgc ctg cct gat caa gac 595
Asn Lys Ser Ser Phe Gly Ile Gln His Arg Arg Leu Pro Asp Gln Asp
      150      155      160      165

agc atc cct gtc atg aaa gca ttc tgg aaa gaa cgc atc gct gca tta 643
Ser Ile Pro Val Met Lys Ala Phe Trp Lys Glu Arg Ile Ala Ala Leu
      170      175      180

gtt gag gtg tca aaa caa ttt tcg ctt taacattaag ttcttagcct 690

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Val Glu Val Ser Lys Gln Phe Ser Leu
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tca

693

<210> 2628

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 2628

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20 25 30

Leu Asp Asp Val Lys Ala Thr Ser Trp Thr His Thr His Ile Ala Lys
35 40 45

His Ile Val Asp Asn Phe Asp Val Ser Gly Trp Trp Ala Gln Gly Ile
50 55 60

Ala Ile Gly Tyr Glu Tyr Glu Arg Gly Met Arg Lys Pro Gly Met Thr
65 70 75 80

Ser Asp Gly Phe Ala Ala Asn Ala Ser Lys Thr Leu Asn Leu Pro Val
85 90 95

Glu Lys Val Trp Lys Leu Phe Gly Asp Asp Asp Leu Arg Ala Gln Trp
100 105 110

Leu Asp Pro Ala Leu Ile Glu Lys Thr Ser Ala Ser Glu Pro Arg Thr
115 120 125

Phe Asn Ala Lys Trp Leu Ala Asp Asp Ser Arg Val Ser Val Asn Phe
130 135 140

Thr Ser Lys Gly Asp Asn Lys Ser Ser Phe Gly Ile Gln His Arg Arg
145 150 155 160

Leu Pro Asp Gln Asp Ser Ile Pro Val Met Lys Ala Phe Trp Lys Glu
165 170 175

Arg Ile Ala Ala Leu Val Glu Val Ser Lys Gln Phe Ser Leu
180 185 190

<210> 2629

<211> 501

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXA02203

<400> 2629

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                                   Met Thr Ile Arg Ala
                                   1 5

act ttc cag cct tcc gta gat gaa ttc atc tcc act ctc gaa gag ttt 163
Thr Phe Gln Pro Ser Val Asp Glu Phe Ile Ser Thr Leu Glu Glu Phe
                                   10 15 20

gca aca ggt tca tac ctt aaa gag gac gaa aag gaa ttc tgg gac gaa 211
Ala Thr Gly Ser Tyr Leu Lys Glu Asp Glu Lys Glu Phe Trp Asp Glu
                                   25 30 35

cct ttc gat gtc aag gca ctt cca gat ctt cgt ttc atc ttg gaa aac 259
Pro Phe Asp Val Lys Ala Leu Pro Asp Leu Arg Phe Ile Leu Glu Asn
                                   40 45 50

tac ctt gat tcc cta gat aag ctc ggt gaa gca cca gac ctt gat gct 307
Tyr Leu Asp Ser Leu Asp Lys Leu Gly Glu Ala Pro Asp Leu Asp Ala
                                   55 60 65

gtt aac gcc tcc gct cag tcc acc ctt gat gag ctg gag aag ttc aac 355
Val Asn Ala Ser Ala Gln Ser Thr Leu Asp Glu Leu Glu Lys Phe Asn
   70 75 80 85

aca aag cac cac ggt gct gtt gtt gag cct gaa gaa aaa gaa gag atc 403
Thr Lys His His Gly Ala Val Val Glu Pro Glu Glu Lys Glu Glu Ile
                                   90 95 100

act aaa ttg atg ttt gat gct gca aag cag act ggt gca gat gat ctt 451
Thr Lys Leu Met Phe Asp Ala Ala Lys Gln Thr Gly Ala Asp Asp Leu
                                   105 110 115

tct gca gag gct ttc cct gag ttt gag taaatttcag tagaagtttt 498
Ser Ala Glu Ala Phe Pro Glu Phe Glu
   120 125

tta 501

<210> 2630
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 2630
Met Thr Ile Arg Ala Thr Phe Gln Pro Ser Val Asp Glu Phe Ile Ser
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Thr Leu Glu Glu Phe Ala Thr Gly Ser Tyr Leu Lys Glu Asp Glu Lys
  20 25 30

Glu Phe Trp Asp Glu Pro Phe Asp Val Lys Ala Leu Pro Asp Leu Arg
  35 40 45

Phe Ile Leu Glu Asn Tyr Leu Asp Ser Leu Asp Lys Leu Gly Glu Ala
  50 55 60

Pro Asp Leu Asp Ala Val Asn Ala Ser Ala Gln Ser Thr Leu Asp Glu
  65 70 75 80

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Leu Glu Lys Phe Asn Thr Lys His His Gly Ala Val Val Glu Pro Glu
 85 90 95

Glu Lys Glu Glu Ile Thr Lys Leu Met Phe Asp Ala Ala Lys Gln Thr
 100 105 110

Gly Ala Asp Asp Leu Ser Ala Glu Ala Phe Pro Glu Phe Glu
 115 120 125

<210> 2631

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXA02206

<400> 2631

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accttatgac ctca gtagtg tgggtgggcgt gaaacagcga atg gtc ggt tca agt 115
                                     Met Val Gly Ser Ser
                                     1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
               10               15               20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
               25               30               35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
               40               45               50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
               55               60               65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
               70               75               80               85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
               90               95               100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
               105               110               115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
               120               125               130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly

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135	140	145	
tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca			595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala			
150	155	160	165
gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg			643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu			
	170	175	180
ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta			691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu			
	185	190	195
ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act			739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr			
	200	205	210
gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca			787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr			
	215	220	225
gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc			835
Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile			
	230	235	245
att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc			883
Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro			
	250	255	260
gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct			931
Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala			
	265	270	275
gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag			979
Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys			
	280	285	290
gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat			1027
Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp			
	295	300	305
gtc tcc ctg tgacttggtc caattacatt cac			1059
Val Ser Leu			
310			

<210> 2632

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 2632

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Ser	Thr	Trp	Gly	Ser	Gly	Thr	Glu	Leu	Ala	Glu	Ala	Gly	Asp	Ile	Phe
			20					25					30		

Lys	Ala	Phe	Ile	Asn	Ser	Gly	Gly	Thr	Leu	Ile	Asp	Val	Ser	Pro	Asn
	35						40					45			

Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140
 Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160
 Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175
 Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190
 Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205
 Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220
 Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240
 Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255
 Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
 260 265 270
 Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
 275 280 285
 Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
 290 295 300
 Gln Ala Leu Asp Asp Val Ser Leu
 305 310

<210> 2633

<211> 553

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(553)

<223> RXA02211

<400> 2633

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tgattcacac tttcagacta caagaactag actaagcggg atg gtt tca gtt ctt 115
               Met Val Ser Val Leu
                               1           5

tta att cag ccc cgt cag gga gaa gca gtc gcc gca gct gag cga cgt 163
Leu Ile Gln Pro Arg Gln Gly Glu Ala Val Ala Ala Glu Arg Arg
               10           15           20

gac ttt ttg cag gcc acc ggt ctt aag cct caa gaa ctg acc tcc cga 211
Asp Phe Leu Gln Ala Thr Gly Leu Lys Pro Gln Glu Leu Thr Ser Arg
               25           30           35

atg ttg gat acc acc act tct cga att ggc agt ctg gaa ggt ttc gac 259
Met Leu Asp Thr Thr Thr Ser Arg Ile Gly Ser Leu Glu Gly Phe Asp
               40           45           50

ggc gtg att gtg ggc gga agc cca ctg aat gcc acc aac ttt gag tac 307
Gly Val Ile Val Gly Gly Ser Pro Leu Asn Ala Thr Asn Phe Glu Tyr
               55           60           65

agc gat tgg caa cgc cac gtc cac cgc gaa ttg tcc ttg ctg atc aat 355
Ser Asp Trp Gln Arg His Val His Arg Glu Leu Ser Leu Leu Ile Asn
               70           75           80           85

cac cca ctg cca aca atc ttt gtc tgc tac ggc aat acc ttt ttg acc 403
His Pro Leu Pro Thr Ile Phe Val Cys Tyr Gly Asn Thr Phe Leu Thr
               90           95           100

ttc ttc tct ggc gga cag att ggt cgc aca cac ccc gaa gat tcc ggc 451
Phe Phe Ser Gly Gly Gln Ile Gly Arg Thr His Pro Glu Asp Ser Gly
               105           110           115

gcc acc aca gtg ttg cta act gac gcc ggc aaa cga gac gta ctc act 499
Ala Thr Thr Val Leu Leu Thr Asp Ala Gly Lys Arg Asp Val Leu Thr
               120           125           130

caa gac cta ccg gat agc ttt acg tcc ttt act ggt cac acg gaa aac 547
Gln Asp Leu Pro Asp Ser Phe Thr Ser Phe Thr Gly His Thr Glu Asn
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tcc gta
Ser Val
150

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<210> 2634

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 2634

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Met Val Ser Val Leu Leu Ile Gln Pro Arg Gln Gly Glu Ala Val Ala
  1           5           10           15

Ala Ala Glu Arg Arg Asp Phe Leu Gln Ala Thr Gly Leu Lys Pro Gln
  20           25           30

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70	75	80	85	
cgg gct cca atg tcg gct gcg gtg gtg agt gat gtt cat tcg agg gcg				403
Arg Ala Pro Met Ser Ala Ala Val Val Ser Asp Val His Ser Arg Ala				
	90	95	100	
gcg ctt gag tca ggg cag cat gat ttg ctt ggg acc act gat tac gtg				451
Ala Leu Glu Ser Gly Gln His Asp Leu Leu Gly Thr Thr Asp Tyr Val				
	105	110	115	
ctg gga acg gag ctt ttg gta cag gat gta acg gaa tcg acg gtg ggg				499
Leu Gly Thr Glu Leu Leu Val Gln Asp Val Thr Glu Ser Thr Val Gly				
	120	125	130	
aat att gat tgg ggt caa ttg ctg att tgg ggg ttg gtt gct ttg gca				547
Asn Ile Asp Trp Gly Gln Leu Leu Ile Trp Gly Leu Val Ala Leu Ala				
	135	140	145	
atc gcc gtg gtt gtt gcg ggt gcg tct gtg cgt cga aaa gca ata tct				595
Ile Ala Val Val Val Ala Gly Ala Ser Val Arg Arg Lys Ala Ile Ser				
	150	155	160	165
tta taagtaaagt tctaaagctt tac				621
Leu				

<210> 2636

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 2636

Met Ile Pro Glu Asn Ile Asp Leu Lys Gln Leu Ala Ser Glu Leu Gly				
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Asp Asp Ala Val Ala Met Gly Glu His Thr Gly Asn Gln Phe Pro Thr				
	20	25	30	
Leu Glu Lys Asp Leu Ile Asn Val Val Thr Asp Ala Lys Glu Ser Asp				
	35	40	45	
Phe Gly Ser Leu Gly Val Val Ile Leu Asp Glu Thr Pro Val Met Thr				
	50	55	60	
Ser Asn Leu Arg Asp Ile Ala Gln Glu Leu Leu Ile Gln Thr Asp Leu				
	65	70	75	80
Asp Thr Val Val Val Arg Ala Pro Met Ser Ala Ala Val Val Ser Asp				
	85	90	95	
Val His Ser Arg Ala Ala Leu Glu Ser Gly Gln His Asp Leu Leu Gly				
	100	105	110	
Thr Thr Asp Tyr Val Leu Gly Thr Glu Leu Leu Val Gln Asp Val Thr				
	115	120	125	
Glu Ser Thr Val Gly Asn Ile Asp Trp Gly Gln Leu Leu Ile Trp Gly				
	130	135	140	
Leu Val Ala Leu Ala Ile Ala Val Val Val Ala Gly Ala Ser Val Arg				

145 150 155 160

Arg Lys Ala Ile Ser Leu
165

<210> 2637
<211> 329
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(306)
<223> RXA02216

<400> 2637
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Val Ala Pro Ala Pro Gly His Val Val Leu Ala Thr Gly Pro Thr Cys
1 5 10 15
ccc atc cag atg ctg cgc gcc aac aag aac acc tgg tca gtt caa ttc 96
Pro Ile Gln Met Leu Arg Ala Asn Lys Asn Thr Trp Ser Val Gln Phe
20 25 30
cat gcg gat atg gat gcc gta ggc atg aaa aac cgc atg gat ttt tac 144
His Ala Asp Met Asp Ala Val Gly Met Lys Asn Arg Met Asp Phe Tyr
35 40 45
tcc aac tac cgg ttc ttc tcc cca gaa gat tat gac cgc atc att gca 192
Ser Asn Tyr Arg Phe Phe Ser Pro Glu Asp Tyr Asp Arg Ile Ile Ala
50 55 60
gag cta ccc tct gtt gac tcc att tat gcc aac agg gtg ctc cgc aac 240
Glu Leu Pro Ser Val Asp Ser Ile Tyr Ala Asn Arg Val Leu Arg Asn
65 70 75 80
ttc gtg gag gtc tgc gaa gga att cgt gtt gct gat ggt gct gag cac 288
Phe Val Glu Val Cys Glu Gly Ile Arg Val Ala Asp Gly Ala Glu His
85 90 95
caa ctc cca aag ctt aac taatcgagga gactggtgat tcg 329
Gln Leu Pro Lys Leu Asn
100

<210> 2638
<211> 102
<212> PRT
<213> Corynebacterium glutamicum

<400> 2638
Val Ala Pro Ala Pro Gly His Val Val Leu Ala Thr Gly Pro Thr Cys
1 5 10 15
Pro Ile Gln Met Leu Arg Ala Asn Lys Asn Thr Trp Ser Val Gln Phe
20 25 30
His Ala Asp Met Asp Ala Val Gly Met Lys Asn Arg Met Asp Phe Tyr
35 40 45

Ser Asn Tyr Arg Phe Phe Ser Pro Glu Asp Tyr Asp Arg Ile Ile Ala
50 55 60

Glu Leu Pro Ser Val Asp Ser Ile Tyr Ala Asn Arg Val Leu Arg Asn
65 70 75 80

Phe Val Glu Val Cys Glu Gly Ile Arg Val Ala Asp Gly Ala Glu His
85 90 95

Gln Leu Pro Lys Leu Asn
100

<210> 2639
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> RXA02217

<400> 2639
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ctttcggcag gaaaaactaa gagttgtag ggtggcgctc atg act aat aaa aca 115
Met Thr Asn Lys Thr
1 5

cga gct cta ctc att ggt ggc cac ggc aag gtg gcc ctc cta gca acc 163
Arg Ala Leu Leu Ile Gly Gly His Gly Lys Val Ala Leu Leu Ala Thr
10 15 20

ccc atg ctt atc gac gcc tcg gtg cag gtc act tcc atg tac cgc aat 211
Pro Met Leu Ile Asp Ala Ser Val Gln Val Thr Ser Met Tyr Arg Asn
25 30 35

ccg gac cac agg tcc gaa att gag gcg ctg ggc gcc aca act tta gag 259
Pro Asp His Arg Ser Glu Ile Glu Ala Leu Gly Ala Thr Thr Leu Glu
40 45 50

cgt gac gtc acc aca ctc agc gtg gag gat tgg gca gat ctg ctc aag 307
Arg Asp Val Thr Thr Leu Ser Val Glu Asp Trp Ala Asp Leu Leu Lys
55 60 65

gac ttc gac gta gtg gtg tgg agc gcc gga aac ggt ggc aag aac ggc 355
Asp Phe Asp Val Val Val Trp Ser Ala Gly Asn Gly Gly Lys Asn Gly
70 75 80 85

gcg gat gca act tat gcc att gat cgt gat gcc gcg atc gca tcc att 403
Ala Asp Ala Thr Tyr Ala Ile Asp Arg Asp Ala Ala Ile Ala Ser Ile
90 95 100

gat ggt gca gct agc cta ggg gag aag gca cct cgc tac atc atg gtg 451
Asp Gly Ala Ala Ser Leu Gly Glu Lys Ala Pro Arg Tyr Ile Met Val
105 110 115

agc tac att gga tcc tcc acg cac acc att gat cct tca gca tcc ttc 499
Ser Tyr Ile Gly Ser Ser Thr His Thr Ile Asp Pro Ser Ala Ser Phe
120 125 130

tac cca tat gca gaa tcc aaa aag gcc gct gat gag cac cta agc tcc 547
 Tyr Pro Tyr Ala Glu Ser Lys Lys Ala Ala Asp Glu His Leu Ser Ser
 135 140 145
 acc aac ctg gat tac ctt atc ctc gca cca gca gcc tta act ctg gat 595
 Thr Asn Leu Asp Tyr Leu Ile Leu Ala Pro Ala Ala Leu Thr Leu Asp
 150 155 160 165
 gaa gtc aat ggc gtt gag gtg atc gcc gat acc aac gaa gca gcc gca 643
 Glu Val Asn Gly Val Glu Val Ile Ala Asp Thr Asn Glu Ala Ala Ala
 170 175 180
 ggc cgc acc aca tca aga gtc ctc gtt gcg gaa gtt atc acc gag ttg 691
 Gly Arg Thr Thr Ser Arg Val Leu Val Ala Glu Val Ile Thr Glu Leu
 185 190 195
 gtg gtt cgc gac ttc cca caa acc cgt gtg ctg cct ttc gtg gat ggc 739
 Val Val Arg Asp Phe Pro Gln Thr Arg Val Leu Pro Phe Val Asp Gly
 200 205 210
 gaa tca cca gtc tcc tcg att agt taagctttgg gagttggtgc tca 786
 Glu Ser Pro Val Ser Ser Ile Ser
 215 220

<210> 2640

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 2640

Met Thr Asn Lys Thr Arg Ala Leu Leu Ile Gly Gly His Gly Lys Val
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 Ala Leu Leu Ala Thr Pro Met Leu Ile Asp Ala Ser Val Gln Val Thr
 20 25 30
 Ser Met Tyr Arg Asn Pro Asp His Arg Ser Glu Ile Glu Ala Leu Gly
 35 40 45
 Ala Thr Thr Leu Glu Arg Asp Val Thr Thr Leu Ser Val Glu Asp Trp
 50 55 60
 Ala Asp Leu Leu Lys Asp Phe Asp Val Val Val Trp Ser Ala Gly Asn
 65 70 75 80
 Gly Gly Lys Asn Gly Ala Asp Ala Thr Tyr Ala Ile Asp Arg Asp Ala
 85 90 95
 Ala Ile Ala Ser Ile Asp Gly Ala Ala Ser Leu Gly Glu Lys Ala Pro
 100 105 110
 Arg Tyr Ile Met Val Ser Tyr Ile Gly Ser Ser Thr His Thr Ile Asp
 115 120 125
 Pro Ser Ala Ser Phe Tyr Pro Tyr Ala Glu Ser Lys Lys Ala Ala Asp
 130 135 140
 Glu His Leu Ser Ser Thr Asn Leu Asp Tyr Leu Ile Leu Ala Pro Ala
 145 150 155 160

<400> 2642

Met Phe Ala Ile Met Thr Val Thr Gly Gln Asp His Thr Gly Ile Ile
 1 5 10 15
 Ala Ala Val Ser Thr Ala Leu Ala Glu Leu Asp Val Asn Ile His Asn
 20 25 30
 Val Ser Gln Thr Ile Met Asp Gln Trp Phe Thr Met Ile Leu His Val
 35 40 45
 Gly Phe Asp Glu Ser Val Leu Asp Ile Ala Thr Val Gln Glu Arg Met
 50 55 60
 Lys Pro Val Glu Lys Glu Gln Gly Leu Val Ile Arg Ile Gln Ser Glu
 65 70 75 80
 Ala Leu Phe Asn Ala Val Asn Glu Ile
 85

<210> 2643

<211> 1509

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1486)

<223> RXA02219

<400> 2643

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 agccttgttc aacgcggtta atgagatcta ggggggtgcac atg gat gat ttt tct 115
 Met Asp Asp Phe Ser
 1 5
 gca tcg cta ggt ttt act gac cgt tcc tcg agg gga att ctg gac acc 163
 Ala Ser Leu Gly Phe Thr Asp Arg Ser Ser Arg Gly Ile Leu Asp Thr
 10 15 20
 atc gag atg att gag aag tat cgt ctt gat att cgc acc gtg acc atg 211
 Ile Glu Met Ile Glu Lys Tyr Arg Leu Asp Ile Arg Thr Val Thr Met
 25 30 35
 gga atc agc ctg ttg gaa tgc gcg cgt ggc tcg atg gaa gag acc gcg 259
 Gly Ile Ser Leu Leu Glu Cys Ala Arg Gly Ser Met Glu Glu Thr Ala
 40 45 50
 acg gct gtt tat gat cgc gtg acg tca cag gct gca cgt ctg gtt gag 307
 Thr Ala Val Tyr Asp Arg Val Thr Ser Gln Ala Ala Arg Leu Val Glu
 55 60 65
 gtt tgt gaa ggc att gag cgt gaa ttg ggc att ccc att gtg aat aag 355
 Val Cys Glu Gly Ile Glu Arg Glu Leu Gly Ile Pro Ile Val Asn Lys
 70 75 80 85
 cgc atc tcg gtg act cca att gcc ctg gtg act gct ggt tgc agt ggc 403
 Arg Ile Ser Val Thr Pro Ile Ala Leu Val Thr Ala Gly Cys Ser Gly
 90 95 100

gat ccc gtt gac gtt gct cga gcc tta gat aag gca gca aaa gat gtc Asp Pro Val Asp Val Ala Arg Ala Leu Asp Lys Ala Ala Lys Asp Val 105 110 115	451
gga gtg aac ttc atc ggc ggg tat tca gca ctg gtt gaa aaa ggt gga Gly Val Asn Phe Ile Gly Gly Tyr Ser Ala Leu Val Glu Lys Gly Gly 120 125 130	499
acc acc tcc gat att cgg ctg atc cgc tcc att ccc gag gca ttg agc Thr Thr Ser Asp Ile Arg Leu Ile Arg Ser Ile Pro Glu Ala Leu Ser 135 140 145	547
aca acc gat gtg gtg tgt gga tcc gtc aat gtg gcg tcg tct cgc gcg Thr Thr Asp Val Val Cys Gly Ser Val Asn Val Ala Ser Ser Arg Ala 150 155 160 165	595
ggt atc aac atg aac gca gtc aat gag atg ggc aag gtg gtc aag caa Gly Ile Asn Met Asn Ala Val Asn Glu Met Gly Lys Val Val Lys Gln 170 175 180	643
gca gct gaa ttg acc aaa gat cgc tcc gcc atc gca tgt gca aag cta Ala Ala Glu Leu Thr Lys Asp Arg Ser Ala Ile Ala Cys Ala Lys Leu 185 190 195	691
gtg gtc ttt gcc aat tct gtg ggc gat aat cca ttc atg gct ggc gct Val Val Phe Ala Asn Ser Val Gly Asp Asn Pro Phe Met Ala Gly Ala 200 205 210	739
ttc cac ggc att gag gag ccg gat tgt gtg gtc agc gtt ggt gtc tca Phe His Gly Ile Glu Glu Pro Asp Cys Val Val Ser Val Gly Val Ser 215 220 225	787
gga cca ggc gtg gtt agt cgc gcg ctg ggc aat ctt caa ggt gcc acc Gly Pro Gly Val Val Ser Arg Ala Leu Gly Asn Leu Gln Gly Ala Thr 230 235 240 245	835
ctt gat caa gtc gca gaa gag atc aag aaa gcg gcc ttc aag atc act Leu Asp Gln Val Ala Glu Glu Ile Lys Lys Ala Ala Phe Lys Ile Thr 250 255 260	883
cgt act gga caa ctg gtt ggt gcg atg gcc tca gaa cgc cta gga gtt Arg Thr Gly Gln Leu Val Gly Ala Met Ala Ser Glu Arg Leu Gly Val 265 270 275	931
cct ttc ggc atc gtt gat ctt tcg ctc gct ccc act gct gaa gtg ggc Pro Phe Gly Ile Val Asp Leu Ser Leu Ala Pro Thr Ala Glu Val Gly 280 285 290	979
gat tcc gtg gca aat atc ctt gag gtc atg ggt ctt gac cag gtg ggc Asp Ser Val Ala Asn Ile Leu Glu Val Met Gly Leu Asp Gln Val Gly 295 300 305	1027
aca cat ggc acc acc gcg gca ctc gca ctg ctc aac gac gcg gtg aaa Thr His Gly Thr Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys 310 315 320 325	1075
aag ggt ggc atg atg gcc tgc tca cgt gtc ggc ggc ttg tcc gga tcc Lys Gly Gly Met Met Ala Cys Ser Arg Val Gly Gly Leu Ser Gly Ser 330 335 340	1123
ttc att cca gtt tct gaa gat aaa ggc atg atc gat gcg gtt cgc aca	1171

Phe Ile Pro Val Ser Glu Asp Lys Gly Met Ile Asp Ala Val Arg Thr
 345 350 355

gga gca att tct att gac aag ctc gaa gcg atg acc gcg atc tgc tca 1219
 Gly Ala Ile Ser Ile Asp Lys Leu Glu Ala Met Thr Ala Ile Cys Ser
 360 365 370

gtt ggt ttg gat atg att gcg atc cct ggc gac acc ccg gcg gaa act 1267
 Val Gly Leu Asp Met Ile Ala Ile Pro Gly Asp Thr Pro Ala Glu Thr
 375 380 385

att tcg ggc atg atc gcg gac gaa gca gcc atc ggt gtg atg aat cat 1315
 Ile Ser Gly Met Ile Ala Asp Glu Ala Ala Ile Gly Val Met Asn His
 390 395 400 405

aag act aca gct gtg cgt gtt att cct gtt cca gga act gtc cct ggc 1363
 Lys Thr Thr Ala Val Arg Val Ile Pro Val Pro Gly Thr Val Pro Gly
 410 415 420

gat gag gta gat ttc ggt ggc ttg ctg ggt tac gcg ccg gtc att cca 1411
 Asp Glu Val Asp Phe Gly Gly Leu Leu Gly Tyr Ala Pro Val Ile Pro
 425 430 435

gta aat acc gtg gga aat agt gag ttt att cac cgc ggc ggc ttc att 1459
 Val Asn Thr Val Gly Asn Ser Glu Phe Ile His Arg Gly Gly Phe Ile
 440 445 450

cca gca ccc gtt cac ggg ttt aga aac taggagatcc ggggccttta 1506
 Pro Ala Pro Val His Gly Phe Arg Asn
 455 460

cct 1509

<210> 2644
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2644
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 20 25 30

Arg Thr Val Thr Met Gly Ile Ser Leu Leu Glu Cys Ala Arg Gly Ser
 35 40 45

Met Glu Glu Thr Ala Thr Ala Val Tyr Asp Arg Val Thr Ser Gln Ala
 50 55 60

Ala Arg Leu Val Glu Val Cys Glu Gly Ile Glu Arg Glu Leu Gly Ile
 65 70 75 80

Pro Ile Val Asn Lys Arg Ile Ser Val Thr Pro Ile Ala Leu Val Thr
 85 90 95

Ala Gly Cys Ser Gly Asp Pro Val Asp Val Ala Arg Ala Leu Asp Lys
 100 105 110

Ala Ala Lys Asp Val Gly Val Asn Phe Ile Gly Gly Tyr Ser Ala Leu
115 120 125

Val Glu Lys Gly Gly Thr Thr Ser Asp Ile Arg Leu Ile Arg Ser Ile
130 135 140

Pro Glu Ala Leu Ser Thr Thr Asp Val Val Cys Gly Ser Val Asn Val
145 150 155 160

Ala Ser Ser Arg Ala Gly Ile Asn Met Asn Ala Val Asn Glu Met Gly
165 170 175

Lys Val Val Lys Gln Ala Ala Glu Leu Thr Lys Asp Arg Ser Ala Ile
180 185 190

Ala Cys Ala Lys Leu Val Val Phe Ala Asn Ser Val Gly Asp Asn Pro
195 200 205

Phe Met Ala Gly Ala Phe His Gly Ile Glu Glu Pro Asp Cys Val Val
210 215 220

Ser Val Gly Val Ser Gly Pro Gly Val Val Ser Arg Ala Leu Gly Asn
225 230 235 240

Leu Gln Gly Ala Thr Leu Asp Gln Val Ala Glu Glu Ile Lys Lys Ala
245 250 255

Ala Phe Lys Ile Thr Arg Thr Gly Gln Leu Val Gly Ala Met Ala Ser
260 265 270

Glu Arg Leu Gly Val Pro Phe Gly Ile Val Asp Leu Ser Leu Ala Pro
275 280 285

Thr Ala Glu Val Gly Asp Ser Val Ala Asn Ile Leu Glu Val Met Gly
290 295 300

Leu Asp Gln Val Gly Thr His Gly Thr Thr Ala Ala Leu Ala Leu Leu
305 310 315 320

Asn Asp Ala Val Lys Lys Gly Gly Met Met Ala Cys Ser Arg Val Gly
325 330 335

Gly Leu Ser Gly Ser Phe Ile Pro Val Ser Glu Asp Lys Gly Met Ile
340 345 350

Asp Ala Val Arg Thr Gly Ala Ile Ser Ile Asp Lys Leu Glu Ala Met
355 360 365

Thr Ala Ile Cys Ser Val Gly Leu Asp Met Ile Ala Ile Pro Gly Asp
370 375 380

Thr Pro Ala Glu Thr Ile Ser Gly Met Ile Ala Asp Glu Ala Ala Ile
385 390 395 400

Gly Val Met Asn His Lys Thr Thr Ala Val Arg Val Ile Pro Val Pro
405 410 415

Gly Thr Val Pro Gly Asp Glu Val Asp Phe Gly Gly Leu Leu Gly Tyr
420 425 430

Ala Pro Val Ile Pro Val Asn Thr Val Gly Asn Ser Glu Phe Ile His

435

440

445

Arg Gly Gly Phe Ile Pro Ala Pro Val His Gly Phe Arg Asn
 450 455 460

<210> 2645

<211> 1485

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1462)

<223> RXA02221

<400> 2645

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ccatcacgac ttcataccca ccaattgaaa gtaaagtcca atg ttt acc gca tcc 115
 Met Phe Thr Ala Ser
 1 5

att cct act tat gaa tta ggg tct ttc agc aag ggc tcc tac gtt gag 163
 Ile Pro Thr Tyr Glu Leu Gly Ser Phe Ser Lys Gly Ser Tyr Val Glu
 10 15 20

atc aaa gga act tac ttc tac cct gac acg cta aat act tta ttt aga 211
 Ile Lys Gly Thr Tyr Phe Tyr Pro Asp Thr Leu Asn Thr Leu Phe Arg
 25 30 35

aat tct ggg gca aaa gac aac gaa gag ttc ttt gta gac gta act ctt 259
 Asn Ser Gly Ala Lys Asp Asn Glu Glu Phe Phe Val Asp Val Thr Leu
 40 45 50

gtt cca gaa cca gat aat ccg cat agc act cga ggc cat gcc att tca 307
 Val Pro Glu Pro Asp Asn Pro His Ser Thr Arg Gly His Ala Ile Ser
 55 60 65

gtc cgc tgg aat gat ctc gta ata gga cat att gcc tcg gat atg act 355
 Val Arg Trp Asn Asp Leu Val Ile Gly His Ile Ala Ser Asp Met Thr
 70 75 80 85

gaa aaa ttc caa caa gtg cga cga gtt gca gct agt ggc tac gat gct 403
 Glu Lys Phe Gln Gln Val Arg Arg Val Ala Ala Ser Gly Tyr Asp Ala
 90 95 100

cga gtc tct gct cgg att tgg acg aat aca aac tat aag aat gaa cga 451
 Arg Val Ser Ala Arg Ile Trp Thr Asn Thr Asn Tyr Lys Asn Glu Arg
 105 110 115

gat ttt tgg gta tct gtt aag ctc ccc gat cca gat ttc ctt gtt cct 499
 Asp Phe Trp Val Ser Val Lys Leu Pro Asp Pro Asp Phe Leu Val Pro
 120 125 130

ctt aat gat cct ccc cat gac ggg ttt acc ctc ctc cct tat gga aca 547
 Leu Asn Asp Pro Pro His Asp Gly Phe Thr Leu Leu Pro Tyr Gly Thr
 135 140 145

gca atc caa gtc acc aag gaa tct gat cac atg gac gtg ctc tca gaa 595
 Ala Ile Gln Val Thr Lys Glu Ser Asp His Met Asp Val Leu Ser Glu

150	155	160	165	
ttc gtg cct cca tct gga caa ggt cag att ctc gta tcg cta cac atc				643
Phe Val Pro Pro Ser Gly Gln Gly Gln Ile Leu Val Ser Leu His Ile				
	170	175	180	
att aac gca ggc gtg aga aaa gaa tgg gat ggc att gaa gtt cgg ctc				691
Ile Asn Ala Gly Val Arg Lys Glu Trp Asp Gly Ile Glu Val Arg Leu				
	185	190	195	
gat aat caa cgg atc gga gag ctt aca aag gcc agt tca gaa aaa ttc				739
Asp Asn Gln Arg Ile Gly Glu Leu Thr Lys Ala Ser Ser Glu Lys Phe				
	200	205	210	
gca ccc gta gtg cga cat ttc gat gac cta gga ctt agt aca cta tgt				787
Ala Pro Val Val Arg His Phe Asp Asp Leu Gly Leu Ser Thr Leu Cys				
	215	220	225	
cgt gcg ctc atc aag ggg tca tca cta gct gct gaa gta act cta tat				835
Arg Ala Leu Ile Lys Gly Ser Ser Leu Ala Ala Glu Val Thr Leu Tyr				
	230	235	240	245
gga gct cgt gca cat gag ctt tcc gaa gaa gac tta gaa cct aaa agc				883
Gly Ala Arg Ala His Glu Leu Ser Glu Glu Asp Leu Glu Pro Lys Ser				
	250	255	260	
tct tcc cca ttg ccc agg ttg gtt gaa tac cag tca aat ccg ttt aat				931
Ser Ser Pro Leu Pro Arg Leu Val Glu Tyr Gln Ser Asn Pro Phe Asn				
	265	270	275	
tat caa gtc ccc aac agg tgg ccc ggc gag cag aat caa cgt gct cct				979
Tyr Gln Val Pro Asn Arg Trp Pro Gly Glu Gln Asn Gln Arg Ala Pro				
	280	285	290	
aag tcg caa aag tct tct tca tca cct ttc gca gcg tat cgc ggg cca				1027
Lys Ser Gln Lys Ser Ser Ser Ser Pro Phe Ala Ala Tyr Arg Gly Pro				
	295	300	305	
tcg caa cct agt aaa tca ctc aca ccg ttt gta gcg cag aca cct gcg				1075
Ser Gln Pro Ser Lys Ser Leu Thr Pro Phe Val Ala Gln Thr Pro Ala				
	310	315	320	325
cct cag cct agt gat cga ttt att gat tgg gat tca ttg ctt caa ccg				1123
Pro Gln Pro Ser Asp Arg Phe Ile Asp Trp Asp Ser Leu Leu Gln Pro				
	330	335	340	
gac gga act cca aga gct acg cca ttc caa aga gga gta acc cgc ggg				1171
Asp Gly Thr Pro Arg Ala Thr Pro Phe Gln Arg Gly Val Thr Arg Gly				
	345	350	355	
tta att ggc aag cat ttt tcg aat caa aaa tct cca aga att gac ttt				1219
Leu Ile Gly Lys His Phe Ser Asn Gln Lys Ser Pro Arg Ile Asp Phe				
	360	365	370	
gca acg gtg ggg caa tgt gat gca att ctc cga act ttc gga gag ccg				1267
Ala Thr Val Gly Gln Cys Asp Ala Ile Leu Arg Thr Phe Gly Glu Pro				
	375	380	385	
acc gac aag ctt tat aaa gac ggc agg act tct tgg cct ttg tgg tgg				1315
Thr Asp Lys Leu Tyr Lys Asp Gly Arg Thr Ser Trp Pro Leu Trp Trp				
	390	395	400	405

gcg ctc atg gcg ata gtc acc ctt ctc gtc atg ttg ctg aac ttt att 1363
 Ala Leu Met Ala Ile Val Thr Leu Leu Val Met Leu Leu Asn Phe Ile
 410 415 420

cca gga att ggt ccg atc ttc cca ctt atc gga ttg atc gta ctt ggt 1411
 Pro Gly Ile Gly Pro Ile Phe Pro Leu Ile Gly Leu Ile Val Leu Gly
 425 430 435

cat cac ttt tgg act cgc cga aaa ctt aac cca cca ttc ggt aga tca 1459
 His His Phe Trp Thr Arg Arg Lys Leu Asn Pro Pro Phe Gly Arg Ser
 440 445 450

aaa tagatattct catcaaatat cgc 1485
 Lys

<210> 2646
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2646
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Asn Thr Leu Phe Arg Asn Ser Gly Ala Lys Asp Asn Glu Glu Phe Phe
 35 40 45

Val Asp Val Thr Leu Val Pro Glu Pro Asp Asn Pro His Ser Thr Arg
 50 55 60

Gly His Ala Ile Ser Val Arg Trp Asn Asp Leu Val Ile Gly His Ile
 65 70 75 80

Ala Ser Asp Met Thr Glu Lys Phe Gln Gln Val Arg Arg Val Ala Ala
 85 90 95

Ser Gly Tyr Asp Ala Arg Val Ser Ala Arg Ile Trp Thr Asn Thr Asn
 100 105 110

Tyr Lys Asn Glu Arg Asp Phe Trp Val Ser Val Lys Leu Pro Asp Pro
 115 120 125

Asp Phe Leu Val Pro Leu Asn Asp Pro Pro His Asp Gly Phe Thr Leu
 130 135 140

Leu Pro Tyr Gly Thr Ala Ile Gln Val Thr Lys Glu Ser Asp His Met
 145 150 155 160

Asp Val Leu Ser Glu Phe Val Pro Pro Ser Gly Gln Gly Gln Ile Leu
 165 170 175

Val Ser Leu His Ile Ile Asn Ala Gly Val Arg Lys Glu Trp Asp Gly
 180 185 190

Ile Glu Val Arg Leu Asp Asn Gln Arg Ile Gly Glu Leu Thr Lys Ala

195	200	205
Ser Ser Glu Lys Phe Ala Pro Val Val Arg His Phe Asp Asp Leu Gly 210 215 220		
Leu Ser Thr Leu Cys Arg Ala Leu Ile Lys Gly Ser Ser Leu Ala Ala 225 230 235 240		
Glu Val Thr Leu Tyr Gly Ala Arg Ala His Glu Leu Ser Glu Glu Asp 245 250 255		
Leu Glu Pro Lys Ser Ser Ser Pro Leu Pro Arg Leu Val Glu Tyr Gln 260 265 270		
Ser Asn Pro Phe Asn Tyr Gln Val Pro Asn Arg Trp Pro Gly Glu Gln 275 280 285		
Asn Gln Arg Ala Pro Lys Ser Gln Lys Ser Ser Ser Ser Pro Phe Ala 290 295 300		
Ala Tyr Arg Gly Pro Ser Gln Pro Ser Lys Ser Leu Thr Pro Phe Val 305 310 315 320		
Ala Gln Thr Pro Ala Pro Gln Pro Ser Asp Arg Phe Ile Asp Trp Asp 325 330 335		
Ser Leu Leu Gln Pro Asp Gly Thr Pro Arg Ala Thr Pro Phe Gln Arg 340 345 350		
Gly Val Thr Arg Gly Leu Ile Gly Lys His Phe Ser Asn Gln Lys Ser 355 360 365		
Pro Arg Ile Asp Phe Ala Thr Val Gly Gln Cys Asp Ala Ile Leu Arg 370 375 380		
Thr Phe Gly Glu Pro Thr Asp Lys Leu Tyr Lys Asp Gly Arg Thr Ser 385 390 395 400		
Trp Pro Leu Trp Trp Ala Leu Met Ala Ile Val Thr Leu Leu Val Met 405 410 415		
Leu Leu Asn Phe Ile Pro Gly Ile Gly Pro Ile Phe Pro Leu Ile Gly 420 425 430		
Leu Ile Val Leu Gly His His Phe Trp Thr Arg Arg Lys Leu Asn Pro 435 440 445		
Pro Phe Gly Arg Ser Lys 450		

<210> 2647

<211> 741

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(718)

<223> RXA02227

<400> 2647

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                               Val Glu Asp Val Asn
                               1 5

gca acg ctg att atc atg cct gga agt ccg gcg ctg gta cct gaa ctg 163
Ala Thr Leu Ile Ile Met Pro Gly Ser Pro Ala Leu Val Pro Glu Leu
                10                15                20

gca cca gcg gat gct gcg ggg gcg cgc ttg ttg gcg tcg tta cgt gca 211
Ala Pro Ala Asp Ala Ala Gly Ala Arg Leu Leu Ala Ser Leu Arg Ala
                25                30                35

gtt ttt gat gcg gaa ctg gct aat gat gat cgc ccg atc gag ttg gtt 259
Val Phe Asp Ala Glu Leu Ala Asn Asp Asp Arg Pro Ile Glu Leu Val
                40                45                50

ggc tcc cgg gat gag gcg tgg ttt acc aag cat gcg gga aat ctg cgg 307
Gly Ser Arg Asp Glu Ala Trp Phe Thr Lys His Ala Gly Asn Leu Arg
                55                60                65

gcc tgg ggt gca ccg agc gtg cag gtt tct gac gga cat tat ttg ccg 355
Ala Trp Gly Ala Pro Ser Val Gln Val Ser Asp Gly His Tyr Leu Pro
                70                75                80                85

gaa att ttg cag cgt gtc gcg ctg ggt ggt ttc gaa tcg cgt gta act 403
Glu Ile Leu Gln Arg Val Ala Leu Gly Gly Phe Glu Ser Arg Val Thr
                90                95                100

cat gtg cgc gat cgg ttg ggt agc gtc aac gac aac acg gtt acg gtg 451
His Val Arg Asp Arg Leu Gly Ser Val Asn Asp Asn Thr Val Thr Val
                105                110                115

ctt gcc ctt gac ggc ccc acg ggc ttg acc acc cgc gcg ccg tcc gca 499
Leu Ala Leu Asp Gly Pro Thr Gly Leu Thr Thr Arg Ala Pro Ser Ala
                120                125                130

ctc gtg ccc ggc gcg tcc aac atc gac gcc tgg tgc cgc tca ttg ctg 547
Leu Val Pro Gly Ala Ser Asn Ile Asp Ala Trp Cys Arg Ser Leu Leu
                135                140                145

tct gga aag ccc ggg gaa gtg ccc agc acc agc acg ctt atc gac gcc 595
Ser Gly Lys Pro Gly Glu Val Pro Ser Thr Ser Thr Leu Ile Asp Ala
                150                155                160                165

tcc ctc cgc gaa cca cag ctc tgg ctc gac tta tcc gcc gtg gca aca 643
Ser Leu Arg Glu Pro Gln Leu Trp Leu Asp Leu Ser Ala Val Ala Thr
                170                175                180

gaa gcg tca act gct caa ctt ctc gac agc gac gac aca cac ggc gtg 691
Glu Ala Ser Thr Ala Gln Leu Leu Asp Ser Asp Asp Thr His Gly Val
                185                190                195

gga cgc tac gtt gct cgc tgg act ttt taacttaagg gagatctaga 738
Gly Arg Tyr Val Ala Arg Trp Thr Phe
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tcg 741

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<212> PRT
<213> Corynebacterium glutamicum

<400> 2648
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Leu Val Pro Glu Leu Ala Pro Ala Asp Ala Ala Gly Ala Arg Leu Leu
20 25 30
Ala Ser Leu Arg Ala Val Phe Asp Ala Glu Leu Ala Asn Asp Asp Arg
35 40 45
Pro Ile Glu Leu Val Gly Ser Arg Asp Glu Ala Trp Phe Thr Lys His
50 55 60
Ala Gly Asn Leu Arg Ala Trp Gly Ala Pro Ser Val Gln Val Ser Asp
65 70 75 80
Gly His Tyr Leu Pro Glu Ile Leu Gln Arg Val Ala Leu Gly Gly Phe
85 90 95
Glu Ser Arg Val Thr His Val Arg Asp Arg Leu Gly Ser Val Asn Asp
100 105 110
Asn Thr Val Thr Val Leu Ala Leu Asp Gly Pro Thr Gly Leu Thr Thr
115 120 125
Arg Ala Pro Ser Ala Leu Val Pro Gly Ala Ser Asn Ile Asp Ala Trp
130 135 140
Cys Arg Ser Leu Leu Ser Gly Lys Pro Gly Glu Val Pro Ser Thr Ser
145 150 155 160
Thr Leu Ile Asp Ala Ser Leu Arg Glu Pro Gln Leu Trp Leu Asp Leu
165 170 175
Ser Ala Val Ala Thr Glu Ala Ser Thr Ala Gln Leu Leu Asp Ser Asp
180 185 190
Asp Thr His Gly Val Gly Arg Tyr Val Ala Arg Trp Thr Phe
195 200 205

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<211> 660
<212> DNA
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<220>
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<222> (101)..(637)
<223> RXA02230

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cgc ttt gct aat ggt tca cgc tcc aac aaa ctg ccg ctc atc gtc atc						163
Pro Phe Ala Asn Gly Ser Arg Ser Asn Lys Leu Pro Leu Ile Val Ile						
ggt ttg tgc tgc ata atg ctg atc ctg tgg ctt aaa ctt ccc ggc gta						211
Gly Leu Cys Cys Ile Met Leu Ile Leu Trp Leu Lys Leu Pro Gly Val						
ctg ctt gcc acc atc att ggg gtt gcc acg atg agt gtg atg cgg atg						259
Leu Leu Ala Thr Ile Ile Gly Val Ala Thr Met Ser Val Met Arg Met						
cgc acc tcc acc cca gaa act gcc tcg ctg gtt act tct att cgg ctg						307
Arg Thr Ser Thr Pro Glu Thr Ala Ser Leu Val Thr Ser Ile Arg Leu						
tct gcg gaa gat att tcc gat gtg caa cat gag tgg cag cag ttt ttg						355
Ser Ala Glu Asp Ile Ser Asp Val Gln His Glu Trp Gln Gln Phe Leu						
acc tcc ccc gag gcc gat gcg ctg gct gat cgc acg ctt gtc cgt ccc						403
Thr Ser Pro Glu Ala Asp Ala Leu Ala Asp Arg Thr Leu Val Arg Pro						
gca ctg gcg gat cca gat tgt ggc gat aag gct atc gag aaa ttt cat						451
Ala Leu Ala Asp Pro Asp Cys Gly Asp Lys Ala Ile Glu Lys Phe His						
tat gaa atc agc aat gcc aat cgc ttc ttg ggc agg ttg gac gct cgt						499
Tyr Glu Ile Ser Asn Ala Asn Arg Phe Leu Gly Arg Leu Asp Ala Arg						
ctg caa caa aac ctc gtg gtc agt gag cta gaa aca ctt ctc aaa gta						547
Leu Gln Gln Asn Leu Val Ser Glu Leu Glu Thr Leu Leu Lys Val						
acg gac gag cgc gca cta gag ctg cgg gaa acg tgg ctg gat gcg cgt						595
Thr Asp Glu Arg Ala Leu Glu Leu Arg Glu Thr Trp Leu Asp Ala Arg						
aaa gcg gcc cag aaa ctt ggg ccg aac tac aat cgc gaa tct						637
Lys Ala Ala Gln Lys Leu Gly Pro Asn Tyr Asn Arg Glu Ser						
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<210> 2650

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 2650

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Pro	Leu	Ile	Val	Ile	Gly	Leu	Cys	Cys	Ile	Met	Leu	Ile	Leu	Trp	Leu
			20				25						30		

gct gtc gag cct ttt gcc acc ttc gcc ggc ttt aac tcc gca aca gtc 307
 Ala Val Glu Pro Phe Ala Thr Phe Ala Gly Phe Asn Ser Ala Thr Val
 55 60 65

gct tac ggc cac gtc agc atg atc aat gat gtg ctg tcc ctg gtc gat 355
 Ala Tyr Gly His Val Ser Met Ile Asn Asp Val Leu Ser Leu Val Asp
 70 75 80 85

atc atc gat cct ttc ggc acc cct gtt gcc acc att acc tgc aac ctt 403
 Ile Ile Asp Pro Phe Gly Thr Pro Val Ala Thr Ile Thr Cys Asn Leu
 90 95 100

gct caa ggc cca ctg ctt gtt gat gaa cca gtg cag cgc tgg cag cag 451
 Ala Gln Gly Pro Leu Leu Val Asp Glu Pro Val Gln Arg Trp Gln Gln
 105 110 115

atc cgc att act gcc ctg ggc att gat gtt gag gtc cac gac aat gca 499
 Ile Arg Ile Thr Ala Leu Gly Ile Asp Val Glu Val His Asp Asn Ala
 120 125 130

gat gct tac atc cgc aat ggt ggc gaa act gtc ggc atg ctg gtt tct 547
 Asp Ala Tyr Ile Arg Asn Gly Gly Glu Thr Val Gly Met Leu Val Ser
 135 140 145

gaa ggt gca gag aag att gcc agc ggc agc ggc gct gtc atc ccg gac 595
 Glu Gly Ala Glu Lys Ile Ala Ser Gly Ser Gly Ala Val Ile Pro Asp
 150 155 160 165

gca tcc gca gag ttt tcc gca cgc gtg ttg tct gcg gag tac cgc acc 643
 Ala Ser Ala Glu Phe Ser Ala Arg Val Leu Ser Ala Glu Tyr Arg Thr
 170 175 180

aac act ctt acc ggc cag cgt ttt atc cac gca aca gtt gat ggc ctc 691
 Asn Thr Leu Thr Gly Gln Arg Phe Ile His Ala Thr Val Asp Gly Leu
 185 190 195

ttc gct ttt gat gtg tgc ctt cct gat gca cca gaa cta cct gcc cgt 739
 Phe Ala Phe Asp Val Cys Leu Pro Asp Ala Pro Glu Leu Pro Ala Arg
 200 205 210

gac agc gtg ttg tct ggc aaa gtc atg ctg act gct gcc gtt atc ccc 787
 Asp Ser Val Leu Ser Gly Lys Val Met Leu Thr Ala Ala Val Ile Pro
 215 220 225

act gag gtc acc ggc tgc ggt ggc tcc ggt ggc ggc tgt ggc tca ggt 835
 Thr Glu Val Thr Gly Cys Gly Gly Ser Gly Gly Gly Cys Gly Ser Gly
 230 235 240 245

agc tgt ggc tgc ggc gga cac taaaattctg cacaattttt taa 879
 Ser Cys Gly Cys Gly Gly His
 250

<210> 2652

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 2652

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Ser Gly Gly Phe Arg Ser Arg Thr Pro Lys Ala Gln Gln Glu Pro Ala						
aag cag aag ccg cag gcg cgt aaa tct ccg tca aag aag gcc ccg gct						211
Lys Gln Lys Pro Gln Ala Arg Lys Ser Pro Ser Lys Lys Ala Pro Ala						
cgg ggg cag ggg cag agt cag ggg cag cgc cag ggc caa agc agt ggc						259
Arg Gly Gln Gly Gln Ser Gln Gly Gln Arg Gln Gly Gln Ser Ser Gly						
aaa ggc ggc gga aac cgc aag ccc cct gcg cag gcc agg gaa gtg agg						307
Lys Gly Gly Gly Asn Arg Lys Pro Pro Ala Gln Ala Arg Glu Val Arg						
gct ctg ggc gtc gat aag ccg aga gaa att gcg ttt gag gtg ctt gat						355
Ala Leu Gly Val Asp Lys Pro Arg Glu Ile Ala Phe Glu Val Leu Asp						
cgt gtg cgt acc ggt gag gcg tat gcc aac ttg gtg ttg cca cga ctg						403
Arg Val Arg Thr Gly Glu Ala Tyr Ala Asn Leu Val Leu Pro Arg Leu						
ctg agc aag cac aat ctt tct ggc cgt gac gcg gcc ttt gct acg gaa						451
Leu Ser Lys His Asn Leu Ser Gly Arg Asp Ala Ala Phe Ala Thr Glu						
att acc tac ggc acc ttg cgt aat gtc ggc ttg ctg gat gag gtc att						499
Ile Thr Tyr Gly Thr Leu Arg Asn Val Gly Leu Leu Asp Glu Val Ile						
aag gct gca tct ggg cgt gaa ctg tct gat att gat cca gag gtt ttg						547
Lys Ala Ala Ser Gly Arg Glu Leu Ser Asp Ile Asp Pro Glu Val Leu						
gac gtg ctg cgt ttg ggc gcg tac cag gtg atg ttt acc cgc gtg gag						595
Asp Val Leu Arg Leu Gly Ala Tyr Gln Val Met Phe Thr Arg Val Glu						
gat cac gct gcg gtc gat act tca gta aag atg gtc ggt ggg ctg aag						643
Asp His Ala Ala Val Asp Thr Ser Val Lys Met Val Gly Gly Leu Lys						
aaa ttc cag gcc act ggt ttt gcc aat gca att ttg cgc aac atc acg						691
Lys Phe Gln Ala Thr Gly Phe Ala Asn Ala Ile Leu Arg Asn Ile Thr						
cgc aag gaa cca gag cag tgg ttg aag gaa ttg gag ccc gcg gaa gag						739
Arg Lys Glu Pro Glu Gln Trp Leu Lys Glu Leu Glu Pro Ala Glu Glu						
ttg gct cgc gtt gcg ttc cgt act gcg cac cca cgc tgg att gcg cag						787
Leu Ala Arg Val Ala Phe Arg Thr Ala His Pro Arg Trp Ile Ala Gln						
agt ttc tca cag gtg ctc ccg gca gat gag ttg gaa gca gcg ctt gct						835
Ser Phe Ser Gln Val Leu Pro Ala Asp Glu Leu Glu Ala Ala Leu Ala						

230	235	240	245	
gcg gac tct gag cgc cca gtg gtg cac ttg gtg gct cgc cca ggt gag Ala Asp Ser Glu Arg Pro Val Val His Leu Val Ala Arg Pro Gly Glu	250	255	260	883
atc agt gca gag gaa ttg gcg ctg atc acc ggt ggt gac gag ggc aag Ile Ser Ala Glu Glu Leu Ala Leu Ile Thr Gly Gly Asp Glu Gly Lys	265	270	275	931
tat tcc cca tac gcg gtg tac ctc gag ggt ggc gac ccg ggt gat att Tyr Ser Pro Tyr Ala Val Tyr Leu Glu Gly Gly Asp Pro Gly Asp Ile	280	285	290	979
gag cca gtg aag gat ggt ctt gca gca gtg caa gat gag ggt tct cag Glu Pro Val Lys Asp Gly Leu Ala Ala Val Gln Asp Glu Gly Ser Gln	295	300	305	1027
ctg att gct cgc gcc ttg gtg gaa atc ccc gtg gag ggc acc gat gcc Leu Ile Ala Arg Ala Leu Val Glu Ile Pro Val Glu Gly Thr Asp Ala	310	315	320	1075
ggc cgt tgg ctg gat atg tgt gca ggt cct ggc ggt aaa gcg gcg ctc Gly Arg Trp Leu Asp Met Cys Ala Gly Pro Gly Gly Lys Ala Ala Leu	330	335	340	1123
att ggt gcg ttg gct cgc atg gat cgt gcc acc gtt gat gcc gtg gag Ile Gly Ala Leu Ala Arg Met Asp Arg Ala Thr Val Asp Ala Val Glu	345	350	355	1171
gtc tct gat cac cgt gcc cga ctg att gaa aag tcc gtg cgt ggt ttg Val Ser Asp His Arg Ala Arg Leu Ile Glu Lys Ser Val Arg Gly Leu	360	365	370	1219
ccc gtc aag gtt cat gtg ggc gat ggc cgc acc atc aac ttg acc ggt Pro Val Lys Val His Val Gly Asp Gly Arg Thr Ile Asn Leu Thr Gly	375	380	385	1267
ggc tac gat cgt gcg cta gtc gat gcg ccg tgt tct ggt ttg ggt gca Gly Tyr Asp Arg Ala Leu Val Asp Ala Pro Cys Ser Gly Leu Gly Ala	390	395	400	1315
ctg cgt cgt cgc cct gag gcg cgt tgg cgc aag cag gaa agc gac att Leu Arg Arg Arg Pro Glu Ala Arg Trp Arg Lys Gln Glu Ser Asp Ile	410	415	420	1363
gtt gag ctc aac acc ctg cag tac gag ctg ctt gaa tcc gct gtg aac Val Glu Leu Asn Thr Leu Gln Tyr Glu Leu Leu Glu Ser Ala Val Asn	425	430	435	1411
aag gtg cgt tcc ggt ggc gtg att gtg tac tcc aca tgt tca cct gat Lys Val Arg Ser Gly Gly Val Ile Val Tyr Ser Thr Cys Ser Pro Asp	440	445	450	1459
ctg cgt gaa acc cgc gga atc gtg gac aag gca ctg ggg gct ctg gag Leu Arg Glu Thr Arg Gly Ile Val Asp Lys Ala Leu Gly Ala Leu Glu	455	460	465	1507
atc gaa gag ctt gag gct gcg gag ttc atg cca ggc atg acc gat acc Ile Glu Glu Leu Glu Ala Ala Glu Phe Met Pro Gly Met Thr Asp Thr	470	475	480	1555
			485	

ggc gat gag aaa tca gtg cag atg tgg cca cac cgc cac ggc acc gat 1603
 Gly Asp Glu Lys Ser Val Gln Met Trp Pro His Arg His Gly Thr Asp
 490 495 500

gcg atg ttt gtg gca gtg ctg cga aag aag tagacctgtg agctaagtgg 1653
 Ala Met Phe Val Ala Val Leu Arg Lys Lys
 505 510

ggt 1656

<210> 2654

<211> 511

<212> PRT

<213> Corynebacterium glutamicum

<400> 2654

Met Ser Leu Glu Lys Ser Gly Gly Phe Arg Ser Arg Thr Pro Lys Ala
 1 5 10 15

Gln Gln Glu Pro Ala Lys Gln Lys Pro Gln Ala Arg Lys Ser Pro Ser
 20 25 30

Lys Lys Ala Pro Ala Arg Gly Gln Gly Gln Ser Gln Gly Gln Arg Gln
 35 40 45

Gly Gln Ser Ser Gly Lys Gly Gly Gly Asn Arg Lys Pro Pro Ala Gln
 50 55 60

Ala Arg Glu Val Arg Ala Leu Gly Val Asp Lys Pro Arg Glu Ile Ala
 65 70 75 80

Phe Glu Val Leu Asp Arg Val Arg Thr Gly Glu Ala Tyr Ala Asn Leu
 85 90 95

Val Leu Pro Arg Leu Leu Ser Lys His Asn Leu Ser Gly Arg Asp Ala
 100 105 110

Ala Phe Ala Thr Glu Ile Thr Tyr Gly Thr Leu Arg Asn Val Gly Leu
 115 120 125

Leu Asp Glu Val Ile Lys Ala Ala Ser Gly Arg Glu Leu Ser Asp Ile
 130 135 140

Asp Pro Glu Val Leu Asp Val Leu Arg Leu Gly Ala Tyr Gln Val Met
 145 150 155 160

Phe Thr Arg Val Glu Asp His Ala Ala Val Asp Thr Ser Val Lys Met
 165 170 175

Val Gly Gly Leu Lys Lys Phe Gln Ala Thr Gly Phe Ala Asn Ala Ile
 180 185 190

Leu Arg Asn Ile Thr Arg Lys Glu Pro Glu Gln Trp Leu Lys Glu Leu
 195 200 205

Glu Pro Ala Glu Glu Leu Ala Arg Val Ala Phe Arg Thr Ala His Pro
 210 215 220

Arg Trp Ile Ala Gln Ser Phe Ser Gln Val Leu Pro Ala Asp Glu Leu

<222> (101)..(1036)

<223> RXA02255

<400> 2655

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gtgtgcagcg ttgctggcaa gttttgctgg agcacgaaag cgттаaggag taggcgtgtc 60

actgacgagt gatatcaaac aagaattggc gcaggtccat gtg gcc aaa aac agt 115
                               Val Ala Lys Asn Ser
                               1 5

gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg 163
Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met
                10                15                20

caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg 211
Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met
                25                30                35

caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct 259
Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser
                40                45                50

cga gtc gat gtg cac acc gtg aac ccg act gtg agc agg aaa acg cca 307
Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro
                55                60                65

cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc 355
Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg
                70                75                80                85

acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct 403
Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro
                90                95                100

tct gtg gtc agc gga aca atc agt gac gct gaa gct gca tgg cgc ggt 451
Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly
                105                110                115

gcg ttt cta gcc aat gga tct tta agt gat cca ggt cgt tcc tct tcg 499
Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro Gly Arg Ser Ser Ser
                120                125                130

ttg gag gtg ttg tgt cct ggt caa gaa tca gca ttg gca ctg gtt gga 547
Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala Leu Ala Leu Val Gly
                135                140                145

tgt gcg cga aga att ggg atc gcg gcg aaa acg aaa gat tct cga gga 595
Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr Lys Asp Ser Arg Gly
                150                155                160                165

ttt gat cgc gtc aat gtt cgt gat gcg gaa gca att ggg gca ctg ctc 643
Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala Ile Gly Ala Leu Leu
                170                175                180

act cga atg ggt gcc cag aaa act cgc atg ttg tgg gaa gaa aaa cgc 691
Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu Trp Glu Glu Lys Arg
                185                190                195

atc aag cgg gaa agt cga act ccg caa acc ggg ttg gcc aac ttc gac 739
Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly Leu Ala Asn Phe Asp
                200                205                210

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gat gcc aat ctg cgc agg tca gcc cga gca gca gtt gcc gct gca gcg 787
Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala Val Ala Ala Ala Ala
215 220 225

agg gta gaa cgc gcc atg aag att ctt ggt gat gat gtt cct gag cat 835
Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp Asp Val Pro Glu His
230 235 240 245

ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg 883
Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu
250 255 260

gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg 931
Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val
265 270 275

gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa 979
Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu
280 285 290

gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg 1027
Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val Thr Glu Asp Leu Leu
295 300 305

gaa gaa att tagatgattg aagcctaaaa acg 1059
Glu Glu Ile
310

<210> 2656

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 2656

Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg
1 5 10 15

Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala
20 25 30

Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln
35 40 45

Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val
50 55 60

Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp
65 70 75 80

Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val
85 90 95

Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu
100 105 110

Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
115 120 125

Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala

130	135	140
Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr 145 150 155 160		
Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala 165 170 175		
Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu 180 185 190		
Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly 195 200 205		
Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala 210 215 220		
Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp 225 230 235 240		
Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His 245 250 255		
Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met 260 265 270		
Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala 275 280 285		
Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val 290 295 300		
Thr Glu Asp Leu Leu Glu Glu Ile 305 310		

<210> 2657
 <211> 636
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> RXA02266

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 tgtaccggcc ttttattgat tttgacgtaa gcttgaccgc atg act caa gat gaa 115
 Met Thr Gln Asp Glu
 1 5
 cac ccc cga cag gcc gac tcc cat ttc aac atg ctt tta ccg gat gga 163
 His Pro Arg Gln Ala Asp Ser His Phe Asn Met Leu Leu Pro Asp Gly
 10 15 20
 aat gaa aac gca cac cag ctt tct gtc gct cta aat cag gtg gca cat 211
 Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu Asn Gln Val Ala His
 25 30 35

Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val
 100 105 110

Leu Ser Leu Ser Glu Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr
 115 120 125

Arg Gln Asn Ala Leu Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile
 130 135 140

Glu Gln Asp Leu Leu Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn
 145 150 155 160

Arg Ala Ser Lys Val Arg Lys Asn Arg Ser Asn
 165 170

<210> 2659

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(973)

<223> RXA02267

<400> 2659

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accaacgatt caagccttat cagttttgta caggaaaata gtg caa aaa tgg ggt 115
 Val Gln Lys Trp Gly
 1 5

tta agc ttc gtg gag agg att gtc atc gtg aac aac gtg caa cag ttt 163
 Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn Asn Val Gln Gln Phe
 10 15 20

cat cga ttt ttt gat gat tcc gca gtc tat tat ccc tgc ttc gtc ccg 211
 His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr Pro Cys Phe Val Pro
 25 30 35

ctt gac cga gcc atc ggc gaa cac ttt gat cgt cag aac aaa ccg atg 259
 Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg Gln Asn Lys Pro Met
 40 45 50

tcc aga ttc atc gga acg ctc att ctg ccg tta gcc aaa ctg gaa gaa 307
 Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu Ala Lys Leu Glu Glu
 55 60 65

gcc gcc caa tac acc ggc gat gaa gtc ctt cgc gtg tcg gca gta atc 355
 Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg Val Ser Ala Val Ile
 70 75 80 85

agt act gat ggg ctc gct gat ctg cga agg gat ttt tac gaa ctc ccc 403
 Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp Phe Tyr Glu Leu Pro
 90 95 100

aac atc gac atc gcc tcg gtg gaa atc aag ctg gtc ggc gca gcc ctc 451
 Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu Val Gly Ala Ala Leu
 105 110 115

acc aac acc gct tgg ttg gga gat gtg gaa aaa ctc atc caa caa cat 499
 Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys Leu Ile Gln Gln His
 120 125 130

cgc aac act ttc gta tgg gtt gag att ccg aca gcc ctg gtc acc gca 547
 Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr Ala Leu Val Thr Ala
 135 140 145

gat att gtc cga aaa ctc cgc cac atg gga gct ggc ctg aaa tac aga 595
 Asp Ile Val Arg Lys Leu Arg His Met Gly Ala Gly Leu Lys Tyr Arg
 150 155 160 165

act gga ggt gat agg gaa gag ctc ttc ccc tca ccg cag gac ttg gtc 643
 Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser Pro Gln Asp Leu Val
 170 175 180

act gtg ctg cgc acc gcc atc gat gct gca ttg ccg ttt aaa ctc act 691
 Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu Pro Phe Lys Leu Thr
 185 190 195

gca ggc ctg cat cgt gct ctc agg tat cgt gac gag aaa acc ggc cga 739
 Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp Glu Lys Thr Gly Arg
 200 205 210

ctt cac ttc gga ttc ctc aac att gca gcc gcc gtg gcg aca ctt cgt 787
 Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala Val Ala Thr Leu Arg
 215 220 225

gct gga aaa ggc gag gca gag gca ctg aag atc ctt gaa ggc gat gat 835
 Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile Leu Glu Gly Asp Asp
 230 235 240 245

gcc gct ccg ctt att cac gca cta caa agc ggc gaa aac tgg cgg gat 883
 Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly Glu Asn Trp Arg Asp
 250 255 260

tcc ttc cgc agc ttc agt acc tgc aat gtt gtt gaa cca ctc aac act 931
 Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val Glu Pro Leu Asn Thr
 265 270 275

ctg att gat ctt gat gtg ttg gcg gaa gga gac gta cat ccc 973
 Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp Val His Pro
 280 285 290

taaggatcga cgctagtttag atc 996

<210> 2660

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 2660

Val Gln Lys Trp Gly Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn
 1 5 10 15

Asn Val Gln Gln Phe His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr
 20 25 30

Pro Cys Phe Val Pro Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg
 35 40 45

Gln Asn Lys Pro Met Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu
50 55 60

Ala Lys Leu Glu Glu Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg
65 70 75 80

Val Ser Ala Val Ile Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp
85 90 95

Phe Tyr Glu Leu Pro Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu
100 105 110

Val Gly Ala Ala Leu Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys
115 120 125

Leu Ile Gln Gln His Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr
130 135 140

Ala Leu Val Thr Ala Asp Ile Val Arg Lys Leu Arg His Met Gly Ala
145 150 155 160

Gly Leu Lys Tyr Arg Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser
165 170 175

Pro Gln Asp Leu Val Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu
180 185 190

Pro Phe Lys Leu Thr Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp
195 200 205

Glu Lys Thr Gly Arg Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala
210 215 220

Val Ala Thr Leu Arg Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile
225 230 235 240

Leu Glu Gly Asp Asp Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly
245 250 255

Glu Asn Trp Arg Asp Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val
260 265 270

Glu Pro Leu Asn Thr Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp
275 280 285

Val His Pro
290

<210> 2661

<211> 776

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(753)

<223> RXA02280

<400> 2661

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cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu 20 25 30	96
gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu 35 40 45	144
aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile 50 55 60	192
cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu 65 70 75 80	240
acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu 85 90 95	288
ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val 100 105 110	336
acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe 115 120 125	384
gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln 130 135 140	432
gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp 145 150 155 160	480
gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala 165 170 175	528
aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn 180 185 190	576
aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val 195 200 205	624
tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys 210 215 220	672
agg cca ctg cgg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala 225 230 235 240	720
gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgctaat	773

Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
245 250

ctt

776

<210> 2662

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 2662

Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser
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Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu
20 25 30

Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu
35 40 45

Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile
50 55 60

His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
65 70 75 80

Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
85 90 95

Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
100 105 110

Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
115 120 125

Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
130 135 140

Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
145 150 155 160

Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
165 170 175

Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
180 185 190

Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
195 200 205

Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
210 215 220

Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
225 230 235 240

Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
245 250

<210> 2663
 <211> 672
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(649)
 <223> RXA02286

<400> 2663

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gcagcgcaca cgctttcccc tcagcctgct gatacccccg ttttgccacc taaaacaacc 60

tctcatcttc atttcatatt cacttcatag ggttgaatac atg aag aac gca aaa 115
                                         Met Lys Asn Ala Lys
                                         1 5

ctt ttc ctc gcg ctc ata tcc gct cct ctt atc ctc gct ggc tgc agc 163
Leu Phe Leu Ala Leu Ile Ser Ala Pro Leu Ile Leu Ala Gly Cys Ser
          10          15          20

tcc acc gat act gga aca gca gaa tcc acc att tcc agc gaa act gct 211
Ser Thr Asp Thr Gly Thr Ala Glu Ser Thr Ile Ser Ser Glu Thr Ala
          25          30          35

tct gca gta gat gcc acc act tct acc tcc tca agt acc gcc acc tct 259
Ser Ala Val Asp Ala Thr Thr Ser Thr Ser Ser Thr Ala Thr Ser
          40          45          50

gcc gtg att gat gac gat ccg gta ttc gac atc atc gac atc gtc ctt 307
Ala Val Ile Asp Asp Asp Pro Val Phe Asp Ile Ile Asp Ile Val Leu
          55          60          65

gcc caa tac ccc gac agg atc atc acc gac att gac cgc gaa gac tcc 355
Ala Gln Tyr Pro Asp Arg Ile Ile Thr Asp Ile Asp Arg Glu Asp Ser
          70          75          80          85

tcc gat caa tac gaa gtc gat gtt gtg gtt ggc caa gaa gtc ctt gaa 403
Ser Asp Gln Tyr Glu Val Asp Val Val Val Gly Gln Glu Val Leu Glu
          90          95          100

ctt gat gtc acc acc agt ggc cag atc cat acc gac gac cgc gac aac 451
Leu Asp Val Thr Thr Ser Gly Gln Ile His Thr Asp Asp Arg Asp Asn
          105          110          115

gat gat gat gac gac atc cgc gaa gct cac gca gcc aca gtc acc gca 499
Asp Asp Asp Asp Asp Ile Arg Glu Ala His Ala Ala Thr Val Thr Ala
          120          125          130

gct caa gcc att ggc cta gcg ctg gat caa tac cca gac gga att att 547
Ala Gln Ala Ile Gly Leu Ala Leu Asp Gln Tyr Pro Asp Gly Ile Ile
          135          140          145

gat tct gtt gaa tta gac gaa gac gac ggc cag ctg aaa tgg aaa ata 595
Asp Ser Val Glu Leu Asp Glu Asp Asp Gly Gln Leu Lys Trp Lys Ile
          150          155          160          165

gac ctc gat gac act tcc ggc aat gat ctt gct gac gtt gaa atc gca 643
Asp Leu Asp Asp Thr Ser Gly Asn Asp Leu Ala Asp Val Glu Ile Ala
          170          175          180
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gca gtt taagcacgcg cacggaaagc cac
Ala Val

672

<210> 2664
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 2664.
Met Lys Asn Ala Lys Leu Phe Leu Ala Leu Ile Ser Ala Pro Leu Ile
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Leu Ala Gly Cys Ser Ser Thr Asp Thr Gly Thr Ala Glu Ser Thr Ile
20 25 30
Ser Ser Glu Thr Ala Ser Ala Val Asp Ala Thr Thr Ser Thr Ser Ser
35 40 45
Ser Thr Ala Thr Ser Ala Val Ile Asp Asp Asp Pro Val Phe Asp Ile
50 55 60
Ile Asp Ile Val Leu Ala Gln Tyr Pro Asp Arg Ile Ile Thr Asp Ile
65 70 75 80
Asp Arg Glu Asp Ser Ser Asp Gln Tyr Glu Val Asp Val Val Val Gly
85 90 95
Gln Glu Val Leu Glu Leu Asp Val Thr Thr Ser Gly Gln Ile His Thr
100 105 110
Asp Asp Arg Asp Asn Asp Asp Asp Asp Ile Arg Glu Ala His Ala
115 120 125
Ala Thr Val Thr Ala Ala Gln Ala Ile Gly Leu Ala Leu Asp Gln Tyr
130 135 140
Pro Asp Gly Ile Ile Asp Ser Val Glu Leu Asp Glu Asp Asp Gly Gln
145 150 155 160
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Asp Val Glu Ile Ala Ala Val
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<223> RXA02287

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Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr Asp His Val Phe Asp
                        10                        15                        20

ctg atg ggc aac gga aac gcc tgg ttc gtc gat gcc cta gaa cgc ctc 211
Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp Ala Leu Glu Arg Leu
                        25                        30                        35

ggg cga ggc atc atc acc gtc cgc ccc aca gtt gaa acc gtg gcc gcc 259
Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val Glu Thr Val Ala Ala
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gcg gac acc tac cac cgc gtc acc cgc cgc ccg gcg gtc gct acc acc 307
Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro Ala Val Ala Thr Thr
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acc tat ggt gct ggt ttc acc aac acc atg acc acg ctt gcc gac gtc 355
Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr Thr Leu Ala Asp Val
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gcc ctc tcc cgt atc cca ctt ctt tta gtt gtg ggc act gcc ccg agc 403
Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val Gly Thr Ala Pro Ser
                        90                        95                        100

gcc ggg cct cgc tgt ttc gac att gac cgg caa gga ctc gca cgt gcc 451
Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln Gly Leu Ala Arg Ala
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Val Gly Val Glu Thr Phe Thr Val His Ala Asp Asp Val Ala Ala Val
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Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn Thr His Val Ile Leu
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Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala Thr Asp Pro Thr Val
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act aca tac ctg ctg cgc ccc gga ttt cag aaa ctc ccg atg tca ccg 643
Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys Leu Pro Met Ser Pro
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<400> 2666

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 Glu Ser Thr Arg Leu Leu Gly Leu Asp Glu Leu His Ile Ile Ala Pro
 55 60 65
 tca gtc cac cta ccc gct ctc gca gta gca gcc gcc gac atc gca cac 355
 Ser Val His Leu Pro Ala Leu Ala Val Ala Ala Asp Ile Ala His
 70 75 80 85
 cat ctg cca gag aaa ttc caa ttc tgt gaa gcc gaa acc tgc act cat 403
 His Leu Pro Glu Lys Phe Gln Phe Cys Glu Ala Glu Thr Cys Thr His
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 ctc cac ccc gac gat gac acc tat ctc acg gct gaa tcc gtt gct caa 451
 Leu His Pro Asp Asp Asp Thr Tyr Leu Thr Ala Glu Ser Val Ala Gln
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<400> 2668

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 35 40 45
 Leu Leu Gly Ala Ala Glu Ser Thr Arg Leu Leu Gly Leu Asp Glu Leu
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 His Ile Ile Ala Pro Ser Val His Leu Pro Ala Leu Ala Val Ala Ala
 65 70 75 80
 Ala Asp Ile Ala His His Leu Pro Glu Lys Phe Gln Phe Cys Glu Ala
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<211> 903

<212> DNA

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 <223> RXA02295

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                                         1           5

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Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly
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tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg 211
Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu
                25                30                35

atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc 259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser
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aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg 307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu
                55                60                65

gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg 355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu
                70                75                80                85

gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att 403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile
                90                95                100

gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt 451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val
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ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa 499
Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys
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gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga 547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly
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ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc 595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe
                150                155                160                165

ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc 643
Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser
                170                175                180

gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta 691
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu
                185                190                195

att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg 739
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215	220	225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt			835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val			
230	235	240	245
gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg			880
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Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val			
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Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser			
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Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu			
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Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu			
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Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val			
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Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly			
115	120	125	
Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala			
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Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro			
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Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln			
165	170	175	
Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr			
180	185	190	
Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp			
195	200	205	

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu
 210 215 220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala
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Ile Gln Gly Met
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cca gac ccc cac gaa caa att cca gag aag cca tcc cgc aag gtt att 163
 Pro Asp Pro His Glu Gln Ile Pro Glu Lys Pro Ser Arg Lys Val Ile
 10 15 20

gca ctt cgt tgg tgc atc gta gcg ccg ctg tcg cta gcc gtg ggg tgg 211
 Ala Leu Arg Trp Cys Ile Val Ala Pro Leu Ser Leu Ala Val Gly Trp
 25 30 35

ctt ttt act atg tgg ggt gtg cca gcc gca tgg atc ctc ggg gcg atc 259
 Leu Phe Thr Met Trp Gly Val Pro Ala Ala Trp Ile Leu Gly Ala Ile
 40 45 50

ctt gtt gcc ggt gta tgt gcg ctg acc aca ggg caa gat ctt ccg atg 307
 Leu Val Ala Gly Val Cys Ala Leu Thr Thr Gly Gln Asp Leu Pro Met
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gcc aag ggg gtg cat gtt ttt ggt cgc tca atc gtg gcg atg ctg gcg 355
 Ala Lys Gly Val His Val Phe Gly Arg Ser Ile Val Ala Met Leu Ala
 70 75 80 85

gcg ctg cct ttg att agt tct tct ggt tcg gaa ctt gtt cgt ttc ctc 403
 Ala Leu Pro Leu Ile Ser Ser Ser Gly Ser Glu Leu Val Arg Phe Leu
 90 95 100

atc ccg ggt ctt gtg att tcc ttt ttc acc atc gcg gta ggc atc gtt 451
 Ile Pro Gly Leu Val Ile Ser Phe Phe Thr Ile Ala Val Gly Ile Val
 105 110 115

ggt ggt ttg ttg ctg gca aga tcc agg ccg gag att ttg ccg gaa act 499
 Gly Gly Leu Leu Leu Ala Arg Ser Arg Pro Glu Ile Leu Pro Glu Thr

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1260

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<211> 379

<212> PRT

<213> Corynebacterium glutamicum

<400> 2672

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20 25 30

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35 40 45

Ile Leu Gly Ala Ile Leu Val Ala Gly Val Cys Ala Leu Thr Thr Gly
50 55 60

Gln Asp Leu Pro Met Ala Lys Gly Val His Val Phe Gly Arg Ser Ile
65 70 75 80

Val Ala Met Leu Ala Ala Leu Pro Leu Ile Ser Ser Ser Gly Ser Glu
85 90 95

Leu Val Arg Phe Leu Ile Pro Gly Leu Val Ile Ser Phe Phe Thr Ile
100 105 110

Ala Val Gly Ile Val Gly Gly Leu Leu Leu Ala Arg Ser Arg Pro Glu
115 120 125

Ile Leu Pro Glu Thr Gly Val Leu Ser Met Leu Ala Gly Gly Ala Ser
130 135 140

Val Met Pro Ile Leu Ala Arg Glu Leu Gly Ala Asp Phe Arg Tyr Val
145 150 155 160

Ala Leu Thr Gln Tyr Leu Arg Leu Leu Val Val Ser Met Thr Leu Pro
165 170 175

Leu Val Thr His Phe Phe Val Pro Gly Gly Ala Asp Leu Gly Ser Pro
180 185 190

Pro Glu Lys Trp Leu Asp Val Leu Ser Leu Gly Glu Phe Gly Thr Ser
195 200 205

Ile Ser Val Leu Ser Leu Leu Val Leu Phe Gly Ile Val Leu Ala Gly
210 215 220

Glu Pro Leu Gly Arg Leu Leu Arg Leu Pro Ala Pro Ala Val Met Gly
225 230 235 240

Pro Leu Ile Leu Thr Val Leu Val Ser Phe Val Ile Pro Asp Asp Leu
245 250 255

Ser Leu Gln Pro Pro Thr Val Phe Lys Ile Ile Ala Phe Met Ala Ile

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Ile	Pro	Glu	Gln	Ala	Arg	Gln	Val	Glu	Cys	Leu	Ile	Asp	Pro	Ala	Gly		
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Trp	Gln	Glu	Leu	Thr	Thr	Val	Phe	His	Glu	Gly	Val	Pro	Gly	His	His		
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Arg	Val	Ala	Cys	Trp	Asn	Ser	Gly	His	Gly	Glu	Gly	Trp	Ala	Leu	Tyr		
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Ala	Glu	Ser	Leu	Met	Lys	Glu	Leu	Gly	Tyr	His	Glu	Asp	Pro	Gly	Asn		
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Leu	Met	Gly	Tyr	Leu	Asp	Ala	Gln	Arg	Leu	Arg	Ala	Ala	Arg	Val	Ala		
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Ile	Asp	Ile	Gly	Ile	His	Leu	Asn	Lys	Arg	Asn	Pro	Glu	Cys	Thr	Gly		
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cca	ggg	cag	gcc	gca	tcg	tat	gcc	att	ggg	cag	cga	ctc	tgg	ttg	aac	1651	
Pro	Gly	Gln	Ala	Ala	Ser	Tyr	Ala	Ile	Gly	Gln	Arg	Leu	Trp	Leu	Asn		
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Leu	Arg	Asp	Glu	Ala	Ile	Ser	Gln	Gly	Gln	Thr	Leu	Ala	Gln	Phe	His		
		520					525					530					
agc	aag	gca	ttg	tcc	tat	ggc	agc	atc	ccg	atg	ggc	att	ttg	cgc	gat	1747	
Ser	Lys	Ala	Leu	Ser	Tyr	Gly	Ser	Ile	Pro	Met	Gly	Ile	Leu	Arg	Asp		
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Gln	Val	Leu	Asn														
550																	

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2674

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35 40 45
Ser Pro Asp Tyr Trp Asn Ala Ile Ala Glu Arg Asn Arg Asp Met Val
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Ala Asp Val Asp Ala Phe Asp Asp Gly Thr Asp Asp Asn Asp Asp Glu
65 70 75 80
Glu Asp Phe Asp Asp Val Asp Arg Val Thr Ala Asp Val Leu Arg Asp
85 90 95
Arg Val Cys Leu Asp Leu Ala Leu His His Gln Gly Glu Thr Leu Ala
100 105 110
Asn Leu Asn Asn Ile Asp Ser Pro Val Gln Thr Ile Arg Asp Thr Phe
115 120 125
Leu Ile Met Pro Arg Glu Thr Asp Asp Asp Val Glu Asn Leu Arg Glu
130 135 140
Arg Leu Ser Arg Val Pro Asp Ala Leu His Gly Tyr Cys Glu Ser Leu
145 150 155 160
Ala Glu Ala Ala Ser Gln Gly His Val Ala Ala Val Arg Gln Val Glu
165 170 175
Glu Val Val Ser Gln Cys Glu Asp Leu Ala Asp Glu Asp Ser Val Leu
180 185 190
Gln His Leu Gly Leu Asp Glu Asn Asp Pro Val Val Val Glu Ala Gln
195 200 205
Glu Ala Phe Ala Arg Val Ala Gly Trp Leu Ala Glu Gln Leu Ala Pro
210 215 220
His Ala Pro His Val Asp Ala Val Gly Arg Asp Arg Tyr Glu Met Phe
225 230 235 240
Ser His Leu His Val Gly Glu Phe Val Asp Leu Asp Glu Ala Tyr Gln
245 250 255
Trp Ser Leu Glu Gln Leu Arg Asp Ile Asp Ala Gln Gln Leu Gln Val
260 265 270
Ala Gln Gln Leu Tyr Gly Pro Gly Thr Thr Ile Arg Glu Ala Met Lys
275 280 285
Lys Leu Asn Ala Asp Glu Arg Tyr Leu Ile Arg Gly Thr Asp Ala Leu
290 295 300

Gln Glu Trp Met Gln Lys Thr Ala Asp Gln Ala Ile Ala Asp Leu Asp
305 310 315 320

Gly Val Ser Phe Asn Ile Pro Glu Gln Ala Arg Gln Val Glu Cys Leu
325 330 335

Ile Asp Pro Ala Gly Thr Gly Gly Ile Phe Tyr Thr Pro Pro Ser Asp
340 345 350

Asp Phe Ser Arg Pro Gly Arg Met Trp Trp Ser Val Pro Lys Thr Gln
355 360 365

Glu Val Phe His Thr Trp Gln Glu Leu Thr Thr Val Phe His Glu Gly
370 375 380

Val Pro Gly His His Leu Gln Ile Ser Gln Thr Leu Val Glu Lys Asp
385 390 395 400

Leu Asn Leu Trp Arg Arg Val Ala Cys Trp Asn Ser Gly His Gly Glu
405 410 415

Gly Trp Ala Leu Tyr Ala Glu Ser Leu Met Lys Glu Leu Gly Tyr His
420 425 430

Glu Asp Pro Gly Asn Leu Met Gly Tyr Leu Asp Ala Gln Arg Leu Arg
435 440 445

Ala Ala Arg Val Ala Ile Asp Ile Gly Ile His Leu Asn Lys Arg Asn
450 455 460

Pro Glu Cys Thr Gly Leu Trp Asp Ala Ser Tyr Ala Arg Ser Phe Leu
465 470 475 480

Arg Glu Asn Thr Ser Met Asn Glu Asp Ala Leu Tyr Phe Glu Leu Asn
485 490 495

Arg Tyr Leu Gly Trp Pro Gly Gln Ala Ala Ser Tyr Ala Ile Gly Gln
500 505 510

Arg Leu Trp Leu Asn Leu Arg Asp Glu Ala Ile Ser Gln Gly Gln Thr
515 520 525

Leu Ala Gln Phe His Ser Lys Ala Leu Ser Tyr Gly Ser Ile Pro Met
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Gly Ile Leu Arg Asp Gln Val Leu Asn
545 550

<210> 2675

<211> 1014

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(991)

<223> RXA02304

<400> 2675

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agtgcaggtt ttttataaca gggcagtaac gtttactggt atg aaa act ccc cgt 115
Met Lys Thr Pro Arg
1 5

ctg ctg aag atc ctc agc gcg atg gtg gct gtc act gga ctt ctc att 163
Leu Leu Lys Ile Leu Ser Ala Met Val Ala Val Thr Gly Leu Leu Ile
10 15 20

cca acg gtg gtc ccc atg gcc gcc gct gat gct gct gaa ctg tcc gac 211
Pro Thr Val Val Pro Met Ala Ala Ala Asp Ala Ala Glu Leu Ser Asp
25 30 35

aac gtt ccc gat cgc acc caa att gcc atc atc aac cct gat ggc agc 259
Asn Val Pro Asp Arg Thr Gln Ile Ala Ile Ile Asn Pro Asp Gly Ser
40 45 50

gtg caa gaa tct gac aac gcc gaa gaa tcc cgc ccg gca tta tcc ctg 307
Val Gln Glu Ser Asp Asn Ala Glu Glu Ser Arg Pro Ala Leu Ser Leu
55 60 65

gcc aag ctg tat ttg ggt tat tat gtg ttg gct caa ggc gcg gaa gaa 355
Ala Lys Leu Tyr Leu Gly Tyr Tyr Val Leu Ala Gln Gly Ala Glu Glu
70 75 80 85

gat att gaa cta gtc cca gat atg atc cgc tac tct gat gat ttc acc 403
Asp Ile Glu Leu Val Pro Asp Met Ile Arg Tyr Ser Asp Asp Phe Thr
90 95 100

gcg gat tat ttg gag agc gaa tac ccg gaa gca att cct gag gtt att 451
Ala Asp Tyr Leu Glu Ser Glu Tyr Pro Glu Ala Ile Pro Glu Val Ile
105 110 115

gat gcc ttc gat ttg gaa gac acc gaa tgg gct ggt ttc tgg ggc aat 499
Asp Ala Phe Asp Leu Glu Asp Thr Glu Trp Ala Gly Phe Trp Gly Asn
120 125 130

gca act acc agt gcg gtg gat att gcg acg ttt gta gca gca ctc atc 547
Ala Thr Thr Ser Ala Val Asp Ile Ala Thr Phe Val Ala Ala Leu Ile
135 140 145

gac gat ccc acg gcg cag ccc ttg ctt gac gca atg tct gac acc gct 595
Asp Asp Pro Thr Ala Gln Pro Leu Leu Asp Ala Met Ser Asp Thr Ala
150 155 160 165

gag tat gcg gcg gat ggc tac gcc cag aac ttt ggc act ttt aca ttg 643
Glu Tyr Ala Ala Asp Gly Tyr Ala Gln Asn Phe Gly Thr Phe Thr Leu
170 175 180

tcc gat gtc acc ggt act aaa ttt ggt tgg tct gat tcc ctc gat gtg 691
Ser Asp Val Thr Gly Thr Lys Phe Gly Trp Ser Asp Ser Leu Asp Val
185 190 195

cat tca tcg gtc agc ttt ggc cct ggt ttt gtg atc gct gcc aac acc 739
His Ser Ser Val Ser Phe Gly Pro Gly Phe Val Ile Ala Ala Asn Thr
200 205 210

tac ggt gac gcc gaa acg ctc acc gaa gat gtc caa gat tcc gtg tct 787
Tyr Gly Asp Ala Glu Thr Leu Thr Glu Asp Val Gln Asp Ser Val Ser
215 220 225

tcg ctg tat ccg gag gaa gta acc acc gcg atc gag gag cag gtg gat 835
 Ser Leu Tyr Pro Glu Glu Val Thr Thr Ala Ile Glu Glu Gln Val Asp
 230 235 240 245
 cag ctg tgt gag tgc gct gca gag act acg cat ttg gga atg cac act 883
 Gln Leu Cys Glu Cys Ala Ala Glu Thr Thr His Leu Gly Met His Thr
 250 255 260
 ggc gcg gag ctg aaa gca cag ctt gag ggc act att tat gga aaa acc 931
 Gly Ala Glu Leu Lys Ala Gln Leu Glu Gly Thr Ile Tyr Gly Lys Thr
 265 270 275
 ctc agc ttt tta cct aat tca gcc cca gcg cca gcg ttt att tac aac 979
 Leu Ser Phe Leu Pro Asn Ser Ala Pro Ala Pro Ala Phe Ile Tyr Asn
 280 285 290
 ctg ctg gca cat tagcaaacag ttttaaggaa ctc 1014
 Leu Leu Ala His
 295

<210> 2676
 <211> 297
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2676
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 20 25 30
 Ala Glu Leu Ser Asp Asn Val Pro Asp Arg Thr Gln Ile Ala Ile Ile
 35 40 45
 Asn Pro Asp Gly Ser Val Gln Glu Ser Asp Asn Ala Glu Glu Ser Arg
 50 55 60
 Pro Ala Leu Ser Leu Ala Lys Leu Tyr Leu Gly Tyr Tyr Val Leu Ala
 65 70 75 80
 Gln Gly Ala Glu Glu Asp Ile Glu Leu Val Pro Asp Met Ile Arg Tyr
 85 90 95
 Ser Asp Asp Phe Thr Ala Asp Tyr Leu Glu Ser Glu Tyr Pro Glu Ala
 100 105 110
 Ile Pro Glu Val Ile Asp Ala Phe Asp Leu Glu Asp Thr Glu Trp Ala
 115 120 125
 Gly Phe Trp Gly Asn Ala Thr Thr Ser Ala Val Asp Ile Ala Thr Phe
 130 135 140
 Val Ala Ala Leu Ile Asp Asp Pro Thr Ala Gln Pro Leu Leu Asp Ala
 145 150 155 160
 Met Ser Asp Thr Ala Glu Tyr Ala Ala Asp Gly Tyr Ala Gln Asn Phe
 165 170 175

Gly Thr Phe Thr Leu Ser Asp Val Thr Gly Thr Lys Phe Gly Trp Ser
 180 185 190
 Asp Ser Leu Asp Val His Ser Ser Val Ser Phe Gly Pro Gly Phe Val
 195 200 205
 Ile Ala Ala Asn Thr Tyr Gly Asp Ala Glu Thr Leu Thr Glu Asp Val
 210 215 220
 Gln Asp Ser Val Ser Ser Leu Tyr Pro Glu Glu Val Thr Thr Ala Ile
 225 230 235 240
 Glu Glu Gln Val Asp Gln Leu Cys Glu Cys Ala Ala Glu Thr Thr His
 245 250 255
 Leu Gly Met His Thr Gly Ala Glu Leu Lys Ala Gln Leu Glu Gly Thr
 260 265 270
 Ile Tyr Gly Lys Thr Leu Ser Phe Leu Pro Asn Ser Ala Pro Ala Pro
 275 280 285
 Ala Phe Ile Tyr Asn Leu Leu Ala His
 290 295

<210> 2677

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXA02308

<400> 2677

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 gagcaaatcc gccaggaaat aaattaagta aggaatatcc atg agt gaa acc cag 115
 Met Ser Glu Thr Gln
 1 5
 tcg aat tca gtg tca gcg gta atg cct gcg cag ctc cct cca ggg cct 163
 Ser Asn Ser Val Ser Ala Val Met Pro Ala Gln Leu Pro Pro Gly Pro
 10 15 20
 gcc gag cgt act gtg tac tcc tac ggt gtt cgc gca ggg gat cag gtg 211
 Ala Glu Arg Thr Val Tyr Ser Tyr Gly Val Arg Ala Gly Asp Gln Val
 25 30 35
 cac att tta aga atg gag gct ttt gat tct gac gcg aat att gtc ggc 259
 His Ile Leu Arg Met Glu Ala Phe Asp Ser Asp Ala Asn Ile Val Gly
 40 45 50
 gaa agg gac att gag gcg cat gct gaa caa gtc ttt aag aac ctg caa 307
 Glu Arg Asp Ile Glu Ala His Ala Glu Gln Val Phe Lys Asn Leu Gln
 55 60 65
 gca gta atc cac gag gca gga gga acg atc aac aac att gtt tcc acc 355
 Ala Val Ile His Glu Ala Gly Gly Thr Ile Asn Asn Ile Val Ser Thr
 70 75 80 85

act act tat ctt gcc gat gtc acc gat gct ccc gtt gtt aac gct gct. 403
 Thr Thr Tyr Leu Ala Asp Val Thr Asp Ala Pro Val Val Asn Ala Ala
 90 95 100

cgc tcc cgc tat ttc acc gga gaa gta ttg ccc acc cac acc gta att 451
 Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro Thr His Thr Val Ile
 105 110 115

gga gtt gct gct ctt gct cgg cca cag ttt cta gtc gag atc tca gcg 499
 Gly Val Ala Ala Leu Ala Arg Pro Gln Phe Leu Val Glu Ile Ser Ala
 120 125 130

gtg gcc tat ttg ggg gac ctt tca aaa gac tagatacatg attatttttg 549
 Val Ala Tyr Leu Gly Asp Leu Ser Lys Asp
 135 140

cat 552

<210> 2678

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 2678

Met Ser Glu Thr Gln Ser Asn Ser Val Ser Ala Val Met Pro Ala Gln
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Leu Pro Pro Gly Pro Ala Glu Arg Thr Val Tyr Ser Tyr Gly Val Arg
 20 25 30

Ala Gly Asp Gln Val His Ile Leu Arg Met Glu Ala Phe Asp Ser Asp
 35 40 45

Ala Asn Ile Val Gly Glu Arg Asp Ile Glu Ala His Ala Glu Gln Val
 50 55 60

Phe Lys Asn Leu Gln Ala Val Ile His Glu Ala Gly Gly Thr Ile Asn
 65 70 75 80

Asn Ile Val Ser Thr Thr Thr Tyr Leu Ala Asp Val Thr Asp Ala Pro
 85 90 95

Val Val Asn Ala Ala Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro
 100 105 110

Thr His Thr Val Ile Gly Val Ala Ala Leu Ala Arg Pro Gln Phe Leu
 115 120 125

Val Glu Ile Ser Ala Val Ala Tyr Leu Gly Asp Leu Ser Lys Asp
 130 135 140

<210> 2679

<211> 1209

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1186)

<223> RXA02324

<400> 2679

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cgactctatt gaaaatgatt cccaaaagga gggctttcac atg gcc aca acg acc 115
 Met Ala Thr Thr Thr
 1 5

cca gtc acc gtg cta tca gga ttt ctc ggc tcc gga aaa acc aca ttg 163
 Pro Val Thr Val Leu Ser Gly Phe Leu Gly Ser Gly Lys Thr Thr Leu
 10 15 20

ctc aac cag atc ctc cac cac cga gga tcc cgg aaa atc gca gtc att 211
 Leu Asn Gln Ile Leu His His Arg Gly Ser Arg Lys Ile Ala Val Ile
 25 30 35

gtc aac gat ttt tca gaa atc aac atc gac gca gcc ctc atc gca tcc 259
 Val Asn Asp Phe Ser Glu Ile Asn Ile Asp Ala Ala Leu Ile Ala Ser
 40 45 50

gaa ggc cac ctc acc cgc ggc gaa gac cgc ttc gtg gaa ctg acc aac 307
 Glu Gly His Leu Thr Arg Gly Glu Asp Arg Phe Val Glu Leu Thr Asn
 55 60 65

gga tgc atc tgc tgc acc ctg cgc gaa gac ctc gtg gat tcc gtc ggc 355
 Gly Cys Ile Cys Cys Thr Leu Arg Glu Asp Leu Val Asp Ser Val Gly
 70 75 80 85

gaa ctc gcc agc agc gac cgc ttc gac cac atc gtc atc gaa tcc acg 403
 Glu Leu Ala Ser Ser Asp Arg Phe Asp His Ile Val Ile Glu Ser Thr
 90 95 100

ggt atc tcc gaa cca atg ccg gta gcc gcc aca ttt gaa tgg cag tgg 451
 Gly Ile Ser Glu Pro Met Pro Val Ala Ala Thr Phe Glu Trp Gln Trp
 105 110 115

gat gac ggc acc cgc ctg gct gac aaa gca ccg atc gac acc atg gtc 499
 Asp Asp Gly Thr Arg Leu Ala Asp Lys Ala Pro Ile Asp Thr Met Val
 120 125 130

acc ctg gtc gat gcc acc caa ttc atc gac ctc atc cgc aaa aac acc 547
 Thr Leu Val Asp Ala Thr Phe Ile Asp Leu Ile Arg Lys Asn Thr
 135 140 145

tcc ctc acc gag gct gac atg ggc gca acc gag gac gat gaa cgc acc 595
 Ser Leu Thr Glu Ala Asp Met Gly Ala Thr Glu Asp Asp Glu Arg Thr
 150 155 160 165

atc gcc gac cta ctc acc gat caa atc gag ttc gcc gac cgc atc tac 643
 Ile Ala Asp Leu Leu Thr Asp Gln Ile Glu Phe Ala Asp Arg Ile Tyr
 170 175 180

atc acc aaa tcc gac ctg gtg gac cgc act gtc ctc gag caa acc cgc 691
 Ile Thr Lys Ser Asp Leu Val Asp Arg Thr Val Leu Glu Gln Thr Arg
 185 190 195

gca cta atc gcc agc atg agt cca cgc gcc cgc att gac tta ctc atc 739
 Ala Leu Ile Ala Ser Met Ser Pro Arg Ala Arg Ile Asp Leu Leu Ile
 200 205 210

gat ggc ctc aat gac ggc tcc ccc atc acc gac gac atc ctc gga gct 787
Asp Gly Leu Asn Asp Gly Ser Pro Ile Thr Asp Asp Ile Leu Gly Ala
215 220 225

ttc ctc tac gac gaa gcc acc gcc cgc gcc tac gag ggc tac acg gaa 835
Phe Leu Tyr Asp Glu Ala Thr Ala Arg Ala Tyr Glu Gly Tyr Thr Glu
230 235 240 245

gaa ctc gaa aac ccg cac act ccc gaa acc gag gaa tac ggc atc agt 883
Glu Leu Glu Asn Pro His Thr Pro Glu Thr Glu Glu Tyr Gly Ile Ser
250 255 260

tcc gtg gta ttc cgc tct gac cgg ccg ttc aac aag gat cgc cta ctt 931
Ser Val Val Phe Arg Ser Asp Arg Pro Phe Asn Lys Asp Arg Leu Leu
265 270 275

cag gta ctg cgt tcc acc act gga ctc gtt cgc tcc aaa ggc tat tgc 979
Gln Val Leu Arg Ser Thr Thr Gly Leu Val Arg Ser Lys Gly Tyr Cys
280 285 290

tgg atc gct gat cac ctc aac atc gtc cag gtc tgg cac caa gcc ggc 1027
Trp Ile Ala Asp His Leu Asn Ile Val Gln Val Trp His Gln Ala Gly
295 300 305

ccc aat ttg agc att cgc ccg gcc gcc tat tgg gcc aat tca gag atc 1075
Pro Asn Leu Ser Ile Arg Pro Ala Ala Tyr Trp Ala Asn Ser Glu Ile
310 315 320 325

acc ccc ggc act gaa ttg gtc ctg atc ggc atc cac atc gac ggc ccc 1123
Thr Pro Gly Thr Glu Leu Val Leu Ile Gly Ile His Ile Asp Gly Pro
330 335 340

acc ttg ctc gca ctg cta caa ggc gcg acg ctt acc gat gcg gaa gtg 1171
Thr Leu Leu Ala Leu Leu Gln Gly Ala Thr Leu Thr Asp Ala Glu Val
345 350 355

gcg gca ctg gtt ttg tgagttcctc aagtcctga att 1209
Ala Ala Leu Val Leu
360

<210> 2680
<211> 362
<212> PRT
<213> Corynebacterium glutamicum

<400> 2680
Met Ala Thr Thr Thr Pro Val Thr Val Leu Ser Gly Phe Leu Gly Ser
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Gly Lys Thr Thr Leu Leu Asn Gln Ile Leu His His Arg Gly Ser Arg
20 25 30
Lys Ile Ala Val Ile Val Asn Asp Phe Ser Glu Ile Asn Ile Asp Ala
35 40 45
Ala Leu Ile Ala Ser Glu Gly His Leu Thr Arg Gly Glu Asp Arg Phe
50 55 60
Val Glu Leu Thr Asn Gly Cys Ile Cys Cys Thr Leu Arg Glu Asp Leu

65	70	75	80
Val Asp Ser Val Gly	Glu Leu Ala Ser Ser Asp Arg Phe Asp His Ile		
	85	90	95
Val Ile Glu Ser Thr Gly Ile Ser Glu Pro Met Pro Val Ala Ala Thr			
	100	105	110
Phe Glu Trp Gln Trp Asp Asp Gly Thr Arg Leu Ala Asp Lys Ala Pro			
	115	120	125
Ile Asp Thr Met Val Thr Leu Val Asp Ala Thr Gln Phe Ile Asp Leu			
	130	135	140
Ile Arg Lys Asn Thr Ser Leu Thr Glu Ala Asp Met Gly Ala Thr Glu			
	145	150	155
Asp Asp Glu Arg Thr Ile Ala Asp Leu Leu Thr Asp Gln Ile Glu Phe			
	165	170	175
Ala Asp Arg Ile Tyr Ile Thr Lys Ser Asp Leu Val Asp Arg Thr Val			
	180	185	190
Leu Glu Gln Thr Arg Ala Leu Ile Ala Ser Met Ser Pro Arg Ala Arg			
	195	200	205
Ile Asp Leu Leu Ile Asp Gly Leu Asn Asp Gly Ser Pro Ile Thr Asp			
	210	215	220
Asp Ile Leu Gly Ala Phe Leu Tyr Asp Glu Ala Thr Ala Arg Ala Tyr			
	225	230	235
Glu Gly Tyr Thr Glu Glu Leu Glu Asn Pro His Thr Pro Glu Thr Glu			
	245	250	255
Glu Tyr Gly Ile Ser Ser Val Val Phe Arg Ser Asp Arg Pro Phe Asn			
	260	265	270
Lys Asp Arg Leu Leu Gln Val Leu Arg Ser Thr Thr Gly Leu Val Arg			
	275	280	285
Ser Lys Gly Tyr Cys Trp Ile Ala Asp His Leu Asn Ile Val Gln Val			
	290	295	300
Trp His Gln Ala Gly Pro Asn Leu Ser Ile Arg Pro Ala Ala Tyr Trp			
	305	310	315
Ala Asn Ser Glu Ile Thr Pro Gly Thr Glu Leu Val Leu Ile Gly Ile			
	325	330	335
His Ile Asp Gly Pro Thr Leu Leu Ala Leu Leu Gln Gly Ala Thr Leu			
	340	345	350
Thr Asp Ala Glu Val Ala Ala Leu Val Leu			
	355	360	

<210> 2681

<211> 993

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(970)

<223> RXA02325

<400> 2681

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				Met Met Asp His Ala	
				1 5	

cac gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc	163
His Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly	
10 15 20	

cag ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg	211
Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly	
25 30 35	

aag gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc	259
Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr	
40 45 50	

atc acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac	307
Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Leu Ile Gly His	
55 60 65	

tcc ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt	355
Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe	
70 75 80 85	

cag gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat	403
Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp	
90 95 100	

gcg agt gca gat gtg gtt gcc aga ttt agg cca aaa cag att ccg gtg	451
Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val	
105 110 115	

gca tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc	499
Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Asn Ser Leu	
120 125 130	

aac aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg ccg gaa	547
Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu	
135 140 145	

acg atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg	595
Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro	
150 155 160 165	

gcg ctg tgg ccg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg	643
Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala	
170 175 180	

gcg ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag ccg	691
Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg	
185 190 195	

gcg cac gcg gcg gtg tcg gta ttg gcg cgg atg tct gtg gcg gat cgg 739
 Ala His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg
 200 205 210

gga gag gat ccg atc gag aag tcg cgc cgg gat cca gac gat gtg aac 787
 Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn
 215 220 225

aag gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac 835
 Lys Ala Leu Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp
 230 235 240 245

aca gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc 883
 Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala
 250 255 260

cgg cgg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc 931
 Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val
 265 270 275

gca ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca 980
 Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met Ser
 280 285 290

ctttaaatat tct 993

<210> 2682
 <211> 290
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2682
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 20 25 30

Ala Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser
 35 40 45

Asn Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val
 50 55 60

Val Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys
 65 70 75 80

Asp Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala
 85 90 95

Ile Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro
 100 105 110

Lys Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala
 115 120 125

Glu Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His
 130 135 140

Phe Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp

10	15	20	
cat ccc gtg aac aag cca ctg gtc acc aaa tcc att atc agg gct cta			211
His Pro Val Asn Lys Pro Leu Val Thr Lys Ser Ile Ile Arg Ala Leu			
25	30	35	
ggc gat gtc ccc gat gtc atg agc aac cag gac atc agc ctt gtg gtg			259
Gly Asp Val Pro Asp Val Met Ser Asn Gln Asp Ile Ser Leu Val Val			
40	45	50	
gtg gat ttg tgg aaa ttc gat acc att act cct cca atc gca gaa tcc			307
Val Asp Leu Trp Lys Phe Asp Thr Ile Thr Pro Pro Ile Ala Glu Ser			
55	60	65	
ctc atg cgt tcc gtc aaa gct gtt aac ggt gag atg cac ccg cag tat			355
Leu Met Arg Ser Val Lys Ala Val Asn Gly Glu Met His Pro Gln Tyr			
70	75	80	85
ccc acc gcg aca gca atg gct gcg atc aag cat ttc tcc aac act ttt			403
Pro Thr Ala Thr Ala Met Ala Ala Ile Lys His Phe Ser Asn Thr Phe			
90	95	100	
gat gga cag att aac gct taaaaggcct gttatagact gat			444
Asp Gly Gln Ile Asn Ala			
105			

<210> 2688

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 2688

Met Asp Glu Leu Gly Val Gly Trp Cys Gln Cys Glu Lys Asp Ser Ile			
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Thr Gly Lys Ala Pro His Pro Val Asn Lys Pro Leu Val Thr Lys Ser			
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Ile Ile Arg Ala Leu Gly Asp Val Pro Asp Val Met Ser Asn Gln Asp			
35	40	45	
Ile Ser Leu Val Val Val Asp Leu Trp Lys Phe Asp Thr Ile Thr Pro			
50	55	60	
Pro Ile Ala Glu Ser Leu Met Arg Ser Val Lys Ala Val Asn Gly Glu			
65	70	75	80
Met His Pro Gln Tyr Pro Thr Ala Thr Ala Met Ala Ala Ile Lys His			
85	90	95	
Phe Ser Asn Thr Phe Asp Gly Gln Ile Asn Ala			
100	105		

<210> 2689

<211> 490

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA02349

<400> 2689

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                                         Met Ser Thr Ala Tyr
                                         1 5
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Gly Ala Trp Arg Asp Asp Glu Leu His Leu Ala Pro Val Ala Gly Leu
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Leu Val Phe Ser Arg Phe Ser Leu Glu Val Leu Gly Gln Ile Ala Arg
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Val Val Gly Asp Ala Leu Val Phe Ser Arg Phe Ser Leu Glu Val Leu
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 Glu Asp Phe Gly Asn Phe Leu Ser Lys Ala Gly Thr Ile Val Met Gly
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 Ser Thr Thr Tyr Glu Trp Leu Leu Lys Asp Leu Asp Phe Ile Ser Asp
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Asp Ala Lys Val Asn Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe
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Glu Val Ala Ala Leu Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val
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Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
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Leu Lys Asp Gly Leu Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr
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Lys Met Leu Val Asn Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala
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Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala Lys Leu Gln Ala Arg
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Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile Thr Arg Pro Thr Pro
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Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu Glu Tyr Glu Thr Ile
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 Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
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 Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile
 405 410 415
 Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu
 420 425 430
 Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
 435 440 445
 Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
 450 455 460
 Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu
 465 470 475 480
 Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr
 485 490 495

Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
500 505 510

Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
515 520 525

Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu
530 535 540

Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp
545 550 555 560

Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
565 570 575

Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr
580 585 590

Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
595 600 605

Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile
610 615 620

Gly Leu Asp Ala Phe Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly
625 630 635 640

Asp Phe Pro Glu Asp Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln
645 650 655

Leu His Tyr Gln Val Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser
660 665 670

Thr Lys Thr Thr Leu Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln
675 680 685

Ile Arg Phe Pro Asn Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys
690 695 700

Met Val Ala Tyr Lys Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser
705 710 715 720

Lys Ile Gly Ser Ser Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys
725 730 735

Glu Leu Met Asp Asp Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe
740 745 750

Ala Glu Ser Lys Asp Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys
755 760 765

Arg Thr Gly Lys Ile Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln
770 775 780

Pro Gln Ala Ser Ser His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu
785 790 795 800

Ala Ala Ala Glu Ile Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg
805 810 815

His Thr Ser Lys Arg Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro

820	825	830
Leu Asp Pro Pro Ile Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu 835 840 845		
Pro Asp Thr His Phe Val Val Gly Pro Leu Ile Val Glu Val Arg Glu 850 855 860		
Lys Glu Phe Leu Ser Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala 865 870 875 880		
Val Val Ala Asn Asp Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro 885 890 895		
Phe Leu Thr His Arg Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu 900 905 910		
Leu Pro Gln Glu Ile Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg 915 920 925		
His Val Leu Ala Gln Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp 930 935 940		
Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala 945 950 955 960		
Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu 965 970 975		
Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp 980 985 990		
Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu 995 1000 1005		
Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu 1010 1015 1020		
Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly 1025 1030 1035 1040		
Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser 1045 1050 1055		
Leu Ala Gln Lys Cys Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg 1060 1065 1070		
Asn Ser Gly Leu Glu Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe 1075 1080 1085		
Ser Ala Glu Phe Ile Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu 1090 1095 1100		
Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr 1105 1110 1115 1120		
Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly 1125 1130 1135		
Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser 1140 1145 1150		

Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val
 1155 1160 1165
 Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile
 1170 1175 1180
 Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala
 1185 1190 1195 1200
 Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu
 1205 1210 1215
 Ala Lys Val Leu Ser Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala
 1220 1225 1230
 Ile

<210> 2699
 <211> 744
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(721)
 <223> RXA02374

<400> 2699

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 attggatagc ccaccgtacg cctatctaca ctgaattacc atg agc tat gac ttt 115
 Met Ser Tyr Asp Phe
 1 5
 gtc ctc ttt gaa acc gat ggc gac cca ggt agc gcc cgt att tcc aaa 163
 Val Leu Phe Glu Thr Asp Gly Asp Pro Gly Ser Ala Arg Ile Ser Lys
 10 15 20
 acc cca ctg acc gaa cgc atc gat ttc gcc acg cca tct aca acc cct 211
 Thr Pro Leu Thr Glu Arg Ile Asp Phe Ala Thr Pro Ser Thr Thr Pro
 25 30 35
 gtg ttg gaa tct ctt tcg gca ggg ctt gcc gaa acg gtg cca gac acc 259
 Val Leu Glu Ser Leu Ser Ala Gly Leu Ala Glu Thr Val Pro Asp Thr
 40 45 50
 gtc aag ctt gaa gaa gac gcc atc cac tta tcc ggt gat cgt tgc ctt 307
 Val Lys Leu Glu Glu Asp Ala Ile His Leu Ser Gly Asp Arg Cys Leu
 55 60 65
 tac gtt gtg acc aac tac aac tcc gcc gaa gaa gca gcc gaa tgg ctc 355
 Tyr Val Val Thr Asn Tyr Asn Ser Ala Glu Glu Ala Ala Glu Trp Leu
 70 75 80 85
 acc gcc atc gct ttc gat tac gga ctg ggc ctt gcc gac atg aac gcg 403
 Thr Ala Ile Ala Phe Asp Tyr Gly Leu Gly Leu Ala Asp Met Asn Ala
 90 95 100

gac acc atc ctg ctt ttc ggc gat gaa gat tcc gac gct gtc gtc caa 451
 Asp Thr Ile Leu Leu Phe Gly Asp Glu Asp Ser Asp Ala Val Val Gln
 105 110 115
 atc gat gac tgg ttc tcc ccc gct ttc tct gcg tac ggc ctt ccc cac 499
 Ile Asp Asp Trp Phe Ser Pro Ala Phe Ser Ala Tyr Gly Leu Pro His
 120 125 130
 ctc ctg gtg gaa gtc atg cgc ctg aag gat tcc aaa acc cct tat ctt 547
 Leu Leu Val Glu Val Met Arg Leu Lys Asp Ser Lys Thr Pro Tyr Leu
 135 140 145
 cga gtc aca ctt gct gca gat gac tcg aaa ttt atc caa acc ctt tac 595
 Arg Val Thr Leu Ala Ala Asp Asp Ser Lys Phe Ile Gln Thr Leu Tyr
 150 155 160 165
 gaa acc gac aac aaa caa tgg ttg gtg gaa acc tct tcc tcc aca ggc 643
 Glu Thr Asp Asn Lys Gln Trp Leu Val Glu Thr Ser Ser Ser Thr Gly
 170 175 180
 acg gac gaa acc cac gtg aag acc att aat gat gtg ctg gaa cgc atc 691
 Thr Asp Glu Thr His Val Lys Thr Ile Asn Asp Val Leu Glu Arg Ile
 185 190 195
 gag aca tgg ttc aac cag gag act gct gtc taaacctttt gtcgtgttct 741
 Glu Thr Trp Phe Asn Gln Glu Thr Ala Val
 200 205
 ggg 744

<210> 2700

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 2700

Met Ser Tyr Asp Phe Val Leu Phe Glu Thr Asp Gly Asp Pro Gly Ser
 1 5 10 15
 Ala Arg Ile Ser Lys Thr Pro Leu Thr Glu Arg Ile Asp Phe Ala Thr
 20 25 30
 Pro Ser Thr Thr Pro Val Leu Glu Ser Leu Ser Ala Gly Leu Ala Glu
 35 40 45
 Thr Val Pro Asp Thr Val Lys Leu Glu Glu Asp Ala Ile His Leu Ser
 50 55 60
 Gly Asp Arg Cys Leu Tyr Val Val Thr Asn Tyr Asn Ser Ala Glu Glu
 65 70 75 80
 Ala Ala Glu Trp Leu Thr Ala Ile Ala Phe Asp Tyr Gly Leu Gly Leu
 85 90 95
 Ala Asp Met Asn Ala Asp Thr Ile Leu Leu Phe Gly Asp Glu Asp Ser
 100 105 110
 Asp Ala Val Val Gln Ile Asp Asp Trp Phe Ser Pro Ala Phe Ser Ala
 115 120 125

Tyr Gly Leu Pro His Leu Leu Val Glu Val Met Arg Leu Lys Asp Ser
 130 135 140
 Lys Thr Pro Tyr Leu Arg Val Thr Leu Ala Ala Asp Asp Ser Lys Phe
 145 150 155 160
 Ile Gln Thr Leu Tyr Glu Thr Asp Asn Lys Gln Trp Leu Val Glu Thr
 165 170 175
 Ser Ser Ser Thr Gly Thr Asp Glu Thr His Val Lys Thr Ile Asn Asp
 180 185 190
 Val Leu Glu Arg Ile Glu Thr Trp Phe Asn Gln Glu Thr Ala Val
 195 200 205

<210> 2701

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXA02390

<400> 2701

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 ggccgcgagg atctcgtagc tcgcttcgag tcataggccg gtg gag tgg acc gct 115
 Val Glu Trp Thr Ala
 1 5
 ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg 163
 Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
 10 15 20
 cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac 211
 Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
 25 30 35
 gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg 259
 Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
 40 45 50
 acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg 307
 Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
 55 60 65
 att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att 355
 Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
 70 75 80 85
 ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc 403
 Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
 90 95 100
 cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa 451
 Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
 105 110 115

gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac 499
 Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
 120 125 130

ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg 547
 Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
 135 140 145

ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg 595
 Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
 150 155 160 165

gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att 643
 Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
 170 175 180

gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg 691
 Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
 185 190 195

ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg 739
 Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
 200 205 210

ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct 789
 Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
 215 220

tcc 792

<210> 2702

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 2702

Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly
 1 5 10 15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr
 20 25 30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
 35 40 45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
 50 55 60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
 65 70 75 80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
 85 90 95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
 100 105 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
 115 120 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
 130 135 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
 145 150 155 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
 165 170 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
 180 185 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
 195 200 205

Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
 210 215 220

<210> 2703
 <211> 405
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(382)
 <223> RXA02393

<220>
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 <223> n = a, t, c, or g

<400> 2703
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tcaaatnngg gacgtccatg cngangtttt agacatcttc atg gcg gaa tct tta 115
 Met Ala Glu Ser Leu
 1 5

gtg att atc aac atc gac gag aaa agc gcc aag ctg ctt atc gac gcc 163
 Val Ile Ile Asn Ile Asp Glu Lys Ser Ala Lys Leu Leu Ile Asp Ala
 10 15 20

gcc cgc cac cac atc ccc acc cgc ttc acc ggg ccc aac gcc cgg ccg 211
 Ala Arg His His Ile Pro Thr Arg Phe Thr Gly Pro Asn Ala Arg Pro
 25 30 35

ctc agc gtc atc ccc atc gag gat ccc cgc tca cgc ccg acg ctc cac 259
 Leu Ser Val Ile Pro Ile Glu Asp Pro Arg Ser Arg Pro Thr Leu His
 40 45 50

cca gat cat ggt tgg atg atg ccg cta agc cca cca gtg gtg gat gaa 307
 Pro Asp His Gly Trp Met Met Pro Leu Ser Pro Pro Val Val Asp Glu
 55 60 65

ctg ctt ggc ggt ggc ttg aaa att gga gaa aca gaa cta gaa agc acc 355
 Leu Leu Gly Gly Gly Leu Lys Ile Gly Glu Thr Glu Leu Glu Ser Thr
 70 75 80 85

aac att gcg ttc att gtt gat gct tcc taaaaatcct gtgccgtgag 402
 Asn Ile Ala Phe Ile Val Asp Ala Ser
 90

gtt 405

<210> 2704
 <211> 94
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2704
 Met Ala Glu Ser Leu Val Ile Ile Asn Ile Asp Glu Lys Ser Ala Lys
 1 5 10 15
 Leu Leu Ile Asp Ala Ala Arg His His Ile Pro Thr Arg Phe Thr Gly
 20 25 30
 Pro Asn Ala Arg Pro Leu Ser Val Ile Pro Ile Glu Asp Pro Arg Ser
 35 40 45
 Arg Pro Thr Leu His Pro Asp His Gly Trp Met Met Pro Leu Ser Pro
 50 55 60
 Pro Val Val Asp Glu Leu Leu Gly Gly Gly Leu Lys Ile Gly Glu Thr
 65 70 75 80
 Glu Leu Glu Ser Thr Asn Ile Ala Phe Ile Val Asp Ala Ser
 85 90

<210> 2705
 <211> 755
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(732)
 <223> RXA02395

<400> 2705
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 Leu Ile Thr Met Ala Ile Pro Ser Phe Ile Leu Ile Leu Ala Phe Thr
 1 5 10 15
 att ttc ggt gga act gcc atc acg atg aac cgc gag aac gta gat ggt 96
 Ile Phe Gly Gly Thr Ala Ile Thr Met Asn Arg Glu Asn Val Asp Gly
 20 25 30
 ttt gac ggc agt tca tcc aag gaa cag gtg ctg ttt gat atg ttc agc 144
 Phe Asp Gly Ser Ser Ser Lys Glu Gln Val Leu Phe Asp Met Phe Ser
 35 40 45
 aac ctt ccg ctg tac tcg atc aca ccg ttc att ttg atc ttt gtg ctg 192
 Asn Leu Pro Leu Tyr Ser Ile Thr Pro Phe Ile Leu Ile Phe Val Leu
 50 55 60
 gca gta ttc ttt gtt acc tct gcc gat tcc gcc tcc gtg gtg atg gga 240
 Ala Val Phe Phe Val Thr Ser Ala Asp Ser Ala Ser Val Val Met Gly

65	70	75	80	
acg atg agc tcc caa ggt aac cct gca cca aac aaa tta atc gtg gtg				288
Thr Met Ser Ser Gln Gly Asn Pro Ala Pro Asn Lys Leu Ile Val Val				
	85	90	95	
ttc tgg gga ctg tgc atg atg ggc atc gcg gtg gtc atg ctg ctt act				336
Phe Trp Gly Leu Cys Met Met Gly Ile Ala Val Val Met Leu Leu Thr				
	100	105	110	
ggt ggc gaa tcc gcg ctg act ggt ctg cag aac ctc acc att ttg atc				384
Gly Gly Glu Ser Ala Leu Thr Gly Leu Gln Asn Leu Thr Ile Leu Ile				
	115	120	125	
gcc att ccg ttt gcg ctg gtg ttg atc gtg atg gct att gcc ttt att				432
Ala Ile Pro Phe Ala Leu Val Leu Ile Val Met Ala Ile Ala Phe Ile				
	130	135	140	
aag gac tta tcc aca gac cca gcc gct att cga caa cgc tat gca aag				480
Lys Asp Leu Ser Thr Asp Pro Ala Ala Ile Arg Gln Arg Tyr Ala Lys				
	145	150	155	160
gca gcc atc tct aac gcg gtg gtt cgt ggc ttg gaa gaa cac ggc gac				528
Ala Ala Ile Ser Asn Ala Val Val Arg Gly Leu Glu Glu His Gly Asp				
	165	170	175	
gac ttc gag ctc tcc atc gaa cct gca gag gaa ggt cgt gga gcg ggt				576
Asp Phe Glu Leu Ser Ile Glu Pro Ala Glu Glu Gly Arg Gly Ala Gly				
	180	185	190	
gct acc ttc gat tcc acc gct gat cac atc acc gac tgg tat cag cgc				624
Ala Thr Phe Asp Ser Thr Ala Asp His Ile Thr Asp Trp Tyr Gln Arg				
	195	200	205	
acc gac gaa gaa ggc aat gat gtt gat tat gac ttc acc acc ggc aaa				672
Thr Asp Glu Glu Gly Asn Asp Val Asp Tyr Asp Phe Thr Thr Gly Lys				
	210	215	220	
tgg gcc gat ggt tgg aca ccg gaa tcg acc gaa gaa ggc gaa gtg gac				720
Trp Ala Asp Gly Trp Thr Pro Glu Ser Thr Glu Glu Gly Glu Val Asp				
	225	230	235	240
gcg aaa aag gat taataataa cgactggctg gga				755
Ala Lys Lys Asp				

<210> 2706

<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 2706

Leu	Ile	Thr	Met	Ala	Ile	Pro	Ser	Phe	Ile	Leu	Ile	Leu	Ala	Phe	Thr
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Ile	Phe	Gly	Gly	Thr	Ala	Ile	Thr	Met	Asn	Arg	Glu	Asn	Val	Asp	Gly
		20						25					30		

Phe	Asp	Gly	Ser	Ser	Ser	Lys	Glu	Gln	Val	Leu	Phe	Asp	Met	Phe	Ser
		35					40					45			

Asn Leu Pro Leu Tyr Ser Ile Thr Pro Phe Ile Leu Ile Phe Val Leu
 50 55 60
 Ala Val Phe Phe Val Thr Ser Ala Asp Ser Ala Ser Val Val Met Gly
 65 70 75 80
 Thr Met Ser Ser Gln Gly Asn Pro Ala Pro Asn Lys Leu Ile Val Val
 85 90 95
 Phe Trp Gly Leu Cys Met Met Gly Ile Ala Val Val Met Leu Leu Thr
 100 105 110
 Gly Gly Glu Ser Ala Leu Thr Gly Leu Gln Asn Leu Thr Ile Leu Ile
 115 120 125
 Ala Ile Pro Phe Ala Leu Val Leu Ile Val Met Ala Ile Ala Phe Ile
 130 135 140
 Lys Asp Leu Ser Thr Asp Pro Ala Ala Ile Arg Gln Arg Tyr Ala Lys
 145 150 155 160
 Ala Ala Ile Ser Asn Ala Val Val Arg Gly Leu Glu Glu His Gly Asp
 165 170 175
 Asp Phe Glu Leu Ser Ile Glu Pro Ala Glu Glu Gly Arg Gly Ala Gly
 180 185 190
 Ala Thr Phe Asp Ser Thr Ala Asp His Ile Thr Asp Trp Tyr Gln Arg
 195 200 205
 Thr Asp Glu Glu Gly Asn Asp Val Asp Tyr Asp Phe Thr Thr Gly Lys
 210 215 220
 Trp Ala Asp Gly Trp Thr Pro Glu Ser Thr Glu Glu Gly Glu Val Asp
 225 230 235 240
 Ala Lys Lys Asp

<210> 2707

<211> 402

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(379)

<223> RXA02396

<400> 2707

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tcaagtatta actccctcgg aaacagaaag gaacacgaca atg gct acc aca gct 115
 Met Ala Thr Thr Ala
 1 5

tcc aag atc tcc acg atc cgt cca gca cag caa gat gct ctt tgg agc 163
 Ser Lys Ile Ser Thr Ile Arg Pro Ala Gln Gln Asp Ala Leu Trp Ser
 10 15 20

gta cgt gag gat ctt cac gct cgc ttc gat ggc ctg gtc gat cct gtc 211
 Val Arg Glu Asp Leu His Ala Arg Phe Asp Gly Leu Val Asp Pro Val
 25 30 35

cag gta gac gca att ttg gac cat gtc gca tct aac cgc gaa gcc aag 259
 Gln Val Asp Ala Ile Leu Asp His Val Ala Ser Asn Arg Glu Ala Lys
 40 45 50

atc acc gtc ttc agc aag att ttc atc gct cgc gag gca acc gct gca 307
 Ile Thr Val Phe Ser Lys Ile Phe Ile Ala Arg Glu Ala Thr Ala Ala
 55 60 65

ctt cag cag att gct ggc aac gtt aac gca gac ctg ctt gac ttc att 355
 Leu Gln Gln Ile Ala Gly Asn Val Asn Ala Asp Leu Leu Asp Phe Ile
 70 75 80 85

gcc ctc aac cgt ggc atg gca gca taagtttttag ctgcccataa att 402
 Ala Leu Asn Arg Gly Met Ala Ala
 90

<210> 2708

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 2708

Met Ala Thr Thr Ala Ser Lys Ile Ser Thr Ile Arg Pro Ala Gln Gln
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Asp Ala Leu Trp Ser Val Arg Glu Asp Leu His Ala Arg Phe Asp Gly
 20 25 30

Leu Val Asp Pro Val Gln Val Asp Ala Ile Leu Asp His Val Ala Ser
 35 40 45

Asn Arg Glu Ala Lys Ile Thr Val Phe Ser Lys Ile Phe Ile Ala Arg
 50 55 60

Glu Ala Thr Ala Ala Leu Gln Gln Ile Ala Gly Asn Val Asn Ala Asp
 65 70 75 80

Leu Leu Asp Phe Ile Ala Leu Asn Arg Gly Met Ala Ala
 85 90

<210> 2709

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> RXA02403

<400> 2709

gcacagaatt aaatcgctgg tgtgcgaact ttcatacctt aacgcagtag tgatgcttaa 60

ggcacaacgt gggggcaatt ccggcctata ctttggaagt atg act act ttt att 115

	Met	Thr	Thr	Phe	Ile	
	1				5	
acc tcc ggt ggc ttg gaa atc tcc ccc gct ggc gct cat att gtt cac						163
Thr Ser Gly Gly Leu Glu Ile Ser Pro Ala Gly Ala His Ile Val His						
	10				20	
gcc gaa tca cct gaa ggt gag ctg ttg ttt gtt agc tcc gct tcc caa						211
Ala Glu Ser Pro Glu Gly Glu Leu Leu Phe Val Ser Ser Ala Ser Gln						
	25				35	
tat ggg gag gga aat gca att agg ggt ggt gtg ccc atc att gct cca						259
Tyr Gly Glu Gly Asn Ala Ile Arg Gly Gly Val Pro Ile Ile Ala Pro						
	40				50	
tgg ttt ggt gga ctg ctt ggt ttg gac cct gca cat ggt tgg gcg aag						307
Trp Phe Gly Gly Leu Leu Gly Leu Asp Pro Ala His Gly Trp Ala Lys						
	55				65	
cgt tcc gcg tgg gac gtg act gaa cat gac ggc caa att cac gct gaa						355
Arg Ser Ala Trp Asp Val Thr Glu His Asp Gly Gln Ile His Ala Glu						
	70				80	85
tat ggc cgc gat ggt tta ctg ctg gat att cgt gcg aac agc act aag						403
Tyr Gly Arg Asp Gly Leu Leu Leu Asp Ile Arg Ala Asn Ser Thr Lys						
	90				95	100
aat ggt ttt gag atc acc ctg cgc gct tac aac gac acc gat gag gca						451
Asn Gly Phe Glu Ile Thr Leu Arg Ala Tyr Asn Asp Thr Asp Glu Ala						
	105				110	115
cgc act gtg cag ttg gcc ttc cac cct tat ttc aag gtg gat gat gta						499
Arg Thr Val Gln Leu Ala Phe His Pro Tyr Phe Lys Val Asp Asp Val						
	120				125	130
gaa aag atc gag gtc cgt ggc ctt gat ggg gtg gac att ctc aat cgc						547
Glu Lys Ile Glu Val Arg Gly Leu Asp Gly Val Asp Ile Leu Asn Arg						
	135				140	145
ctg aac aat gag gtg gag acc caa gat ggt ccc gtt act ttt gat ggc						595
Leu Asn Asn Glu Val Glu Thr Gln Asp Gly Pro Val Thr Phe Asp Gly						
	150				155	160
gag ttc gat cgc att gcg cta ggg act ccg gtt gtg agg att ttt gat						643
Glu Phe Asp Arg Ile Ala Leu Gly Thr Pro Val Val Arg Ile Phe Asp						
	170				175	180
acc gat cgc atc atc acc att gag ggc gat ggt cat gat tcc act gtg						691
Thr Asp Arg Ile Ile Thr Ile Glu Gly Asp Gly His Asp Ser Thr Val						
	185				190	195
gtg tgg aat cca ggc gaa agt cgc gcc tcc acc gtg gcc gat att ggc						739
Val Trp Asn Pro Gly Glu Ser Arg Ala Ser Thr Val Ala Asp Ile Gly						
	200				205	210
gaa ggt gaa tgg cgc gac ttt gtg tgt gtt gaa ccg gcg ctt ttg ggt						787
Glu Gly Glu Trp Arg Asp Phe Val Cys Val Glu Pro Ala Leu Leu Gly						
	215				220	225
gct gac caa aaa gga gtg agg gtg gct ccg ggg cag tca gtc acc gtt						835
Ala Asp Gln Lys Gly Val Arg Val Ala Pro Gly Gln Ser Val Thr Val						

230 235 240 245
 ggg atg cag gta agc gtc gaa aag cgt gct tagtttttttg ctttgaactc 885
 Gly Met Gln Val Ser Val Glu Lys Arg Ala
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 gcg 888

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 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 2710
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 Ser Ser Ala Ser Gln Tyr Gly Glu Gly Asn Ala Ile Arg Gly Gly Val
 35 40 45
 Pro Ile Ile Ala Pro Trp Phe Gly Gly Leu Leu Gly Leu Asp Pro Ala
 50 55 60
 His Gly Trp Ala Lys Arg Ser Ala Trp Asp Val Thr Glu His Asp Gly
 65 70 75 80
 Gln Ile His Ala Glu Tyr Gly Arg Asp Gly Leu Leu Leu Asp Ile Arg
 85 90 95
 Ala Asn Ser Thr Lys Asn Gly Phe Glu Ile Thr Leu Arg Ala Tyr Asn
 100 105 110
 Asp Thr Asp Glu Ala Arg Thr Val Gln Leu Ala Phe His Pro Tyr Phe
 115 120 125
 Lys Val Asp Asp Val Glu Lys Ile Glu Val Arg Gly Leu Asp Gly Val
 130 135 140
 Asp Ile Leu Asn Arg Leu Asn Asn Glu Val Glu Thr Gln Asp Gly Pro
 145 150 155 160
 Val Thr Phe Asp Gly Glu Phe Asp Arg Ile Ala Leu Gly Thr Pro Val
 165 170 175
 Val Arg Ile Phe Asp Thr Asp Arg Ile Ile Thr Ile Glu Gly Asp Gly
 180 185 190
 His Asp Ser Thr Val Val Trp Asn Pro Gly Glu Ser Arg Ala Ser Thr
 195 200 205
 Val Ala Asp Ile Gly Glu Gly Glu Trp Arg Asp Phe Val Cys Val Glu
 210 215 220
 Pro Ala Leu Leu Gly Ala Asp Gln Lys Gly Val Arg Val Ala Pro Gly
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 Gln Ser Val Thr Val Gly Met Gln Val Ser Val Glu Lys Arg Ala

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603

<210> 2712

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 2712

Val Ala Ile Ile Val Ile Ala Phe Val Leu Leu Phe Asn Ser Leu Val
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 20 25 30

Ser Val Glu Gln Thr Ile Ser Glu Ser Pro Glu Ser Pro Ser Ala Thr
 35 40 45

Glu Asp Gln Pro Pro Ser Ser Ala Thr Glu Thr Pro Arg Asn Arg Pro
 50 55 60

Ala Gln Pro Ser Leu Pro Ala Gly Ala Ser Pro Ala Asn Asp Ala Ala
 65 70 75 80

Ala Thr Gln Thr Asp Ala Gly Asn Leu Asn Asn Val Tyr Thr Gly Ser
 85 90 95

Ala Ser Thr Ser Ala Gly Phe Ala Gln Ala Val Arg Asp Ala Phe Val
 100 105 110

Asn His Tyr Leu Asp Thr Asn Glu Leu Ser Gly Arg Val Thr Ala Thr
 115 120 125

Ser Pro Val Thr Gly Gly Asn Tyr Thr Met Asn Cys Glu Asp Asn Gly
 130 135 140

Glu Tyr Val Thr Cys Thr Gly Gly Asn Asn Ala Val Val Tyr Ile Ser
 145 150 155 160

<210> 2713

<211> 2247

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2224)

<223> RXA02417

<400> 2713

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 Met Asp Met Asn Ser
 1 5

tct gac cga ttg gct cta cgc acc gcg tta gag aaa ttg tcg gca tcg 163
 Ser Asp Arg Leu Ala Leu Arg Thr Ala Leu Glu Lys Leu Ser Ala Ser
 10 15 20

gct acc gcc atg gcg tca gcg agc aat gac atc aaa gat ctc gtt gca 211

Ala Thr Ala Met Ala Ser Ala Ser Asn Asp Ile Lys Asp Leu Val Ala	
25 30 35	
cgc ctt gat gcc caa gag atg tcg ctt atc gac gca aac ccg gct ccc	259
Arg Leu Asp Ala Gln Glu Met Ser Leu Ile Asp Ala Asn Pro Ala Pro	
40 45 50	
acc cca gcg ccc act gcc cca ccc gag gct cag ctt gag ccc caa cca	307
Thr Pro Ala Pro Thr Ala Pro Glu Ala Gln Leu Glu Pro Gln Pro	
55 60 65	
ctg gtg tat gca acc gcc tca acg gcg cct gca ctg gcg gat gtt tcc	355
Leu Val Tyr Ala Thr Ala Ser Thr Ala Pro Ala Leu Ala Asp Val Ser	
70 75 80 85	
ggg acc aac cgt att cca cgt ttc gtt cgg cat cgc gcc ctg gat cca	403
Gly Thr Asn Arg Ile Pro Arg Phe Val Arg His Arg Ala Leu Asp Pro	
90 95 100	
gcg agc gaa ggc tgg cca ctt ggc gtc gag aag caa aaa gtg cag gct	451
Ala Ser Glu Gly Trp Pro Leu Gly Val Glu Lys Gln Lys Val Gln Ala	
105 110 115	
cct gcg tac ccg cac ccc gtc cgg cca gct cgt ccg gca aag ccg ccg	499
Pro Ala Tyr Pro His Pro Val Arg Pro Ala Arg Pro Ala Lys Pro Pro	
120 125 130	
atg acg tcg gag gaa aag atc atg cgt ggc gtg gcg atc ggc ggt ggt	547
Met Thr Ser Glu Glu Lys Ile Met Arg Gly Val Ala Ile Gly Gly Gly	
135 140 145	
gtg atc acc gtg gcc ggc gtg att ttg ctg gtg tcg gtg gcg att caa	595
Val Ile Thr Val Ala Gly Val Ile Leu Leu Val Ser Val Ala Ile Gln	
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Arg Gly Trp Leu Gly Pro Leu Gly Arg Val Ile Gly Ala Tyr Leu Leu	
170 175 180	
gcg gtg ctg ctt ctt ggc gcc gca cat tat gtg cgc aag cgc gga acc	691
Ala Val Leu Leu Leu Gly Ala Ala His Tyr Val Arg Lys Arg Gly Thr	
185 190 195	
cgt gtg gaa gca ctc gtt gcg ttg acg gtt acc tcc cag att gcg ttt	739
Arg Val Glu Ala Leu Val Ala Leu Thr Val Thr Ser Gln Ile Ala Phe	
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ctt gcc aca acg agt gca atc atc ttc att ttg gaa tgg tgg ccg cct	787
Leu Ala Thr Thr Ser Ala Ile Ile Phe Ile Leu Glu Trp Trp Pro Pro	
215 220 225	
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Gly Leu Gly Ser Leu Val Ala Leu Ile Gly Asn Ile Gly Phe Leu Ile	
230 235 240 245	
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Val Gly Arg Leu Trp Ser Leu Ser Lys Thr Glu Lys Ser Ala Ala Glu	
250 255 260	
ggc cac aca gta ttt gtg gga gcc atc gcc gtt tca gga ttc tcc gcg	931
Gly His Thr Val Phe Val Gly Ala Ile Ala Val Ser Gly Phe Ser Ala	

265	270	275	
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gtt gcg gca ttg ttg ctg tgc tac cgc atc tcc acg aat atc atc cga Val Ala Ala Leu Leu Leu Ser Tyr Arg Ile Ser Thr Asn Ile Ile Arg 295 300 305			1027
gcg agc atg gcg gca ttc gcg gtc att ctg cag ttt gtt ttg tgc gca Ala Ser Met Ala Ala Phe Ala Val Ile Leu Gln Phe Val Leu Ser Ala 310 315 320 325			1075
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ctg tgg ctc acc gat acc caa gcg ctc atc caa gca ttg ctg atc ttg Leu Trp Leu Thr Asp Thr Gln Ala Leu Ile Gln Ala Leu Leu Ile Leu 520 525 530	1699
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gcg ggc acc ttc aag ctg gtg ttc ttt gac ctg gtc gcg ctg tcc gga Ala Gly Thr Phe Lys Leu Val Phe Phe Asp Leu Val Ala Leu Ser Gly 630 635 640 645	2035
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gct aga cct cag gtg gct aga cat ggg gcg act agc cat aaa aat gag Ala Arg Pro Gln Val Ala Arg His Gly Ala Thr Ser His Lys Asn Glu 680 685 690	2179
gag cct tcc cat gaa agc ccc tca tct tct cct aca aca act ctt Glu Pro Ser His Glu Ser Pro Ser Ser Ser Pro Thr Thr Thr Leu 695 700 705	2224
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<212> PRT

<213> Corynebacterium glutamicum

<400> 2714

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20 25 30

Lys Asp Leu Val Ala Arg Leu Asp Ala Gln Glu Met Ser Leu Ile Asp
35 40 45

Ala Asn Pro Ala Pro Thr Pro Ala Pro Thr Ala Pro Pro Glu Ala Gln
50 55 60

Leu Glu Pro Gln Pro Leu Val Tyr Ala Thr Ala Ser Thr Ala Pro Ala
65 70 75 80

Leu Ala Asp Val Ser Gly Thr Asn Arg Ile Pro Arg Phe Val Arg His
85 90 95

Arg Ala Leu Asp Pro Ala Ser Glu Gly Trp Pro Leu Gly Val Glu Lys
100 105 110

Gln Lys Val Gln Ala Pro Ala Tyr Pro His Pro Val Arg Pro Ala Arg
115 120 125

Pro Ala Lys Pro Pro Met Thr Ser Glu Glu Lys Ile Met Arg Gly Val
130 135 140

Ala Ile Gly Gly Gly Val Ile Thr Val Ala Gly Val Ile Leu Leu Val
145 150 155 160

Ser Val Ala Ile Gln Arg Gly Trp Leu Gly Pro Leu Gly Arg Val Ile
165 170 175

Gly Ala Tyr Leu Leu Ala Val Leu Leu Leu Gly Ala Ala His Tyr Val
180 185 190

Arg Lys Arg Gly Thr Arg Val Glu Ala Leu Val Ala Leu Thr Val Thr
195 200 205

Ser Gln Ile Ala Phe Leu Ala Thr Thr Ser Ala Ile Ile Phe Ile Leu
210 215 220

Glu Trp Trp Pro Pro Gly Leu Gly Ser Leu Val Ala Leu Ile Gly Asn
225 230 235 240

Ile Gly Phe Leu Ile Val Gly Arg Leu Trp Ser Leu Ser Lys Thr Glu
245 250 255

Lys Ser Ala Ala Glu Gly His Thr Val Phe Val Gly Ala Ile Ala Val
260 265 270

Ser Gly Phe Ser Ala Ile Leu Phe Ala Leu Ser Ala Asp Ala Trp Trp
275 280 285

Pro Ile Phe Ser Ile Val Ala Ala Leu Leu Leu Ser Tyr Arg Ile Ser
290 295 300

Thr Asn Ile Ile Arg Ala Ser Met Ala Ala Phe Ala Val Ile Leu Gln
305 310 315 320

Phe Val Leu Ser Ala Ser Trp Gln Thr Met Glu Trp Pro Ala Thr Ile
325 330 335

Val Gly Thr Ile Thr Ala Val Leu Leu Val Ala Leu Thr Leu Trp Asp

340 345 350
Pro Phe Lys Ile Thr Ala Thr Asp Ser His Asp Ile Ala Leu Glu Glu
355 360 365
Tyr Trp Arg Ser Phe Glu Thr Asn Pro Val Ser Thr Trp Val Gly Ala
370 375 380
Val Ser Pro Val Leu Ile Val Phe Ile Thr Thr Ser Met Phe Ile Ala
385 390 395 400
Val Asp Trp Pro Trp Leu Ala Leu Ile Pro Ala Cys Ala Val Ala Ala
405 410 415
Leu Gly Ile Phe Ala Leu Arg Ser Ser Asp Thr Ala Ser Ile Glu Asn
420 425 430
Gln Arg Met Ser Arg Leu Ile Ala Val Val Gly Leu Ala Leu Ile Ala
435 440 445
Glu Thr Phe Val Gln Leu Phe Tyr Gly Asp Leu Pro Thr Asn Pro Leu
450 455 460
Leu Val Met Val Phe Leu Ile Ala Gly Ala Ala Leu Phe Met Trp Leu
465 470 475 480
Arg Met Leu Pro Pro Gln Arg Gln Leu Gly Val Val Pro Trp Val Ala
485 490 495
Trp Leu Ile Ala Ala Val Ala Met Thr Gly Val Leu Leu Arg Asn Val
500 505 510
Val Ser Ile Ser Pro Leu Trp Leu Thr Asp Thr Gln Ala Leu Ile Gln
515 520 525
Ala Leu Leu Ile Leu Val Phe Ile Ala Ala Thr Ile Gln Val Arg Arg
530 535 540
Ser Phe Tyr Gly His Lys Leu Trp Leu Gln Ile Leu Val Gly Leu Thr
545 550 555 560
Leu Leu Thr Leu Ser Ala Ile Ser Ile Val Thr Ile Thr Thr Phe Ile
565 570 575
Gly Arg Leu Ile Ala Gly Asn Ala Gly Met Met Leu Gly Phe Leu Ile
580 585 590
Gly His Ala Thr Val Ser Ile Leu Trp Met Val Ile Ala Ala Ala Leu
595 600 605
Met Leu Asn Arg Lys Leu Leu Asp Ala Pro Gly Ala Leu Trp Thr Gly
610 615 620
Val Gly Leu Ala Val Ala Gly Thr Phe Lys Leu Val Phe Phe Asp Leu
625 630 635 640
Val Ala Leu Ser Gly Val Pro Arg Ala Ile Ala Phe Leu Leu Ser Gly
645 650 655
Ile Ala Leu Leu Thr Ile Ala Ala Met Arg Gly Arg Arg Thr Ser Glu
660 665 670

Asn Lys Ala Asp Val Ala Arg Pro Gln Val Ala Arg His Gly Ala Thr
 675 680 685

Ser His Lys Asn Glu Glu Pro Ser His Glu Ser Pro Ser Ser Ser Pro
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Thr Thr Thr Leu
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<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> RXA02421

<400> 2715

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 Met Thr Leu Leu Leu
 1 5
 aag cca att ttg cag gct gcg gga atc aat cct gaa gat gcg tta gca 163
 Lys Pro Ile Leu Gln Ala Ala Gly Ile Asn Pro Glu Asp Ala Leu Ala
 10 15 20
 atg cgt cat gta ttt att tcg atc cac gag gac acc aat tcc aat ggt 211
 Met Arg His Val Phe Ile Ser Ile His Glu Asp Thr Asn Ser Asn Gly
 25 30 35
 att acc cgt gaa tct aaa gac gaa gag att ctc gcc tac aca gct agc 259
 Ile Thr Arg Glu Ser Lys Asp Glu Glu Ile Leu Ala Tyr Thr Ala Ser
 40 45 50
 cag tca agt gat ccg cgt aga ttc cca ctg aat ccg cca cgc ttt tgg 307
 Gln Ser Ser Asp Pro Arg Arg Phe Pro Leu Asn Pro Pro Arg Phe Trp
 55 60 65
 atg gtg ttc atc cga gaa ggt ggc tcg cag gct cga cta tgg aaa gtg 355
 Met Val Phe Ile Arg Glu Gly Gly Ser Gln Ala Arg Leu Trp Lys Val
 70 75 80 85
 gtg gaa aac cac ggc gaa gtc acc aat gat ggc gta cgc aga gtc ttc 403
 Val Glu Asn His Gly Glu Val Thr Asn Asp Gly Val Arg Arg Val Phe
 90 95 100
 aac ctt act gag att gaa ctc atg gat gac ctt gca ggc aga ctc gtt 451
 Asn Leu Thr Glu Ile Glu Leu Met Asp Asp Leu Ala Gly Arg Leu Val
 105 110 115
 att cgt tgg aat tca cca cgc aag tgg tgg att aag ggc act act gct 499
 Ile Arg Trp Asn Ser Pro Arg Lys Trp Trp Ile Lys Gly Thr Thr Ala
 120 125 130
 gcc cta tac acc gtg gat act att gcc gat gcg gag cct att ccg ttt 547

Ala Leu Tyr Thr Val Asp Thr Ile Ala Asp Ala Glu Pro Ile Pro Phe
 135 140 145

cca ggt ttc gac aat ctt gtc ctg agc tac cca ttt ctt caa gaa gtg 595
 Pro Gly Phe Asp Asn Leu Val Leu Ser Tyr Pro Phe Leu Gln Glu Val
 150 155 160 165

atg cgt gaa cct gcc tat gct tgc tgg cgc aca gct ctt ggt gct gtc 643
 Met Arg Glu Pro Ala Tyr Ala Ser Trp Arg Thr Ala Leu Gly Ala Val
 170 175 180

aaa ggt att tac ctc att acc gat acc cgt act ggc cgc cac tat gtc 691
 Lys Gly Ile Tyr Leu Ile Thr Asp Thr Arg Thr Gly Arg His Tyr Val
 185 190 195

ggc aaa gct gaa gga cta gaa aac ata cgc caa cgc tgg aac agc tac 739
 Gly Lys Ala Glu Gly Leu Glu Asn Ile Arg Gln Arg Trp Asn Ser Tyr
 200 205 210

gcc acc aat gga cat ggc gga aac gta aaa ctc aaa cag ctt aag ccc 787
 Ala Thr Asn Gly His Gly Gly Asn Val Lys Leu Lys Gln Leu Lys Pro
 215 220 225

gac aca ttt cgt ttt tgc ttg ctt cgg gtc ttt gat ccc gca act cca 835
 Asp Thr Phe Arg Phe Ser Leu Leu Arg Val Phe Asp Pro Ala Thr Pro
 230 235 240 245

act agc att att aac gct gct gaa agc cac ttt aaa att gct ctc gac 883
 Thr Ser Ile Ile Asn Ala Ala Glu Ser His Phe Lys Ile Ala Leu Asp
 250 255 260

acg atc aag cac gga tta aac gca aac taatcgcagc tccccaaccc 930
 Thr Ile Lys His Gly Leu Asn Ala Asn
 265 270

caa 933

<210> 2716

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 2716

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Thr Asn Ser Asn Gly Ile Thr Arg Glu Ser Lys Asp Glu Glu Ile Leu
 35 40 45

Ala Tyr Thr Ala Ser Gln Ser Ser Asp Pro Arg Arg Phe Pro Leu Asn
 50 55 60

Pro Pro Arg Phe Trp Met Val Phe Ile Arg Glu Gly Gly Ser Gln Ala
 65 70 75 80

Arg Leu Trp Lys Val Val Glu Asn His Gly Glu Val Thr Asn Asp Gly
 85 90 95

Val Arg Arg Val Phe Asn Leu Thr Glu Ile Glu Leu Met Asp Asp Leu
 100 105 110

Ala Gly Arg Leu Val Ile Arg Trp Asn Ser Pro Arg Lys Trp Trp Ile
 115 120 125

Lys Gly Thr Thr Ala Ala Leu Tyr Thr Val Asp Thr Ile Ala Asp Ala
 130 135 140

Glu Pro Ile Pro Phe Pro Gly Phe Asp Asn Leu Val Leu Ser Tyr Pro
 145 150 155 160

Phe Leu Gln Glu Val Met Arg Glu Pro Ala Tyr Ala Ser Trp Arg Thr
 165 170 175

Ala Leu Gly Ala Val Lys Gly Ile Tyr Leu Ile Thr Asp Thr Arg Thr
 180 185 190

Gly Arg His Tyr Val Gly Lys Ala Glu Gly Leu Glu Asn Ile Arg Gln
 195 200 205

Arg Trp Asn Ser Tyr Ala Thr Asn Gly His Gly Gly Asn Val Lys Leu
 210 215 220

Lys Gln Leu Lys Pro Asp Thr Phe Arg Phe Ser Leu Leu Arg Val Phe
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Asp Pro Ala Thr Pro Thr Ser Ile Ile Asn Ala Ala Glu Ser His Phe
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Lys Ile Ala Leu Asp Thr Ile Lys His Gly Leu Asn Ala Asn
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<211> 653

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(630)

<223> RXA02425

<400> 2717

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agt tgg gcc gct gtt atc ggc ttc ttc ggt ggc atc gcg ctg atc gcc 96
 Ser Trp Ala Ala Val Ile Gly Phe Phe Gly Gly Ile Ala Leu Ile Ala
 20 25 30

atc atc gac cgc tta gtc ccc acg gcg att aac ccc cac gag ccc tcc 144
 Ile Ile Asp Arg Leu Val Pro Thr Ala Ile Asn Pro His Glu Pro Ser
 35 40 45

acc gtg gga ggc gcc gtt gaa gga ttc gag cgc cgc aac cgc atg atg 192
 Thr Val Gly Gly Ala Val Glu Gly Phe Glu Arg Arg Asn Arg Met Met
 50 55 60

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Lys Met Gly Val Leu Thr Ala Leu Ala Ile Ala Ile His Asn Phe Pro
65 70 75 80

gaa ggt ttc gct aca ttc ttg gcc gga ttg tcc gat cca atg atc gcg 288
Glu Gly Phe Ala Thr Phe Leu Ala Gly Leu Ser Asp Pro Met Ile Ala
85 90 95

atc cct gtg gcc gtg gca att gcc att cac aat att cca gag ggc att 336
Ile Pro Val Ala Val Ala Ile Ala Ile His Asn Ile Pro Glu Gly Ile
100 105 110

gcg gtg ccg gtg cca ctg agg gaa gct aca ggg tca cgt cga aaa gca 384
Ala Val Pro Val Pro Leu Arg Glu Ala Thr Gly Ser Arg Arg Lys Ala
115 120 125

tta ggt tgg gcg acc ctc tcc ggc ctt gct gag ccc gcc ggc gcc ctc 432
Leu Gly Trp Ala Thr Leu Ser Gly Leu Ala Glu Pro Ala Gly Ala Leu
130 135 140

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Ile Gly Phe Leu Leu Leu Met Pro Phe Ile Gly Pro Glu Ala Leu Gly
145 150 155 160

ctg tgc ttc gcc gca gtt gcc ggc gtg atg gtg ttc atc agc gtc gat 528
Leu Cys Phe Ala Ala Val Ala Gly Val Met Val Phe Ile Ser Val Asp
165 170 175

gaa cta ctg ccc act gcc atc tcc agc ggc aaa cac cac acc gcc atc 576
Glu Leu Leu Pro Thr Ala Ile Ser Ser Gly Lys His His Thr Ala Ile
180 185 190

tac gga ctc atc gct ggc atg gca gtc atg gcg atc agc ctg ctg ctg 624
Tyr Gly Leu Ile Ala Gly Met Ala Val Met Ala Ile Ser Leu Leu Leu
195 200 205

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Phe Ile
210

<210> 2718
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<212> PRT
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Pro Gly Ala Phe Asp Glu Leu Thr Ser Val Trp Gly Glu Lys Gly Gly
1 5 10 15

Ser Trp Ala Ala Val Ile Gly Phe Phe Gly Gly Ile Ala Leu Ile Ala
20 25 30

Ile Ile Asp Arg Leu Val Pro Thr Ala Ile Asn Pro His Glu Pro Ser
35 40 45

Thr Val Gly Gly Ala Val Glu Gly Phe Glu Arg Arg Asn Arg Met Met
50 55 60

Lys Met Gly Val Leu Thr Ala Leu Ala Ile Ala Ile His Asn Phe Pro

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65	70	75	80
Glu Gly Phe Ala Thr Phe Leu Ala Gly Leu Ser Asp Pro Met Ile Ala	85	90	95
Ile Pro Val Ala Val Ala Ile Ala Ile His Asn Ile Pro Glu Gly Ile	100	105	110
Ala Val Pro Val Pro Leu Arg Glu Ala Thr Gly Ser Arg Arg Lys Ala	115	120	125
Leu Gly Trp Ala Thr Leu Ser Gly Leu Ala Glu Pro Ala Gly Ala Leu	130	135	140
Ile Gly Phe Leu Leu Leu Met Pro Phe Ile Gly Pro Glu Ala Leu Gly	145	150	155
Leu Cys Phe Ala Ala Val Ala Gly Val Met Val Phe Ile Ser Val Asp	165	170	175
Glu Leu Leu Pro Thr Ala Ile Ser Ser Gly Lys His His Thr Ala Ile	180	185	190
Tyr Gly Leu Ile Ala Gly Met Ala Val Met Ala Ile Ser Leu Leu Leu	195	200	205
Phe Ile	210		

<210> 2719

<211> 510

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(487)

<223> RXA02427

<400> 2719

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agcgatgctg acagtgcttc acttcgggcc gcatctaatt cctgctcgat tacccaactg 60
ctcgcgcagg gaatcgtcac cgacgacgag gtgaactagc gtg gat ttt gag ttg 115
                               Val Asp Phe Glu Leu
                               1           5

ggt aaa cgc tgc ccc tgc gga act ggc ctt acc tac ggt gag tgc tgc 163
Gly Lys Arg Cys Pro Cys Gly Thr Gly Leu Thr Tyr Gly Glu Cys Cys
                10                15                20

tac cgc ttt cac tcc ggc gaa tgg gtg gcc ccc acc gct gaa gcg ctc 211
Tyr Arg Phe His Ser Gly Glu Trp Val Ala Pro Thr Ala Glu Ala Leu
                25                30                35

atg cga tct cgg ttc acc gcc ttt gct gtt gga aat tcc cag tac ctt 259
Met Arg Ser Arg Phe Thr Ala Phe Ala Val Gly Asn Ser Gln Tyr Leu
                40                45                50

ctt gac act tgg gat cca gaa acc cgg cca agc gaa ctc ggc ctc gat 307
Leu Asp Thr Trp Asp Pro Glu Thr Arg Pro Ser Glu Leu Gly Leu Asp

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<221> CDS

<222> (101)..(286)

<223> RXA02430

<400> 2721

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cttgtagtca agcgtggacc aaatgcaggc gctcgattcc ttctggacca gcccaaccacg 60
accgctggtc gtcacccaga aagtgcacatc ttccttgatg atg tca ccc gtt tca 115
                                         Met Ser Pro Val Ser
                                         1           5

cgt cgc cac gca gag ttc cgc atc aat gaa ggt gaa ttt gaa gtc gtg 163
Arg Arg His Ala Glu Phe Arg Ile Asn Glu Gly Glu Phe Glu Val Val
              10              15              20

gac gta ggg tcc ctc aac gga acc tac gtt aac cgc gag cca cgc aac 211
Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Arg Asn
              25              30              35

gct cag gtc atg cag acc ggt gat gag atc cag att ggc aag ttc cgc 259
Ala Gln Val Met Gln Thr Gly Asp Glu Ile Gln Ile Gly Lys Phe Arg
              40              45              50

ctg gtt ttc ctc gca ggc cct gct gag taaaaacact tcctaggaaa 306
Leu Val Phe Leu Ala Gly Pro Ala Glu
              55              60

gtt 309

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<210> 2722

<211> 62

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2722

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Met Ser Pro Val Ser Arg Arg His Ala Glu Phe Arg Ile Asn Glu Gly
 1           5           10           15

Glu Phe Glu Val Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn
      20           25           30

Arg Glu Pro Arg Asn Ala Gln Val Met Gln Thr Gly Asp Glu Ile Gln
      35           40           45

Ile Gly Lys Phe Arg Leu Val Phe Leu Ala Gly Pro Ala Glu
      50           55           60

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<210> 2723

<211> 723

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(700)

<223> RXA02433

<400> 2723

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aggcagcaga tcattcatcg tcggttccat agaatgggta gctgtcgaat gctgatagat 60

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atttggtgac cagagattag agcaaaggat cattttcatc gtg aag ctt ttc aag 115
                                   Val Lys Leu Phe Lys
                                   1 5

gca acc gca gtt act ttt act gtt gca gca gca ttg gcg ctc agc gcg 163
Ala Thr Ala Val Thr Phe Thr Val Ala Ala Ala Leu Ala Leu Ser Ala
                                   10 15 20

tgc tcc agc agt gat gat tcc tct tcg gag tca agc acc tct tct tcc 211
Cys Ser Ser Ser Asp Asp Ser Ser Ser Glu Ser Ser Thr Ser Ser Ser
                                   25 30 35

acc tct tcg gct gcg tct gat gct gcg act cag tac cca act gct gag 259
Thr Ser Ser Ala Ala Ser Asp Ala Ala Thr Gln Tyr Pro Thr Ala Glu
                                   40 45 50

gaa ctg aat gca att ttg gct gtg gca acc gac cct gag gca cca atc 307
Glu Leu Asn Ala Ile Leu Ala Val Ala Thr Asp Pro Glu Ala Pro Ile
                                   55 60 65

gag gag aag gtg aag act gtt cag ggt tct gag aac gct cct gag ctg 355
Glu Glu Lys Val Lys Thr Val Gln Gly Ser Glu Asn Ala Pro Glu Leu
                                   70 75 80 85

ttt gag acc atg act cag gca aag gtg gag tcg ggt gct gag ttc cag 403
Phe Glu Thr Met Thr Gln Ala Lys Val Glu Ser Gly Ala Glu Phe Gln
                                   90 95 100

gtt gtt ggt tct gtg ctt cct ggc tat gac cca acc tct gag gtt ctg 451
Val Val Gly Ser Val Leu Pro Gly Tyr Asp Pro Thr Ser Glu Val Leu
                                   105 110 115

acc acc gtc atg ttc cag ctt ccg gac cgc gct gag cag gaa gct gaa 499
Thr Thr Val Met Phe Gln Leu Pro Asp Arg Ala Glu Gln Glu Ala Glu
                                   120 125 130

ggc gtg gag ttt gtg aac act gat ggt aat tgg cag ctg tcc cag gat 547
Gly Val Glu Phe Val Asn Thr Asp Gly Asn Trp Gln Leu Ser Gln Asp
                                   135 140 145

tgg gct tgt atc ttg atc acc aat act gtt gct cct gag cag gtt cct 595
Trp Ala Cys Ile Leu Ile Thr Asn Thr Val Ala Pro Glu Gln Val Pro
                                   150 155 160 165

gca atg tgt gtt gga act gat gct tct tcc gct ggt att gaa gag gcc 643
Ala Met Cys Val Gly Thr Asp Ala Ser Ser Ala Gly Ile Glu Glu Ala
                                   170 175 180

cca gct gaa gag ggt gct gtt gtt gag gaa gcc cct gtt gaa gag gtt 691
Pro Ala Glu Glu Gly Ala Val Val Glu Glu Ala Pro Val Glu Glu Val
                                   185 190 195

cct gtt cag tagggtttaa cggctcaggc tga 723
Pro Val Gln
                                   200

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<210> 2724

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 2724

Val Lys Leu Phe Lys Ala Thr Ala Val Thr Phe Thr Val Ala Ala Ala
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 Leu Ala Leu Ser Ala Cys Ser Ser Ser Asp Asp Ser Ser Ser Glu Ser
 20 25 30
 Ser Thr Ser Ser Ser Thr Ser Ser Ala Ala Ser Asp Ala Ala Thr Gln
 35 40 45
 Tyr Pro Thr Ala Glu Glu Leu Asn Ala Ile Leu Ala Val Ala Thr Asp
 50 55 60
 Pro Glu Ala Pro Ile Glu Glu Lys Val Lys Thr Val Gln Gly Ser Glu
 65 70 75 80
 Asn Ala Pro Glu Leu Phe Glu Thr Met Thr Gln Ala Lys Val Glu Ser
 85 90 95
 Gly Ala Glu Phe Gln Val Val Gly Ser Val Leu Pro Gly Tyr Asp Pro
 100 105 110
 Thr Ser Glu Val Leu Thr Thr Val Met Phe Gln Leu Pro Asp Arg Ala
 115 120 125
 Glu Gln Glu Ala Glu Gly Val Glu Phe Val Asn Thr Asp Gly Asn Trp
 130 135 140
 Gln Leu Ser Gln Asp Trp Ala Cys Ile Leu Ile Thr Asn Thr Val Ala
 145 150 155 160
 Pro Glu Gln Val Pro Ala Met Cys Val Gly Thr Asp Ala Ser Ser Ala
 165 170 175
 Gly Ile Glu Glu Ala Pro Ala Glu Glu Gly Ala Val Val Glu Glu Ala
 180 185 190
 Pro Val Glu Glu Val Pro Val Gln
 195 200

<210> 2725

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> RXA02437

<400> 2725

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 gggctcttaga agaacgcgac caattttaagg agagttgaat atg agc acg att ggc 115
 Met Ser Thr Ile Gly
 1 5
 aac ctc aag tta gta gtg gat ggc gca cgt aaa gct tat gga act tat 163

Asn	Leu	Lys	Leu	Val	Val	Asp	Gly	Ala	Arg	Lys	Ala	Tyr	Gly	Thr	Tyr		
				10					15					20			
gcg	gat	tac	cgc	gac	cgc	aag	gtg	tct	gag	act	tat	gat	gcg	ttg	tcc	211	
Ala	Asp	Tyr	Arg	Asp	Arg	Lys	Val	Ser	Glu	Thr	Tyr	Asp	Ala	Leu	Ser		
			25					30					35				
caa	gct	gct	ggc	gaa	tat	gca	cca	aaa	gct	gag	cag	gct	gta	gag	act	259	
Gln	Ala	Ala	Gly	Glu	Tyr	Ala	Pro	Lys	Ala	Glu	Gln	Ala	Val	Glu	Thr		
			40				45					50					
gcg	cgg	gaa	tca	gcg	aag	gaa	ttt	tat	act	gag	tcg	cgc	gat	aag	gct	307	
Ala	Arg	Glu	Ser	Ala	Lys	Glu	Phe	Tyr	Thr	Glu	Ser	Arg	Asp	Lys	Ala		
		55				60					65						
gga	aat	gtc	acc	aag	gct	gct	cgt	gct	cgt	ctg	gaa	aag	gcg	ctc	gct	355	
Gly	Asn	Val	Thr	Lys	Ala	Ala	Arg	Ala	Arg	Leu	Glu	Lys	Ala	Leu	Ala		
	70				75					80					85		
gag	gct	gac	aag	cag	ggc	act	tct	gcg	ttg	aag	gac	gca	cgt	gaa	tcg	403	
Glu	Ala	Asp	Lys	Gln	Gly	Thr	Ser	Ala	Leu	Lys	Asp	Ala	Arg	Glu	Ser		
				90					95					100			
ggc	aag	aaa	ttg	aac	cgg	aag	gcg	cgt	cga	aaa	gca	gac	aag	gcc	gct	451	
Gly	Lys	Lys	Leu	Asn	Arg	Lys	Ala	Arg	Arg	Lys	Ala	Asp	Lys	Ala	Ala		
			105					110					115				
aag	gca	gcc	cgc	aag	gcg	act	gaa	aag	aag	gag	tcg	cac	tgg	gtg	cgc	499	
Lys	Ala	Ala	Arg	Lys	Ala	Thr	Glu	Lys	Lys	Glu	Ser	His	Trp	Val	Arg		
		120					125					130					
aat	ctg	tcg	ttg	gcg	gcg	cta	gcg	acc	tcc	ggc	atc	gtc	gcg	gtg	gcc	547	
Asn	Leu	Ser	Leu	Ala	Ala	Leu	Ala	Thr	Ser	Gly	Ile	Val	Ala	Val	Ala		
		135				140					145						
tac	gcg	ttt	ttg	aac	aag	acc	aag	aag	gaa	acc	cca	ggc	acc	cag	cct	595	
Tyr	Ala	Phe	Leu	Asn	Lys	Thr	Lys	Lys	Glu	Thr	Pro	Gly	Thr	Gln	Pro		
		150			155					160				165			
cca	cgg	gtt	gag	gtt	cag	ttg	aag	aag	gcc	gtg	gag	cag	gat	gag	cct	643	
Pro	Arg	Val	Glu	Val	Gln	Leu	Lys	Lys	Ala	Val	Glu	Gln	Asp	Glu	Pro		
				170					175					180			
gag	gtt	gtg	gct	gag	gct	gct	gtg	gag	gag	cca	gag	ttg	gtg	tac	tcc	691	
Glu	Val	Val	Ala	Glu	Ala	Ala	Val	Glu	Glu	Pro	Glu	Leu	Val	Tyr	Ser		
			185					190					195				
aca	gaa	agc	cca	gaa	acc	act	gaa	gcc	cca	gct	gag	gcc	acc	gaa	act	739	
Thr	Glu	Ser	Pro	Glu	Thr	Thr	Glu	Ala	Pro	Ala	Glu	Ala	Thr	Glu	Thr		
		200					205					210					
cca	gca	gaa	acc	acc	gaa	gaa	gaa	gcc	aaa	acc	gaa	gct	gaa	cta	gag	787	
Pro	Ala	Glu	Thr	Thr	Glu	Glu	Glu	Ala	Lys	Thr	Glu	Ala	Glu	Leu	Glu		
		215				220					225						
gca	gag	ctc	gag	gct	gag	gcc	gat	gcg	gag	cag	gaa	gcg	gca	gaa	gag	835	
Ala	Glu	Leu	Glu	Ala	Glu	Ala	Asp	Ala	Glu	Gln	Glu	Ala	Ala	Glu	Glu		
		230			235				240					245			
gcg	gaa	gct	gag	gcc	att	cag	gct	gag	ttt	gat	aag	aag	aat	gca	cct	883	
Ala	Glu	Ala	Glu	Ala	Ile	Gln	Ala	Glu	Phe	Asp	Lys	Lys	Asn	Ala	Pro		

250 255 260
 cag cgc acc cag agc gaa aag aag aag taggttaacg cttcaattcg 930
 Gln Arg Thr Gln Ser Glu Lys Lys Lys
 265 270
 tgg 933

 <210> 2726
 <211> 270
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 2726
 Met Ser Thr Ile Gly Asn Leu Lys Leu Val Val Asp Gly Ala Arg Lys
 1 5 10 15
 Ala Tyr Gly Thr Tyr Ala Asp Tyr Arg Asp Arg Lys Val Ser Glu Thr
 20 25 30
 Tyr Asp Ala Leu Ser Gln Ala Ala Gly Glu Tyr Ala Pro Lys Ala Glu
 35 40 45
 Gln Ala Val Glu Thr Ala Arg Glu Ser Ala Lys Glu Phe Tyr Thr Glu
 50 55 60
 Ser Arg Asp Lys Ala Gly Asn Val Thr Lys Ala Ala Arg Ala Arg Leu
 65 70 75 80
 Glu Lys Ala Leu Ala Glu Ala Asp Lys Gln Gly Thr Ser Ala Leu Lys
 85 90 95
 Asp Ala Arg Glu Ser Gly Lys Lys Leu Asn Arg Lys Ala Arg Arg Lys
 100 105 110
 Ala Asp Lys Ala Ala Lys Ala Ala Arg Lys Ala Thr Glu Lys Lys Glu
 115 120 125
 Ser His Trp Val Arg Asn Leu Ser Leu Ala Ala Leu Ala Thr Ser Gly
 130 135 140
 Ile Val Ala Val Ala Tyr Ala Phe Leu Asn Lys Thr Lys Lys Glu Thr
 145 150 155 160
 Pro Gly Thr Gln Pro Pro Arg Val Glu Val Gln Leu Lys Lys Ala Val
 165 170 175
 Glu Gln Asp Glu Pro Glu Val Val Ala Glu Ala Ala Val Glu Glu Pro
 180 185 190
 Glu Leu Val Tyr Ser Thr Glu Ser Pro Glu Thr Thr Glu Ala Pro Ala
 195 200 205
 Glu Ala Thr Glu Thr Pro Ala Glu Thr Thr Glu Glu Glu Ala Lys Thr
 210 215 220
 Glu Ala Glu Leu Glu Ala Glu Leu Glu Ala Glu Ala Asp Ala Glu Gln
 225 230 235 240
 Glu Ala Ala Glu Glu Ala Glu Ala Glu Ala Ile Gln Ala Glu Phe Asp

50	55	60
Val Gly Asp Ser Ala Asp Val Gln Val Leu Met Lys Pro Asn Ala Asp 65 70 75 80		
Pro His Ser Phe Gly Val Ser Ala Gln Asp Ala Ala Ala Met Glu His 85 90 95		
Ala Asp Leu Ile Val Ala Asn Gly Leu Gly Leu Glu Glu Gly Leu Gln 100 105 110		
Ser Asn Val Asp Asn Ala Lys Ser Gln Gly Val Pro Val Leu Glu Val 115 120 125		
Gly Glu His Ile Asp Val Ile Asp Tyr Ser Pro Gly Val Pro Asp Pro 130 135 140		
His Phe Trp Thr Asp Pro Ala Arg Met Ile Ala Ala Thr Glu Val Ile 145 150 155 160		
Glu Ala Glu Leu Ile Lys Glu Leu Asp Pro Ser Leu Thr Glu Ser Ile 165 170 175		
Thr Gln Ser Ala Gln His Tyr Arg Glu Glu Leu Val Ala Leu Asp Glu 180 185 190		
Glu Val Thr Glu Leu Leu Ser Gly Val Ala Pro Glu Asn Arg Lys Leu 195 200 205		
Val Thr Asn His Asn Val Phe Gly Tyr Leu Ala Ser Arg Phe Asn Tyr 210 215 220		
Thr Val Ile Asp Thr Ile Ile Pro Gly Gly Ser Thr Leu Ala Ala Pro 225 230 235 240		
Ser Ala Ser Asp Leu Asn Asp Ile Ser Thr Ala Ile Glu Asp Asn Asn 245 250 255		
Val Pro Ala Ile Phe Thr Asp Thr Ser Ser Pro Gln Arg Leu Ala Glu 260 265 270		
Val Leu Ala Ser Asn Ala Gly Ile Asp Val Gln Val Val Ser Ile Phe 275 280 285		
Thr Glu Ser Leu Thr Asp Ala Asp Gly Glu Ala Pro Thr Tyr Ile Ser 290 295 300		
Met Gln Lys Ile Asn Ala Glu Arg Ile Ala Ser Thr Leu Ser 305 310 315		

<210> 2729

<211> 1401

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1378)

<223> RXA02444

<400> 2729

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cagtccccgt tttactaaat gttttactaa aaggagaacc atg aaa aac tcc aag 115
                                         Met Lys Asn Ser Lys
                                         1           5

cta ctt ctt att gct gcg gta tcc acc gca tct atc ctg ctg gca agc 163
Leu Leu Leu Ile Ala Ala Val Ser Thr Ala Ser Ile Leu Leu Ala Ser
              10              15              20

tgt ggc act gac agc tct gca gat act gca act gcg tct agc tct gca 211
Cys Gly Thr Asp Ser Ser Ala Asp Thr Ala Thr Ala Ser Ser Ser Ala
              25              30              35

aca gca agc tcc gag gca cac gat cat gat ggc cac gaa gcc gaa ggc 259
Thr Ala Ser Ser Glu Ala His Asp His Asp Gly His Glu Ala Glu Gly
              40              45              50

agc agc act gcc gtt gag gtg tcc tcc ccg cag gcc cgc atc gtc acc 307
Ser Ser Thr Ala Val Glu Val Ser Ser Pro Gln Ala Arg Ile Val Thr
              55              60              65

acc tac gac ggt ggc atc att acc ctc gac gcc aac act ctg gaa atc 355
Thr Tyr Asp Gly Gly Ile Ile Thr Leu Asp Ala Asn Thr Leu Glu Ile
              70              75              80              85

ctg gaa gac acc gaa cta gca ggt ttt aac cgc ctc aac agt gca gga 403
Leu Glu Asp Thr Glu Leu Ala Gly Phe Asn Arg Leu Asn Ser Ala Gly
              90              95              100

gac gga cgc cac gta ttt gtc tcc aca ggt ggc ggc ttc cag ctc ttt 451
Asp Gly Arg His Val Phe Val Ser Thr Gly Gly Gly Phe Gln Leu Phe
              105              110              115

gat acc ggc gca tgg acc gaa cca cac ggc gat cac acc cac agc tac 499
Asp Thr Gly Ala Trp Thr Glu Pro His Gly Asp His Thr His Ser Tyr
              120              125              130

acc gcc acc cca gaa ctc acc gac atc acc tac tcc acc gat aag cct 547
Thr Ala Thr Pro Glu Leu Thr Asp Ile Thr Tyr Ser Thr Asp Lys Pro
              135              140              145

ggc cat gta gtg aac cac gcc ggc aag acc gtg ctg ttc ggc gat ggt 595
Gly His Val Val Asn His Ala Gly Lys Thr Val Leu Phe Gly Asp Gly
150              155              160              165

gac ggc aaa atc cag atc ttc gac acc gct tcc ctc ctc aag ggc gat 643
Asp Gly Lys Ile Gln Ile Phe Asp Thr Ala Ser Leu Leu Lys Gly Asp
              170              175              180

gaa gta gaa cct gag atc aaa aac gcc ctc aaa gcc cac cac ggc gtg 691
Glu Val Glu Pro Glu Ile Lys Asn Ala Leu Lys Ala His His Gly Val
              185              190              195

gca gta gtc ctc gaa aac ggc gac ctg ctg cac act ttg ggc gat gag 739
Ala Val Val Leu Glu Asn Gly Asp Leu Leu His Thr Leu Gly Asp Glu
              200              205              210

gat tcc cgc aac ggc gcc gtc gta ttc aac gca gcc ggt gaa gaa atc 787
Asp Ser Arg Asn Gly Ala Val Val Phe Asn Ala Ala Gly Glu Glu Ile

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215	220	225	
gcc cgc aac gaa cag tgc ccc ggc gtt cac ggt gaa agc gca gca ctc Ala Arg Asn Glu Gln Cys Pro Gly Val His Gly Glu Ser Ala Ala Leu 230 235 240 245			835
ggt gac gcc atc gca gtt ggc tgt gaa gac ggt gta ctg atc tac aag Gly Asp Ala Ile Ala Val Gly Cys Glu Asp Gly Val Leu Ile Tyr Lys 250 255 260			883
gac ggc gag ttc acc aag gtc cag gca cct gat tcc tac ggt cgc atc Asp Gly Glu Phe Thr Lys Val Gln Ala Pro Asp Ser Tyr Gly Arg Ile 265 270 275			931
ggc aac caa tca ggc agc gac gtc tct cct gtc gtc ctc ggc gat tac Gly Asn Gln Ser Gly Ser Asp Val Ser Pro Val Val Leu Gly Asp Tyr 280 285 290			979
aag gta gat aaa gac gcc gac ttg gag cgc cca gag cgc gtt tcc ctc Lys Val Asp Lys Asp Ala Asp Leu Glu Arg Pro Glu Arg Val Ser Leu 295 300 305			1027
acc aac acc gag acc ggc gag ctc acc ctc gtt gac ctc ggc acc tcc Thr Asn Thr Glu Thr Gly Glu Leu Thr Leu Val Asp Leu Gly Thr Ser 310 315 320 325			1075
tac tcc ttc cgc tca ctt ggc cgt ggc cct gca ggc gaa gca gta gtt Tyr Ser Phe Arg Ser Leu Gly Arg Gly Pro Ala Gly Glu Ala Val Val 330 335 340			1123
cta ggc acc gac ggc gca ctc cac atc atc gat gcc aac acc ggc gcc Leu Gly Thr Asp Gly Ala Leu His Ile Ile Asp Ala Asn Thr Gly Ala 345 350 355			1171
atc acc aac acc tac ccc gtc atc gat gcc tgg acc gaa cca gaa gta Ile Thr Asn Thr Tyr Pro Val Ile Asp Ala Trp Thr Glu Pro Glu Val 360 365 370			1219
tgg caa gaa gca cgc cca acc ctg ttc atc aac aag gac cgc gca tac Trp Gln Glu Ala Arg Pro Thr Leu Phe Ile Asn Lys Asp Arg Ala Tyr 375 380 385			1267
gtc tcc gac cca tca aac aac gaa ctc cat gtt gtt gac ctg gcc aac Val Ser Asp Pro Ser Asn Asn Glu Leu His Val Val Asp Leu Ala Asn 390 395 400 405			1315
ggc aac atc ctt gcc agc gcc acc ctg cca gga acc ccc aac gag ctc Gly Asn Ile Leu Ala Ser Ala Thr Leu Pro Gly Thr Pro Asn Glu Leu 410 415 420			1363
acc gga gtg agc ggc taaaaagaaa ttgcttttcg acg Thr Gly Val Ser Gly 425			1401

<210> 2730

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 2730

Met Lys Asn Ser Lys Leu Leu Leu Ile Ala Ala Val Ser Thr Ala Ser
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 Ile Leu Leu Ala Ser Cys Gly Thr Asp Ser Ser Ala Asp Thr Ala Thr
 20 25 30
 Ala Ser Ser Ser Ala Thr Ala Ser Ser Glu Ala His Asp His Asp Gly
 35 40 45
 His Glu Ala Glu Gly Ser Ser Thr Ala Val Glu Val Ser Ser Pro Gln
 50 55 60
 Ala Arg Ile Val Thr Thr Tyr Asp Gly Gly Ile Ile Thr Leu Asp Ala
 65 70 75 80
 Asn Thr Leu Glu Ile Leu Glu Asp Thr Glu Leu Ala Gly Phe Asn Arg
 85 90 95
 Leu Asn Ser Ala Gly Asp Gly Arg His Val Phe Val Ser Thr Gly Gly
 100 105 110
 Gly Phe Gln Leu Phe Asp Thr Gly Ala Trp Thr Glu Pro His Gly Asp
 115 120 125
 His Thr His Ser Tyr Thr Ala Thr Pro Glu Leu Thr Asp Ile Thr Tyr
 130 135 140
 Ser Thr Asp Lys Pro Gly His Val Val Asn His Ala Gly Lys Thr Val
 145 150 155 160
 Leu Phe Gly Asp Gly Asp Gly Lys Ile Gln Ile Phe Asp Thr Ala Ser
 165 170 175
 Leu Leu Lys Gly Asp Glu Val Glu Pro Glu Ile Lys Asn Ala Leu Lys
 180 185 190
 Ala His His Gly Val Ala Val Val Leu Glu Asn Gly Asp Leu Leu His
 195 200 205
 Thr Leu Gly Asp Glu Asp Ser Arg Asn Gly Ala Val Val Phe Asn Ala
 210 215 220
 Ala Gly Glu Glu Ile Ala Arg Asn Glu Gln Cys Pro Gly Val His Gly
 225 230 235 240
 Glu Ser Ala Ala Leu Gly Asp Ala Ile Ala Val Gly Cys Glu Asp Gly
 245 250 255
 Val Leu Ile Tyr Lys Asp Gly Glu Phe Thr Lys Val Gln Ala Pro Asp
 260 265 270
 Ser Tyr Gly Arg Ile Gly Asn Gln Ser Gly Ser Asp Val Ser Pro Val
 275 280 285
 Val Leu Gly Asp Tyr Lys Val Asp Lys Asp Ala Asp Leu Glu Arg Pro
 290 295 300
 Glu Arg Val Ser Leu Thr Asn Thr Glu Thr Gly Glu Leu Thr Leu Val
 305 310 315 320
 Asp Leu Gly Thr Ser Tyr Ser Phe Arg Ser Leu Gly Arg Gly Pro Ala

325 330 335
 Gly Glu Ala Val Val Leu Gly Thr Asp Gly Ala Leu His Ile Ile Asp
 340 345 350
 Ala Asn Thr Gly Ala Ile Thr Asn Thr Tyr Pro Val Ile Asp Ala Trp
 355 360 365
 Thr Glu Pro Glu Val Trp Gln Glu Ala Arg Pro Thr Leu Phe Ile Asn
 370 375 380
 Lys Asp Arg Ala Tyr Val Ser Asp Pro Ser Asn Asn Glu Leu His Val
 385 390 395 400
 Val Asp Leu Ala Asn Gly Asn Ile Leu Ala Ser Ala Thr Leu Pro Gly
 405 410 415
 Thr Pro Asn Glu Leu Thr Gly Val Ser Gly
 420 425

<210> 2731
 <211> 303
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(280)
 <223> RXA02452

<400> 2731
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 taggggtggaa tgcagaaata tttcctacgg aaggtccggtt atg acg cct gca ggt 115
 Met Thr Pro Ala Gly
 1 5
 cca gca caa tta ctc att gtt gct ctt gta gta att gtc ctc ttt ggt 163
 Pro Ala Gln Leu Leu Ile Val Ala Leu Val Val Ile Val Leu Phe Gly
 10 15 20
 tcc aat aag ttg cct gat gtt gct cgg tcc gtt ggc cgt tcg atg cgc 211
 Ser Asn Lys Leu Pro Asp Val Ala Arg Ser Val Gly Arg Ser Met Arg
 25 30 35
 att ttc aaa tct gag atc aaa gag atg aac aag gat cag atc gaa agc 259
 Ile Phe Lys Ser Glu Ile Lys Glu Met Asn Lys Asp Gln Ile Glu Ser
 40 45 50
 tcc gat cag acc ttg aag aac taagggttcct cgcatctaaa aac 303
 Ser Asp Gln Thr Leu Lys Asn
 55 60

<210> 2732
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2732

Met Thr Pro Ala Gly Pro Ala Gln Leu Leu Ile Val Ala Leu Val Val
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Ile Val Leu Phe Gly Ser Asn Lys Leu Pro Asp Val Ala Arg Ser Val
 20 25 30

Gly Arg Ser Met Arg Ile Phe Lys Ser Glu Ile Lys Glu Met Asn Lys
 35 40 45

Asp Gln Ile Glu Ser Ser Asp Gln Thr Leu Lys Asn
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<210> 2733

<211> 858

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(835)

<223> RXA02459

<400> 2733

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aaaactttcc ctggttttga aaatgtttgg gaggagatgg ttg gct aga cgc agc 115
 Leu Ala Arg Arg Ser
 1 5

tat gac gaa tcc gat gtt cgt gtt cgc cca ggt aaa ggt acc cgc cct 163
 Tyr Asp Glu Ser Asp Val Arg Val Arg Pro Gly Lys Gly Thr Arg Pro
 10 15 20

cgt acg aag gat cgg cca tcg cat gag aat gct cta gtg ggc atg gtt 211
 Arg Thr Lys Asp Arg Pro Ser His Glu Asn Ala Leu Val Gly Met Val
 25 30 35

gtg acg aag gat cgt ggt cgt tgg ggt gtt gtt ctc gat ggt cgt caa 259
 Val Thr Lys Asp Arg Gly Arg Trp Gly Val Val Leu Asp Gly Arg Gln
 40 45 50

gat gcc att gtg acg atg cgt gcc cgt gag ttg ggg cgt acg gct atc 307
 Asp Ala Ile Val Thr Met Arg Ala Arg Glu Leu Gly Arg Thr Ala Ile
 55 60 65

gaa gtg ggt gat cgt gtc gga gtt gtc ggc gat acg tct ggc cgt ccg 355
 Glu Val Gly Asp Arg Val Gly Val Val Gly Asp Thr Ser Gly Arg Pro
 70 75 80 85

ggc tcg ttg gct cga att gtc cgc ctt gag gag cgc acg agt gtg ttg 403
 Gly Ser Leu Ala Arg Ile Val Arg Leu Glu Arg Thr Ser Val Leu
 90 95 100

cgt cgt acg gct gat gac acg gac ccg ttt gag cgg att gtg gtg gct 451
 Arg Arg Thr Ala Asp Asp Thr Asp Pro Phe Glu Arg Ile Val Val Ala
 105 110 115

aat gcg gat cag ttg ttg att gtt tct gct gtc gcc gat ccg ccg cct 499
 Asn Ala Asp Gln Leu Leu Ile Val Ser Ala Val Ala Asp Pro Pro Pro
 120 125 130

cgg gcg ggt ttt gtg gag cgt gct cta att gct gcg ttt gtt ggt aat 547
 Arg Ala Gly Phe Val Glu Arg Ala Leu Ile Ala Ala Phe Val Gly Asn
 135 140 145

ttg cag ccg gtg ttg tgt ttg acg aag tct gat ttg gcg gat cct gcg 595
 Leu Gln Pro Val Leu Cys Leu Thr Lys Ser Asp Leu Ala Asp Pro Ala
 150 155 160 165

gag ttc gct gcg gag ttt gag gct ttg gaa gtg ccg gtt gtt gtt tgt 643
 Glu Phe Ala Ala Glu Phe Glu Ala Leu Glu Val Pro Val Val Val Cys
 170 175 180

ggg gtt gat gat cct ctt gat cct gtt ttg gag gtc gtg gaa ggc cat 691
 Gly Val Asp Asp Pro Leu Asp Pro Val Leu Glu Val Val Glu Gly His
 185 190 195

att acg gcg ctt att ggg caa tct ggt gtg ggt aag tcg acg ttg gtt 739
 Ile Thr Ala Leu Ile Gly Gln Ser Gly Val Gly Lys Ser Thr Leu Val
 200 205 210

aat cgt ttg gtg ccg gaa tgc cga tcg tta aac tgg tgt cgt gtc ggg 787
 Asn Arg Leu Val Pro Glu Cys Arg Ser Leu Asn Trp Cys Arg Val Gly
 215 220 225

ggg tgg caa ggg tcg gca tac gtc gac gca gtc ggt cgc tct tgc cat 835
 Gly Trp Gln Gly Ser Ala Tyr Val Asp Ala Val Gly Arg Ser Cys His
 230 235 240 245

tgataatggt tggattatcg aaa 858

<210> 2734

<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 2734

Leu Ala Arg Arg Ser Tyr Asp Glu Ser Asp Val Arg Val Arg Pro Gly
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 20 25 30

Leu Val Gly Met Val Val Thr Lys Asp Arg Gly Arg Trp Gly Val Val
 35 40 45

Leu Asp Gly Arg Gln Asp Ala Ile Val Thr Met Arg Ala Arg Glu Leu
 50 55 60

Gly Arg Thr Ala Ile Glu Val Gly Asp Arg Val Gly Val Val Gly Asp
 65 70 75 80

Thr Ser Gly Arg Pro Gly Ser Leu Ala Arg Ile Val Arg Leu Glu Glu
 85 90 95

Arg Thr Ser Val Leu Arg Arg Thr Ala Asp Asp Thr Asp Pro Phe Glu
 100 105 110

Arg Ile Val Val Ala Asn Ala Asp Gln Leu Leu Ile Val Ser Ala Val
 115 120 125

Ala Asp Pro Pro Pro Arg Ala Gly Phe Val Glu Arg Ala Leu Ile Ala
 130 135 140

Ala Phe Val Gly Asn Leu Gln Pro Val Leu Cys Leu Thr Lys Ser Asp
 145 150 155 160

Leu Ala Asp Pro Ala Glu Phe Ala Ala Glu Phe Glu Ala Leu Glu Val
 165 170 175

Pro Val Val Val Cys Gly Val Asp Asp Pro Leu Asp Pro Val Leu Glu
 180 185 190

Val Val Glu Gly His Ile Thr Ala Leu Ile Gly Gln Ser Gly Val Gly
 195 200 205

Lys Ser Thr Leu Val Asn Arg Leu Val Pro Glu Cys Arg Ser Leu Asn
 210 215 220

Trp Cys Arg Val Gly Gly Trp Gln Gly Ser Ala Tyr Val Asp Ala Val
 225 230 235 240

Gly Arg Ser Cys His
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<210> 2735

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA02461

<400> 2735

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acgactatta tgtcacgaag aaaccaaaga aagggaata atg cgc gga cta att 115
 Met Arg Gly Leu Ile
 1 5

gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc 163
 Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg
 10 15 20

tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg 211
 Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
 25 30 35

atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa 259
 Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
 40 45 50

ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt 307
 Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
 55 60 65

ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc 355
 Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala

70	75	80	85	
atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc				403
Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu				
	90	95	100	
aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag				451
Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln				
	105	110	115	
caa ttt gac cgt gca gtc gtc gaa atc gtc gga ctg ttc ggg cta gaa				499
Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu				
	120	125	130	
gga gaa ttc taatcttgcg cgtctacatc cca				531
Gly Glu Phe				
135				

<210> 2736

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 2736

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Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala				
	35	40	45	
Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu				
	50	55	60	
Leu Ser Gly Glu Leu Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln				
	65	70	75	80
Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val				
	85	90	95	
Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val				
	100	105	110	
Gly Val Tyr Tyr Gln Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly				
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Leu Phe Gly Leu Glu Gly Glu Phe				
	130	135		

<210> 2737

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA02467

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aatagggtca ttccaatata acgattcttt taggagagct atg gat atc aag atc 115
Met Asp Ile Lys Ile
1 5
gga ttt gcc gat act gcc cgt gaa ctg gtc att tct tct gct ttg cag 163
Gly Phe Ala Asp Thr Ala Arg Glu Leu Val Ile Ser Ser Ala Leu Gln
10 15 20
cag gat gag gcc gct gcg aag gtg tcg gag gct ttg gct aat gat tct 211
Gln Asp Glu Ala Ala Ala Lys Val Ser Glu Ala Leu Ala Asn Asp Ser
25 30 35
ggc gtt tta gat ttg agc gat gaa aag ggt cgc cgt tac att att cgt 259
Gly Val Leu Asp Leu Ser Asp Glu Lys Gly Arg Arg Tyr Ile Ile Arg
40 45 50
aat agc cga atc gct tat gtt gag gtc ggc acg agt gct cct cgt act 307
Asn Ser Arg Ile Ala Tyr Val Glu Val Gly Thr Ser Ala Pro Arg Thr
55 60 65
gtc ggc ttc gct ggc gca taggggcttt tagacacgtg tcg 348
Val Gly Phe Ala Gly Ala
70 75

<210> 2738

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 2738

Met Asp Ile Lys Ile Gly Phe Ala Asp Thr Ala Arg Glu Leu Val Ile
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Ser Ser Ala Leu Gln Gln Asp Glu Ala Ala Ala Lys Val Ser Glu Ala
20 25 30
Leu Ala Asn Asp Ser Gly Val Leu Asp Leu Ser Asp Glu Lys Gly Arg
35 40 45
Arg Tyr Ile Ile Arg Asn Ser Arg Ile Ala Tyr Val Glu Val Gly Thr
50 55 60
Ser Ala Pro Arg Thr Val Gly Phe Ala Gly Ala
65 70 75

<210> 2739

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXA02472

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				Met Ser Phe Val Asn	5	
atc acg gct ctt acg ttc cct gca ggg gct gaa aaa gaa atc gaa caa	163					
Ile Thr Ala Leu Thr Phe Pro Ala Gly Ala Glu Lys Glu Ile Glu Gln	20					
cgc ttc gcg gct cgt aag aag gct gta gat acg gcc aaa gga ttc caa	211					
Arg Phe Ala Ala Arg Lys Lys Ala Val Asp Thr Ala Lys Gly Phe Gln	35					
gaa ttt gag ttg ttg cgt cca caa ttt ggt gag gat cgc tac ttc gta	259					
Glu Phe Glu Leu Leu Arg Pro Gln Phe Gly Glu Asp Arg Tyr Phe Val	50					
gtt act cgt tgg gat tcc cgc gaa gac tat caa gca tgg tcg gat gcc	307					
Val Thr Arg Trp Asp Ser Arg Glu Asp Tyr Gln Ala Trp Ser Asp Ala	65					
cgc cct gcc ggt aac cat gct gat gat gaa caa cgt ggc atg agc gtg	355					
Arg Pro Ala Gly Asn His Ala Asp Asp Glu Gln Arg Gly Met Ser Val	85					
gaa gtt ctt ggt ttc gat gtg gtt cct ttg gaa ggc taaaagtcct	401					
Glu Val Leu Gly Phe Asp Val Val Pro Leu Glu Gly	95					
tggcgtggca tag	414					

Gly

<210> 2741

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> RXA02473

<400> 2741

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                                         Met Val Ala Glu Tyr
                                         1                               5

cct gac gga tcc tcg gaa ata ttc ccg gta acg tta aat tta att ccg 163
Pro Asp Gly Ser Ser Glu Ile Phe Pro Val Thr Leu Asn Leu Ile Pro
                        10                               15                               20

gaa gat acc ctc gtt tat gac gcc gtc tac aaa ttc aaa agc atc cga 211
Glu Asp Thr Leu Val Tyr Asp Ala Val Tyr Lys Phe Lys Ser Ile Arg
                        25                               30                               35

act ggt tcc gaa gat caa ata acc cca ttt gta tca aac caa cct gat 259
Thr Gly Ser Glu Asp Gln Ile Thr Pro Phe Val Ser Asn Gln Pro Asp
                        40                               45                               50

gtg cct ttc cct gca gga aca tcg ttc aca tta act gga tat tat gaa 307
Val Pro Phe Pro Ala Gly Thr Ser Phe Thr Leu Thr Gly Tyr Tyr Glu
                        55                               60                               65

att gat cag ctg aga agt gca gga tgg aaa ttt gag ctt aat cct gta 355
Ile Asp Gln Leu Arg Ser Ala Gly Trp Lys Phe Glu Leu Asn Pro Val
                        70                               75                               80                               85

aca ggt gaa ctt tca gtc aca gtt cct atc tct gta att tac cct gat 403
Thr Gly Glu Leu Ser Val Thr Val Pro Ile Ser Val Ile Tyr Pro Asp
                        90                               95                               100

ggg tct cgt gat aac aca atc gcg acc atg gaa tcc gta ggc cct gat 451
Gly Ser Arg Asp Asn Thr Ile Ala Thr Met Glu Ser Val Gly Pro Asp
                        105                               110                               115

gat tct gag ctt ttc aaa cca gac ttt gat tta atc cca ata aaa tca 499
Asp Ser Glu Leu Phe Lys Pro Asp Phe Asp Leu Ile Pro Ile Lys Ser
                        120                               125                               130

ggt gac tat ata gag ata ggt gta ctc gca cca ggg ctt cct gct ggt 547
Gly Asp Tyr Ile Glu Ile Gly Val Leu Ala Pro Gly Leu Pro Ala Gly
                        135                               140                               145

acg gaa ttc cat ctc gat tac tac gca ctt ccg gat cga ttc ttt gac 595
Thr Glu Phe His Leu Asp Tyr Tyr Ala Leu Pro Asp Arg Phe Phe Asp
                        150                               155                               160                               165

tta ggc ggt tct aca agc ctt tca ggc aac ggt aag ttc tct ctt gga 643
Leu Gly Gly Ser Thr Ser Leu Ser Gly Asn Gly Lys Phe Ser Leu Gly

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170	175	180	
gtt cca ctt acc tgg aat gat gat	ctc cag ctc ccg atc tcg att act	691	
Val Pro Leu Thr Trp Asn Asp Asp	Leu Gln Leu Pro Ile Ser Ile Thr		
185	190 195		
ttt cct gac gga agc cac aca gtt gag aat ttg cat gtt gac gta acc	739		
Phe Pro Asp Gly Ser His Thr Val Glu Asn Leu His Val Asp Val Thr			
200	205 210		
ccc gca aac ttt gct ggc aac ccc att gac gag cct aag gac gat gac	787		
Pro Ala Asn Phe Ala Gly Asn Pro Ile Asp Glu Pro Lys Asp Asp Asp			
215	220 225		
aag gat cat cca caa ccg gct cct aaa cca agt ggc agc tca ttt ggt	835		
Lys Asp His Pro Gln Pro Ala Pro Lys Pro Ser Gly Ser Ser Phe Gly			
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Ser Ser			

<210> 2742

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 2742

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35 40 45	
Ser Asn Gln Pro Asp Val Pro Phe Pro Ala Gly Thr Ser Phe Thr Leu	
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Thr Gly Tyr Tyr Glu Ile Asp Gln Leu Arg Ser Ala Gly Trp Lys Phe	
65 70 75 80	
Glu Leu Asn Pro Val Thr Gly Glu Leu Ser Val Thr Val Pro Ile Ser	
85 90 95	
Val Ile Tyr Pro Asp Gly Ser Arg Asp Asn Thr Ile Ala Thr Met Glu	
100 105 110	
Ser Val Gly Pro Asp Asp Ser Glu Leu Phe Lys Pro Asp Phe Asp Leu	
115 120 125	
Ile Pro Ile Lys Ser Gly Asp Tyr Ile Glu Ile Gly Val Leu Ala Pro	
130 135 140	
Gly Leu Pro Ala Gly Thr Glu Phe His Leu Asp Tyr Tyr Ala Leu Pro	
145 150 155 160	
Asp Arg Phe Phe Asp Leu Gly Gly Ser Thr Ser Leu Ser Gly Asn Gly	
165 170 175	

Lys Phe Ser Leu Gly Val Pro Leu Thr Trp Asn Asp Asp Leu Gln Leu
 180 185 190
 Pro Ile Ser Ile Thr Phe Pro Asp Gly Ser His Thr Val Glu Asn Leu
 195 200 205
 His Val Asp Val Thr Pro Ala Asn Phe Ala Gly Asn Pro Ile Asp Glu
 210 215 220
 Pro Lys Asp Asp Asp Lys Asp His Pro Gln Pro Ala Pro Lys Pro Ser
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 Gly Ser Ser Phe Gly Ser Ser
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<210> 2743

<211> 1278

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1255)

<223> RXA02475

<400> 2743

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 Met Leu Gly Leu Ser 5
 cgt cgt aag ttt gcc atg ctc gct gcc tta act gcg gga atc gtt ggc 163
 Arg Arg Lys Phe Ala Met Leu Ala Ala Leu Thr Ala Gly Ile Val Gly 20
 10 15
 gtt gtt gcc act ggt tgt agt acg ccc gca gaa cct gaa acg atc gat 211
 Val Val Ala Thr Gly Cys Ser Thr Pro Ala Glu Pro Glu Thr Ile Asp 35
 25 30
 aat ccg gtg ttc att ggt atc tcc atc gat cca att aaa aac cta agt 259
 Asn Pro Val Phe Ile Gly Ile Ser Ile Asp Pro Ile Lys Asn Leu Ser 50
 40 45
 ccg aat cac gct gca aac ctc ttc gct tta tct gca gat ggc tcg gga 307
 Pro Asn His Ala Ala Asn Leu Phe Ala Leu Ser Ala Asp Gly Ser Gly 65
 55 60
 gga att ttc caa gaa ctc gct ccc aca tac ttt ccg tcg atc cat cga 355
 Gly Ile Phe Gln Glu Leu Ala Pro Thr Tyr Phe Pro Ser Ile His Arg 85
 70 75 80
 tta gga aac gga ttc atc gca ccc gat aga gat tct ttg gta gtt gtc 403
 Leu Gly Asn Gly Phe Ile Ala Pro Asp Arg Asp Ser Leu Val Val Val 100
 90 95
 gac gct tct cta aag gaa gtt tat cga cac gaa gtg gcc agg ctt ggt 451
 Asp Ala Ser Leu Lys Glu Val Tyr Arg His Glu Val Ala Arg Leu Gly 115
 105 110

gtt gga atg caa act caa tca gct agg tct cca ctg cat aaa tca gtt	499
Val Gly Met Gln Thr Gln Ser Ala Arg Ser Pro Leu His Lys Ser Val	
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Ala Phe Ser Phe Asn Glu Gly Thr Ala Glu Ala Pro Tyr Arg His Arg	
135 140 145	
atc gtc tcc gca act gag aaa aca tca gct tcc gca atg aca gat cag	595
Ile Val Ser Ala Thr Glu Lys Thr Ser Ala Ser Ala Met Thr Asp Gln	
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Arg His Phe Ala Leu Thr Ala Cys Asp Asp Gly Ser Thr Arg Trp Val	
170 175 180	
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Glu Tyr Ser Pro Asp Arg Gly Met Glu Asp Pro Met Gly Pro Gly Ser	
185 190 195	
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Ala Arg Ile Val Thr Leu Gln Ala Asp Gly Glu Leu Ser Glu Ile Asp	
200 205 210	
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Val Glu Trp Asn Phe Pro Asp Arg Pro Ser Ala Pro Ile Ile Leu Ser	
215 220 225	
tgc gaa gat cca agc gct tat ata gtt tca gaa gaa gac atc atc tat	835
Cys Glu Asp Pro Ser Ala Tyr Ile Val Ser Glu Glu Asp Ile Ile Tyr	
230 235 240 245	
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Val Lys Asp Glu Val Ser Pro Ala Glu Ser Ile Gly Lys Leu Pro Ala	
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Tyr Glu Ile Pro Asp Arg Ala Arg Phe Asp Thr Val Ser Gly Glu Asp	
265 270 275	
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Tyr Phe Ala Phe Thr Ser Thr Gly Met Leu Thr Arg Ile Asn Ile Pro	
280 285 290	
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Gln Ala Lys Ile Val Tyr Ala Gln Ser Ile Asp Leu Tyr Gly Lys His	
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Pro Val Ser Ile Thr Phe Asp Ser Asp Arg Ala Tyr Val Val Thr Ser	
310 315 320 325	
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Gly Asp Ser Gly Glu Ser Leu Leu Glu Ile Asp Leu Asn Asp Pro Thr	
330 335 340	
tgc act tca gat cag ctc tcg ctc act ggt ttc aac aaa tta ctc aca	1171
Cys Thr Ser Asp Gln Leu Ser Leu Thr Gly Phe Asn Lys Leu Leu Thr	
345 350 355	

Glu Asp Ile Ile Tyr Val Lys Asp Glu Val Ser Pro Ala Glu Ser Ile
 245 250 255

Gly Lys Leu Pro Ala Tyr Glu Ile Pro Asp Arg Ala Arg Phe Asp Thr
 260 265 270

Val Ser Gly Glu Asp Tyr Phe Ala Phe Thr Ser Thr Gly Met Leu Thr
 275 280 285

Arg Ile Asn Ile Pro Gln Ala Lys Ile Val Tyr Ala Gln Ser Ile Asp
 290 295 300

Leu Tyr Gly Lys His Pro Val Ser Ile Thr Phe Asp Ser Asp Arg Ala
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Tyr Val Val Thr Ser Gly Asp Ser Gly Glu Ser Leu Leu Glu Ile Asp
 325 330 335

Leu Asn Asp Pro Thr Cys Thr Ser Asp Gln Leu Ser Leu Thr Gly Phe
 340 345 350

Asn Lys Leu Leu Thr Ala Arg Lys Pro Lys Pro Glu Pro Ser Ile Ile
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Ile Glu Thr Ile Leu Pro Ile Asp Pro Asn Tyr Ser Leu Gly Cys Lys
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Ser
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<210> 2745

<211> 1345

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1336)

<223> RXA02478

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 Met Arg Thr Ser Leu
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 10 15 20
 Ile Ala Arg Gly Leu Tyr Arg Ile Pro Ala Leu Val Trp Asp Gln Gly

ctt tta acg ctt ttc gac gcc cgc ctc agt gtt gac gac ctc ccc gca 211
 25 30 35
 Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val Asp Asp Leu Pro Ala

ccc atc gac gtg gtg tca gcg cga tcc tca gac ggc atc acc tgg acc 259
 40 45 50
 Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp Gly Ile Thr Trp Thr

acc cca gaa cca gca atc gtc gaa act gaa cac cgc ggt gtg ggc gat	307
Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His Arg Gly Val Gly Asp	
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Val Cys Leu Val Thr Gly Asp Leu Cys Phe His Gly Leu Ser Asn Leu	
70 75 80 85	
gca gga ttt ttt gag gat ccc acc gac ctt gaa ccc cgg ctg gcg cgc	403
Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu Pro Arg Leu Ala Arg	
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Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met Ala His Tyr Phe Ala	
105 110 115	
gat gtt gat gcc gcg ttc gcc tcg tcg ggg acg gga ctt gtc ctg gcg	499
Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr Gly Leu Val Leu Ala	
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gat ggg cgg tgg att cag agt ttt gtg gtg cgg cgc ggg cgc gag att	547
Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg Arg Gly Arg Glu Ile	
135 140 145	
tcg ctt cgg att ctg cgc agc gat ggc cac atc acc gat att gcc ggc	595
Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile Thr Asp Ile Ala Gly	
150 155 160 165	
ggt aac gaa tcc gcg atg acg cag ctg ccg agc ggt cgg att gtg ctg	643
Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser Gly Arg Ile Val Leu	
170 175 180	
cat tcc agg ggg gtg gga cac cgt ctg agc agt gtg tcc gat gat ttc	691
His Ser Arg Gly Val Gly His Arg Leu Ser Ser Val Ser Asp Asp Phe	
185 190 195	
ggg gag aca ttc act ccg ctg gag cct gtg cct gaa cta atc gac ccc	739
Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro Glu Leu Ile Asp Pro	
200 205 210	
ggc tgc aac ggc cac gtg ttc tac tgg aaa gcg gct gga atg ctc gcc	787
Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala Ala Gly Met Leu Ala	
215 220 225	
gca acg cac ctg gcg gac cct gat ctg cga cgc cac ttg gtg gtt gat	835
Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg His Leu Val Val Asp	
230 235 240 245	
tta tcc agc gac gaa gga gcg acc tgg gcg cat cgc atc acc atc gag	883
Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His Arg Ile Thr Ile Glu	
250 255 260	
cgc gaa gaa gcc gcc tat tca acc gct gcg gaa atg ccc aac gga gat	931
Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu Met Pro Asn Gly Asp	
265 270 275	
gtt gcc gtg gtg tgg gaa gca gag gga acg cgc gcg ata aaa tgc acg	979
Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg Ala Ile Lys Cys Thr	
280 285 290	
gtg atc agc gta aat gat att tcg ctg cgg atc gat gag ccc att tcc	1027

Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile Asp Glu Pro Ile Ser
 295 300 305

gat gcc ata tcc ctc cgc cat gtg gtg atc aac gat gac cat gac ggc 1075
 Asp Ala Ile Ser Leu Arg His Val Val Ile Asn Asp Asp His Asp Gly
 310 315 320 325

atc gaa gtc gca ctg cct gac gca tcg caa tgg ggt gaa ggt gta ttc 1123
 Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp Gly Glu Gly Val Phe
 330 335 340

aaa att gtg tcc aat cca gac gcg agc acc caa aaa atc cgc act cga 1171
 Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln Lys Ile Arg Thr Arg
 345 350 355

ggc aag ccc gcg cga cag acc ctg gaa att ggg gat gaa ttg gtt ttt 1219
 Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly Asp Glu Leu Val Phe
 360 365 370

gat atc cgc aag ggt gga gaa gtg gct tac ggc gtc acg gtt cct tat 1267
 Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly Val Thr Val Pro Tyr
 375 380 385

gat ggt cgc tcg ttg ggg aag tta aac agg att ttg gag tgg ggc tgt 1315
 Asp Gly Arg Ser Leu Gly Lys Leu Asn Arg Ile Leu Glu Trp Gly Cys
 390 395 400 405

aga ggc cga ttt gcg gtc ctt taattgcgg 1345
 Arg Gly Arg Phe Ala Val Leu
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<210> 2746

<211> 412

<212> PRT

<213> Corynebacterium glutamicum

<400> 2746

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Val Trp Asp Gln Gly Leu Leu Thr Leu Phe Asp Ala Arg Leu Ser Val
 20 25 30

Asp Asp Leu Pro Ala Pro Ile Asp Val Val Ser Ala Arg Ser Ser Asp
 35 40 45

Gly Ile Thr Trp Thr Thr Pro Glu Pro Ala Ile Val Glu Thr Glu His
 50 55 60

Arg Gly Val Gly Asp Val Cys Leu Val Thr Gly Asp Leu Cys Phe His
 65 70 75 80

Gly Leu Ser Asn Leu Ala Gly Phe Phe Glu Asp Pro Thr Asp Leu Glu
 85 90 95

Pro Arg Leu Ala Arg Arg Asp Val Ser Gly Trp Thr Ser Ile Ser Met
 100 105 110

Ala His Tyr Phe Ala Asp Val Asp Ala Ala Phe Ala Ser Ser Gly Thr
 115 120 125

Gly Leu Val Leu Ala Asp Gly Arg Trp Ile Gln Ser Phe Val Val Arg
130 135 140

Arg Gly Arg Glu Ile Ser Leu Arg Ile Leu Arg Ser Asp Gly His Ile
145 150 155 160

Thr Asp Ile Ala Gly Gly Asn Glu Ser Ala Met Thr Gln Leu Pro Ser
165 170 175

Gly Arg Ile Val Leu His Ser Arg Gly Val Gly His Arg Leu Ser Ser
180 185 190

Val Ser Asp Asp Phe Gly Glu Thr Phe Thr Pro Leu Glu Pro Val Pro
195 200 205

Glu Leu Ile Asp Pro Gly Cys Asn Gly His Val Phe Tyr Trp Lys Ala
210 215 220

Ala Gly Met Leu Ala Ala Thr His Leu Ala Asp Pro Asp Leu Arg Arg
225 230 235 240

His Leu Val Val Asp Leu Ser Ser Asp Glu Gly Ala Thr Trp Ala His
245 250 255

Arg Ile Thr Ile Glu Arg Glu Glu Ala Ala Tyr Ser Thr Ala Ala Glu
260 265 270

Met Pro Asn Gly Asp Val Ala Val Val Trp Glu Ala Glu Gly Thr Arg
275 280 285

Ala Ile Lys Cys Thr Val Ile Ser Val Asn Asp Ile Ser Leu Arg Ile
290 295 300

Asp Glu Pro Ile Ser Asp Ala Ile Ser Leu Arg His Val Val Ile Asn
305 310 315 320

Asp Asp His Asp Gly Ile Glu Val Ala Leu Pro Asp Ala Ser Gln Trp
325 330 335

Gly Glu Gly Val Phe Lys Ile Val Ser Asn Pro Asp Ala Ser Thr Gln
340 345 350

Lys Ile Arg Thr Arg Gly Lys Pro Ala Arg Gln Thr Leu Glu Ile Gly
355 360 365

Asp Glu Leu Val Phe Asp Ile Arg Lys Gly Gly Glu Val Ala Tyr Gly
370 375 380

Val Thr Val Pro Tyr Asp Gly Arg Ser Leu Gly Lys Leu Asn Arg Ile
385 390 395 400

Leu Glu Trp Gly Cys Arg Gly Arg Phe Ala Val Leu
405 410

<210> 2747

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> RXA02482

<400> 2747

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ggtttgcaac tttccaacct cagccggata aggaacacta gtg ggc gtg gct aaa 115
                                   Val Gly Val Ala Lys
                                   1           5

tca aag aaa tct gct tta cct aaa gtc ctg ctc acc atc gtg gtg atc 163
Ser Lys Lys Ser Ala Leu Pro Lys Val Leu Leu Thr Ile Val Val Ile
                        10                        15                        20

ctg ctc ctg ctc gtg ctg gta gca gaa ttc ggg ctg cgc ttc atg atc 211
Leu Leu Leu Leu Val Leu Val Ala Glu Phe Gly Leu Arg Phe Met Ile
                        25                        30                        35

gga aaa caa ctg aaa gat gag ttc caa gct cag gct tcc tca caa gga 259
Gly Lys Gln Leu Lys Asp Glu Phe Gln Ala Gln Ala Ser Ser Gln Gly
                        40                        45                        50

atc tct gca act gaa gag ccc tcc atc agc ttc ggc gca tcc cca ctc 307
Ile Ser Ala Thr Glu Glu Pro Ser Ile Ser Phe Gly Ala Ser Pro Leu
                        55                        60                        65

ctg tta ggc atc gct cgg gga agc atc aat gaa gtc aca atc gac acc 355
Leu Leu Gly Ile Ala Arg Gly Ser Ile Asn Glu Val Thr Ile Asp Thr
                        70                        75                        80                        85

ccc gac tcc gta tcc atc act aac caa gac ggt gtc ccc tcc atc agt 403
Pro Asp Ser Val Ser Ile Thr Asn Gln Asp Gly Val Pro Ser Ile Ser
                        90                        95                        100

ggc aca cca gag tca act atc caa ctc caa ggg ctt gat atc ggt gac 451
Gly Thr Pro Glu Ser Thr Ile Gln Leu Gln Gly Leu Asp Ile Gly Asp
                        105                        110                        115

cgc gac aac cca gtc gca gac cac ctc acc tta acc aca ttg gca acc 499
Arg Asp Asn Pro Val Ala Asp His Leu Thr Leu Thr Thr Leu Ala Thr
                        120                        125                        130

gac gat ttc atc ctg gca acc atc caa cag cag atg gcc gaa gca acc 547
Asp Asp Phe Ile Leu Ala Thr Ile Gln Gln Gln Met Ala Glu Ala Thr
                        135                        140                        145

ggc ggg aac agc acc tcc caa gga ttc gca gaa cag ctt atc cag gaa 595
Gly Gly Asn Ser Thr Ser Gln Gly Phe Ala Glu Gln Leu Ile Gln Glu
                        150                        155                        160                        165

ctc atc aaa gtc acc gac att act tcc gat gca gct aat caa acc atc 643
Leu Ile Lys Val Thr Asp Ile Thr Ser Asp Ala Ala Asn Gln Thr Ile
                        170                        175                        180

gaa gtt gaa ttc acc gac ggc gcc gcc cga gcc tca ctg cac ccc atc 691
Glu Val Glu Phe Thr Asp Gly Ala Ala Arg Ala Ser Leu His Pro Ile
                        185                        190                        195

gta acg aac ggc caa ctc ggc ttt gag atc gta gat tcc caa ctc ttc 739

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Val Thr Asn Gly Gln Leu Gly Phe Glu Ile Val Asp Ser Gln Leu Phe
 200 205 210

gga ttc ggc ctc ccc gat gaa atc tcc caa atg ctc acc gac gca ctg 787
 Gly Phe Gly Leu Pro Asp Glu Ile Ser Gln Met Leu Thr Asp Ala Leu
 215 220 225

caa tca tca atc aat gaa gta gcc ggt ggc ctg caa atc caa agc ctc 835
 Gln Ser Ser Ile Asn Glu Val Ala Gly Gly Leu Gln Ile Gln Ser Leu
 230 235 240 245

gaa gtt gtc gac gct ggc atc aac gtc acc ctg acc gga gac aac atc 883
 Glu Val Val Asp Ala Gly Ile Asn Val Thr Leu Thr Gly Asp Asn Ile
 250 255 260

aac atc cag acc cta gaa gcc gca cag taaagagcgc tttcgcgtct 930
 Asn Ile Gln Thr Leu Glu Ala Ala Gln
 265 270

gtg 933

<210> 2748

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 2748

Val Gly Val Ala Lys Ser Lys Lys Ser Ala Leu Pro Lys Val Leu Leu
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Thr Ile Val Val Ile Leu Leu Leu Leu Val Leu Val Ala Glu Phe Gly
 20 25 30

Leu Arg Phe Met Ile Gly Lys Gln Leu Lys Asp Glu Phe Gln Ala Gln
 35 40 45

Ala Ser Ser Gln Gly Ile Ser Ala Thr Glu Glu Pro Ser Ile Ser Phe
 50 55 60

Gly Ala Ser Pro Leu Leu Leu Gly Ile Ala Arg Gly Ser Ile Asn Glu
 65 70 75 80

Val Thr Ile Asp Thr Pro Asp Ser Val Ser Ile Thr Asn Gln Asp Gly
 85 90 95

Val Pro Ser Ile Ser Gly Thr Pro Glu Ser Thr Ile Gln Leu Gln Gly
 100 105 110

Leu Asp Ile Gly Asp Arg Asp Asn Pro Val Ala Asp His Leu Thr Leu
 115 120 125

Thr Thr Leu Ala Thr Asp Asp Phe Ile Leu Ala Thr Ile Gln Gln Gln
 130 135 140

Met Ala Glu Ala Thr Gly Gly Asn Ser Thr Ser Gln Gly Phe Ala Glu
 145 150 155 160

Gln Leu Ile Gln Glu Leu Ile Lys Val Thr Asp Ile Thr Ser Asp Ala
 165 170 175

Ala Asn Gln Thr Ile Glu Val Glu Phe Thr Asp Gly Ala Ala Arg Ala
 180 185 190

Ser Leu His Pro Ile Val Thr Asn Gly Gln Leu Gly Phe Glu Ile Val
 195 200 205

Asp Ser Gln Leu Phe Gly Phe Gly Leu Pro Asp Glu Ile Ser Gln Met
 210 215 220

Leu Thr Asp Ala Leu Gln Ser Ser Ile Asn Glu Val Ala Gly Gly Leu
 225 230 235 240

Gln Ile Gln Ser Leu Glu Val Val Asp Ala Gly Ile Asn Val Thr Leu
 245 250 255

Thr Gly Asp Asn Ile Asn Ile Gln Thr Leu Glu Ala Ala Gln
 260 265 270

<210> 2749

<211> 936

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(913)

<223> RXA02483

<400> 2749

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aggcgctctg accgaaaagt ggatctccga gaacctctaa atg gct gat cac gcc 115
 Met Ala Asp His Ala
 1 5

cac aat ctg cgc gcc tct ttc cgc aag ggt gca aac gga aag cag aag 163
 His Asn Leu Arg Ala Ser Phe Arg Lys Gly Ala Asn Gly Lys Gln Lys
 10 15 20

cca atc ggc gtg atc acc cgc ggc acc acc ggt gtg aac cgc cta cgg 211
 Pro Ile Gly Val Ile Thr Arg Gly Thr Thr Gly Val Asn Arg Leu Arg
 25 30 35

cgc ttc gat cgg tgg tgc ttt cat cat ccc aaa ata cgt tcg ctt ctc 259
 Arg Phe Asp Arg Trp Cys Phe His His Pro Lys Ile Arg Ser Leu Leu
 40 45 50

gac gcc act tcc ctg gcg tta gat gtc ggg tac ggc gcc agc cac aca 307
 Asp Ala Thr Ser Leu Ala Leu Asp Val Gly Tyr Gly Ala Ser His Thr
 55 60 65

acc acc gtc gaa tgg gga cgt tgg ctc cac cgc ctc caa ccc gac atg 355
 Thr Thr Val Glu Trp Gly Arg Trp Leu His Arg Leu Gln Pro Asp Met
 70 75 80 85

gat gtc atc ggc cta gaa atc aac ccc gaa cga gtc ctc gaa ccc caa 403
 Asp Val Ile Gly Leu Glu Ile Asn Pro Glu Arg Val Leu Glu Pro Gln
 90 95 100

aac ggc gtg tcc ttt gaa ctc ggc gga ttc gaa ctt gcc ggc tac acc 451

Asn Gly Val Ser Phe Glu Leu Gly Gly Phe Glu Leu Ala Gly Tyr Thr
 105 110 115
 cca caa ctc gtg cgc gcc ttc aac gtg ctg cgc caa tac gac gtg gac 499
 Pro Gln Leu Val Arg Ala Phe Asn Val Leu Arg Gln Tyr Asp Val Asp
 120 125 130
 caa gtc gaa gcc gca tgg gaa acc gtc acc tcc aga ctt gcc cca ggc 547
 Gln Val Glu Ala Ala Trp Glu Thr Val Thr Ser Arg Leu Ala Pro Gly
 135 140 145
 gga ctg ttt ttc gaa ggc acc tgc gat gaa atc ggc aaa cgc tgc acc 595
 Gly Leu Phe Phe Glu Gly Thr Cys Asp Glu Ile Gly Lys Arg Cys Thr
 150 155 160 165
 tgg atc aca ctt aac tca gac ggc cca caa gaa ctc acc ctt gca tgg 643
 Trp Ile Thr Leu Asn Ser Asp Gly Pro Gln Glu Leu Thr Leu Ala Trp
 170 175 180
 gat cct tgg gga atc tcc acc ccc tcc gat gtg gcc gaa cga ctg ccc 691
 Asp Pro Trp Gly Ile Ser Thr Pro Ser Asp Val Ala Glu Arg Leu Pro
 185 190 195
 aaa atg ctc atc cac cgc aac att cct ggt gaa aag att cac gca ctg 739
 Lys Met Leu Ile His Arg Asn Ile Pro Gly Glu Lys Ile His Ala Leu
 200 205 210
 cta gca gcc gct gat tta gcc tgg gac tac tgc gcc ggc tgg gaa ccc 787
 Leu Ala Ala Ala Asp Leu Ala Trp Asp Tyr Cys Ala Gly Trp Glu Pro
 215 220 225
 cac gga ccg cgc gtg cgc tgg gaa aaa gcc cgc gag atg ctc atc gac 835
 His Gly Pro Arg Val Arg Trp Glu Lys Ala Arg Glu Met Leu Ile Asp
 230 235 240 245
 caa ggt tgg ccc atc gca gtg tcc agg cga cgc gtg ggc gat agc ctg 883
 Gln Gly Trp Pro Ile Ala Val Ser Arg Arg Val Gly Asp Ser Leu
 250 255 260
 ctg act gta ccg tgg gaa acg gtg gcg cct taattgtttt acgcgtgctg 933
 Leu Thr Val Pro Trp Glu Thr Val Ala Pro
 265 270
 aca 936

<210> 2750

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 2750

Met Ala Asp His Ala His Asn Leu Arg Ala Ser Phe Arg Lys Gly Ala
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Asn Gly Lys Gln Lys Pro Ile Gly Val Ile Thr Arg Gly Thr Thr Gly
 20 25 30

Val Asn Arg Leu Arg Arg Phe Asp Arg Trp Cys Phe His His Pro Lys
 35 40 45

Ile Arg Ser Leu Leu Asp Ala Thr Ser Leu Ala Leu Asp Val Gly Tyr
 50 55 60
 Gly Ala Ser His Thr Thr Thr Val Glu Trp Gly Arg Trp Leu His Arg
 65 70 75 80
 Leu Gln Pro Asp Met Asp Val Ile Gly Leu Glu Ile Asn Pro Glu Arg
 85 90 95
 Val Leu Glu Pro Gln Asn Gly Val Ser Phe Glu Leu Gly Gly Phe Glu
 100 105 110
 Leu Ala Gly Tyr Thr Pro Gln Leu Val Arg Ala Phe Asn Val Leu Arg
 115 120 125
 Gln Tyr Asp Val Asp Gln Val Glu Ala Ala Trp Glu Thr Val Thr Ser
 130 135 140
 Arg Leu Ala Pro Gly Gly Leu Phe Phe Glu Gly Thr Cys Asp Glu Ile
 145 150 155 160
 Gly Lys Arg Cys Thr Trp Ile Thr Leu Asn Ser Asp Gly Pro Gln Glu
 165 170 175
 Leu Thr Leu Ala Trp Asp Pro Trp Gly Ile Ser Thr Pro Ser Asp Val
 180 185 190
 Ala Glu Arg Leu Pro Lys Met Leu Ile His Arg Asn Ile Pro Gly Glu
 195 200 205
 Lys Ile His Ala Leu Leu Ala Ala Ala Asp Leu Ala Trp Asp Tyr Cys
 210 215 220
 Ala Gly Trp Glu Pro His Gly Pro Arg Val Arg Trp Glu Lys Ala Arg
 225 230 235 240
 Glu Met Leu Ile Asp Gln Gly Trp Pro Ile Ala Val Ser Arg Arg Arg
 245 250 255
 Val Gly Asp Ser Leu Leu Thr Val Pro Trp Glu Thr Val Ala Pro
 260 265 270

<210> 2751

<211> 624

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXA02484

<400> 2751

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gcgatgaatc caacacccca ctaacggtag tcttatacctc atg gca acg cgt aca 115
 Met Ala Thr Arg Thr
 1 5

gaa aac acc att acg atc aat cag ccc gtc ggc aag gtg cac caa gca 163

Glu Asn Thr Ile Thr Ile Asn Gln Pro Val Gly Lys Val His Gln Ala
 10 15 20
 ctg acc acc gaa gcc tac tgg gca tac atc gca gag aac ctc tcc ccc 211
 Leu Thr Thr Glu Ala Tyr Trp Ala Tyr Ile Ala Glu Asn Leu Ser Pro
 25 30 35
 gaa gct ggc gag gtc aac gag ttc acc gca gct gac ggt ggc gca acc 259
 Glu Ala Gly Glu Val Asn Glu Phe Thr Ala Ala Asp Gly Gly Ala Thr
 40 45 50
 gca acc ctt ttt gag gtc ctc cca ctc gag gtc ctc cca gag gca gtt 307
 Ala Thr Leu Phe Glu Val Leu Pro Leu Glu Val Leu Pro Glu Ala Val
 55 60 65
 cgc gca atg atc agc cag gca ctg aag gtc aag cga gtc ctc acg gtt 355
 Arg Ala Met Ile Ser Gln Ala Leu Lys Val Lys Arg Val Leu Thr Val
 70 75 80 85
 cct gca ctg acc aac aac gcc aca acc gtc gag tac aac gct gac gtc 403
 Pro Ala Leu Thr Asn Asn Ala Thr Thr Val Glu Tyr Asn Ala Asp Val
 90 95 100
 aag ggc acc cct gtt gat ttc aag ggc acc atc gcc atc aac ggc gac 451
 Lys Gly Thr Pro Val Asp Phe Lys Gly Thr Ile Ala Ile Asn Gly Asp
 105 110 115
 gac gca gca acc acc ttc gac tac agc aac gaa gtg tcc gtg aac atc 499
 Asp Ala Ala Thr Thr Phe Asp Tyr Ser Asn Glu Val Ser Val Asn Ile
 120 125 130
 cca ttc atg ggc cct gca atc gag cct aag gtt gcc gac gca ctc ggc 547
 Pro Phe Met Gly Pro Ala Ile Glu Pro Lys Val Ala Asp Ala Leu Gly
 135 140 145
 gag ctc ttc gca aac gaa ggc gct ctg acc gaa aag tgg atc tcc gag 595
 Glu Leu Phe Ala Asn Glu Gly Ala Leu Thr Glu Lys Trp Ile Ser Glu
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 Asn Leu

<210> 2752

<211> 167

<212> PRT

<213> Corynebacterium glutamicum

<400> 2752

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 20 25 30
 Glu Asn Leu Ser Pro Glu Ala Gly Glu Val Asn Glu Phe Thr Ala Ala
 35 40 45
 Asp Gly Gly Ala Thr Ala Thr Leu Phe Glu Val Leu Pro Leu Glu Val
 50 55 60

Leu Pro Glu Ala Val Arg Ala Met Ile Ser Gln Ala Leu Lys Val Lys
 65 70 75 80
 Arg Val Leu Thr Val Pro Ala Leu Thr Asn Asn Ala Thr Thr Val Glu
 85 90 95
 Tyr Asn Ala Asp Val Lys Gly Thr Pro Val Asp Phe Lys Gly Thr Ile
 100 105 110
 Ala Ile Asn Gly Asp Asp Ala Ala Thr Thr Phe Asp Tyr Ser Asn Glu
 115 120 125
 Val Ser Val Asn Ile Pro Phe Met Gly Pro Ala Ile Glu Pro Lys Val
 130 135 140
 Ala Asp Ala Leu Gly Glu Leu Phe Ala Asn Glu Gly Ala Leu Thr Glu
 145 150 155 160
 Lys Trp Ile Ser Glu Asn Leu
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<210> 2753

<211> 759

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> RXA02486

<400> 2753

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 Met Thr Glu Phe Ser
 1 5
 gac gtc cct ggc acc gcc gcc cca ctg cac agg gcg ttg gaa aat gcc 163
 Asp Val Pro Gly Thr Ala Ala Pro Leu His Arg Ala Leu Glu Asn Ala
 10 15 20
 gga tac tcc act tta gaa tcc ctc gac ggt gtt ccc tac aag acg ttg 211
 Gly Tyr Ser Thr Leu Glu Ser Leu Asp Gly Val Pro Tyr Lys Thr Leu
 25 30 35
 att gcc ctg cat ggt gtc gga aaa act ggc ctc ggc agg atc cag gca 259
 Ile Ala Leu His Gly Val Gly Lys Thr Gly Leu Gly Arg Ile Gln Ala
 40 45 50
 gca ttg ttg gaa cgt ggc ctt tcc ctg ggg gaa gaa aca aaa ggc gcc 307
 Ala Leu Leu Glu Arg Gly Leu Ser Leu Gly Glu Glu Thr Lys Gly Ala
 55 60 65
 acc atc acc cca ggt cac acc ggt aaa gtg gcc tca gat atc aaa act 355
 Thr Ile Thr Pro Gly His Thr Gly Lys Val Ala Ser Asp Ile Lys Thr
 70 75 80 85
 cac atc act tcc gtg gat ccc gtc gca tac gtc gat ggt cta gag ggg 403

His Ile Thr Ser Val Asp Pro Val Ala Tyr Val Asp Gly Leu Glu Gly
 90 95 100
 cgt cgg gtt gct cac ggg cac caa ttg cta tcg atc ttc ggt cgc gtc 451
 Arg Arg Val Ala His Gly His Gln Leu Leu Ser Ile Phe Gly Arg Val
 105 110 115
 acc ggc gcg gaa ccc aaa atg tgg gga ccc tcc atg atc gga tac ggc 499
 Thr Gly Ala Glu Pro Lys Met Trp Gly Pro Ser Met Ile Gly Tyr Gly
 120 125 130
 tca gtc cac tac gtt tcc cac acc gga agg gaa ggc gat tgg ttt cag 547
 Ser Val His Tyr Val Ser His Thr Gly Arg Glu Gly Asp Trp Phe Gln
 135 140 145
 tgt ggt ttc agc ccg gcg aag tcc aaa atc tgc ctg tat ggc ctg aag 595
 Cys Gly Phe Ser Pro Ala Lys Ser Lys Ile Cys Leu Tyr Gly Leu Lys
 150 155 160 165
 gat tcg cct cgc ggt gag gaa ttg ctg cag aaa ctt gga aaa tac acc 643
 Asp Ser Pro Arg Gly Glu Glu Leu Leu Gln Lys Leu Gly Lys Tyr Thr
 170 175 180
 gaa ggc cgc gga tgc gtg tac atc aat aaa ccg gaa gac atc gat ttg 691
 Glu Gly Arg Gly Cys Val Tyr Ile Asn Lys Pro Glu Asp Ile Asp Leu
 185 190 195
 gat gtt tta gag gcc atg atc agc gag tca tgg gcc ggc caa ggc 736
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<210> 2754

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 2754

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 20 25 30
 Pro Tyr Lys Thr Leu Ile Ala Leu His Gly Val Gly Lys Thr Gly Leu
 35 40 45
 Gly Arg Ile Gln Ala Ala Leu Leu Glu Arg Gly Leu Ser Leu Gly Glu
 50 55 60
 Glu Thr Lys Gly Ala Thr Ile Thr Pro Gly His Thr Gly Lys Val Ala
 65 70 75 80
 Ser Asp Ile Lys Thr His Ile Thr Ser Val Asp Pro Val Ala Tyr Val
 85 90 95
 Asp Gly Leu Glu Gly Arg Arg Val Ala His Gly His Gln Leu Leu Ser
 100 105 110

ctg gta gct agc gga ttc ctt gca gcg ttt aag taaatgaatc gttttcctag 389
 Leu Val Ala Ser Gly Phe Leu Ala Ala Phe Lys
 115 120

tgc

392

<210> 2756
 <211> 123
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2756
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 Cys Asp Glu Pro Glu Thr Pro Val Glu Pro Glu Val Pro Val Glu Pro
 35 40 45
 Glu Thr Pro Val Asp Pro Glu Thr Ser Val Asp Pro Glu Thr Pro Val
 50 55 60
 Asp Pro Glu Thr Ser Val Asp Pro Glu Lys Pro Gly Asp Asp Asn Lys
 65 70 75 80
 Asp Asp Gly Ser Asn Ser Ser Ser Asn Gly Asp Ile Leu Gly Ile Leu
 85 90 95
 Gly Ile Leu Ala Ala Leu Gly Gly Val Gly Ala Leu Val Tyr Asn Phe
 100 105 110
 Leu Val Ala Ser Gly Phe Leu Ala Ala Phe Lys
 115 120

<210> 2757
 <211> 724
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(724)
 <223> RXA02489

<400> 2757
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 Met Asn Arg Phe Pro
 1 5
 agt gcc tta tta gca gcc tct gtc gcg ggg gct gcg ttg gcc att cca 163
 Ser Ala Leu Leu Ala Ala Ser Val Ala Gly Ala Ala Leu Ala Ile Pro
 10 15 20
 gcg acc tct gca cat gca gca gaa tct att tgt aca ttc acc ggc gat 211
 Ala Thr Ser Ala His Ala Ala Glu Ser Ile Cys Thr Phe Thr Gly Asp

25	30	35	
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atc gca aat ggt agt gct tat aaa tat aag ggc ggg ttg gac gtt cgt Ile Ala Asn Gly Ser Ala Tyr Lys Tyr Lys Gly Gly Leu Asp Val Arg 55 60 65			307
gac ggc gtc cag acc gac ggt aac ggc aaa act cca gca ctg acc tgg Asp Gly Val Gln Thr Asp Gly Asn Gly Lys Thr Pro Ala Leu Thr Trp 70 75 80 85			355
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cac tgg acc gga cac aac ctg tac ccc ggt gat gac ctc gcg gaa gtc His Trp Thr Gly His Asn Leu Tyr Pro Gly Asp Asp Leu Ala Glu Val 105 110 115			451
cct aac aat ttc acg ttg gat ctt gat ttt tcc aac atc act gtg gag Pro Asn Asn Phe Thr Leu Asp Leu Asp Phe Ser Asn Ile Thr Val Glu 120 125 130			499
ctg agt ggt tct aca ggt cgg ttg ttg gtg gat tac aca tct cgg gaa Leu Ser Gly Ser Thr Gly Arg Leu Leu Val Asp Tyr Thr Ser Arg Glu 135 140 145			547
tac atc aac acc cac acg ttg ggt gag ttt caa act ggt gaa cag gct Tyr Ile Asn Thr His Thr Leu Gly Glu Phe Gln Thr Gly Glu Gln Ala 150 155 160 165			595
gag ctt gcc acg att act ttt gcc aaa gct cca gac ctc acc tct aat Glu Leu Ala Thr Ile Thr Phe Ala Lys Ala Pro Asp Leu Thr Ser Asn 170 175 180			643
tca gtc aac gtg act ggc gat gtg gca ttg act gct gat ggt gtg gaa Ser Val Asn Val Thr Gly Asp Val Ala Leu Thr Ala Asp Gly Val Glu 185 190 195			691
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<400> 2758

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Thr	Phe	Thr	Gly	Asp	Val	Gly	Trp	Asn	Val	Arg	Asp	Ser	Phe	Asn	Ser
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Tyr Leu Leu Gly Asn Ile Ala Asn Gly Ser Ala Tyr Lys Tyr Lys Gly
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 Gly Leu Asp Val Arg Asp Gly Val Gln Thr Asp Gly Asn Gly Lys Thr
 65 70 75 80
 Pro Ala Leu Thr Trp Pro Val Asp Ser Val Thr Ser Ser Lys Ile Ser
 85 90 95
 Thr Ser Gly Gly Ala His Trp Thr Gly His Asn Leu Tyr Pro Gly Asp
 100 105 110
 Asp Leu Ala Glu Val Pro Asn Asn Phe Thr Leu Asp Leu Asp Phe Ser
 115 120 125
 Asn Ile Thr Val Glu Leu Ser Gly Ser Thr Gly Arg Leu Leu Val Asp
 130 135 140
 Tyr Thr Ser Arg Glu Tyr Ile Asn Thr His Thr Leu Gly Glu Phe Gln
 145 150 155 160
 Thr Gly Glu Gln Ala Glu Leu Ala Thr Ile Thr Phe Ala Lys Ala Pro
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<211> 2691

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2668)

<223> RXA02495

<400> 2759

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 Met Ala Leu Thr Val
 1 5

ctt tcg gtt gtg cta gga acc gca ttt ttg tgt ggc tcc ctc ctc ctc 163
 Leu Ser Val Val Leu Gly Thr Ala Phe Leu Cys Gly Ser Leu Leu Leu
 10 15 20

aca cat tcc ctt gaa aga aca ttt tcc tcc atc gtt gat gcc ggc gtg 211
 Thr His Ser Leu Glu Arg Thr Phe Ser Ser Ile Val Asp Ala Gly Val
 25 30 35

gag ggc gtt gac gtg ggc gtt atc gcg caa caa aac aac ccc gac ggc 259
 Glu Gly Val Asp Val Gly Val Ile Ala Gln Gln Asn Asn Pro Asp Gly
 40 45 50

gta cct ttc tcc gtc atc gcc gaa att gag cag tat ccg gaa gtc cgc Val Pro Phe Ser Val Ile Ala Glu Ile Glu Gln Tyr Pro Glu Val Arg 55 60 65	307
gcc gtc aac atc atc ggc gac ggc ccc ggc atg ccc tcc ggc acc acc Ala Val Asn Ile Ile Gly Asp Gly Pro Gly Met Pro Ser Gly Thr Thr 70 75 80 85	355
atg acc ggc caa tcc gcg ctg atc ctc acc gac tcc gac ggc aat ccc Met Thr Gly Gln Ser Ala Leu Ile Leu Thr Asp Ser Asp Gly Asn Pro 90 95 100	403
ctg caa gca ggc agc tcc ggc acg cac ccg cta gcc att tat ccg cag Leu Gln Ala Gly Ser Ser Gly Thr His Pro Leu Ala Ile Tyr Pro Gln 105 110 115	451
ggc gag tgg gtc tcg ccc gag cca acg ctt atc gac ggc cac ttc ccc Gly Glu Trp Val Ser Pro Glu Pro Thr Leu Ile Asp Gly His Phe Pro 120 125 130	499
aca aaa ccc gac gag gta gta gtc aac gct tcg gcc gcc aaa cgt ggc Thr Lys Pro Asp Glu Val Val Val Asn Ala Ser Ala Ala Lys Arg Gly 135 140 145	547
ggg ctc tcc ctc ggt gat cac cta acg atc gtc aca ccc acc gaa cgc Gly Leu Ser Leu Gly Asp His Leu Thr Ile Val Thr Pro Thr Glu Arg 150 155 160 165	595
atc gac gcc acc ctg tct gga acc ttc gaa tca aac acc gac gtc gca Ile Asp Ala Thr Leu Ser Gly Thr Phe Glu Ser Asn Thr Asp Val Ala 170 175 180	643
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Gly Val Ser Thr Phe Gln Ile Gly Phe Ser Val Ile Met Glu Ala Val	
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Phe Val Gly Leu Ile Gly Gly Phe Ile Gly Ile Ala Val Gly Phe Gly	
310 315 320 325	
gtg gtc aat gca ctt gtc caa gtg ctc aac caa ttc ggc gac acc ctc	1123
Val Val Asn Ala Leu Val Gln Val Leu Asn Gln Phe Gly Asp Thr Leu	
330 335 340	
tcc tcc atc gac atc acc tac aac gcc gga tcc ttc atc ttc cct gtc	1171
Ser Ser Ile Asp Ile Thr Tyr Asn Ala Gly Ser Phe Ile Phe Pro Val	
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ctc ttc gcc gtc act gcc acc gta cta agc tcc ata tcg cct gct cac	1219
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cgc gcc ggt aac ctc cca cca gtc caa gca ttc gaa tcc tcc gat gca	1267
Arg Ala Gly Asn Leu Pro Pro Val Gln Ala Phe Glu Ser Ser Asp Ala	
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cgc agc gac gcc ctc gga agg atc cgc ttc ctc gtc gcc gcc gtc atg	1315
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Ile Asn Gly Asp Glu Phe Lys Thr Glu Thr Arg Leu Ala Phe Ile Gly	
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Leu Met Val Ala Thr Ser Gln Thr Leu Gly Val Ala Ile Met Ser Pro	
455 460 465	
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Phe Arg Ala Val Gly Lys Leu Ala Gln Arg Asn Thr Leu Arg Asn Pro	
470 475 480 485	
cga cgc tcc gca acc acc gca ctg gcc gtc act ttg agc gtt ggc ctc	1603
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Val Ala Cys Val Gly Val Ile Gly Ala Thr Thr Arg Ala Ser Val Phe	
505 510 515	
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Gly Ser Met Glu Ser Thr Ile Lys Ser Pro Tyr Val Leu Asp Ser Ile	
520 525 530	
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Gly Gly Thr Met Ile Pro Gly Gln Pro Ala Gly Gly Ser Arg Ser Leu	

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cac cgg tcc caa atc ttc gtc aac ggc gac ggc tcc acc acc aac gaa His Arg Ser Gln Ile Phe Val Asn Gly Asp Gly Ser Thr Thr Asn Glu 680 685 690			2179
gaa ctc cgc gac atc ctc gtc gac gcc gta gcc ccc ttc ctc atc gtc Glu Leu Arg Asp Ile Leu Val Asp Ala Val Ala Pro Phe Leu Ile Val 695 700 705			2227
caa gtg aaa tcc aaa gat gaa ttc cgc gga agc ctc ggc acc caa atc Gln Val Lys Ser Lys Asp Glu Phe Arg Gly Ser Leu Gly Thr Gln Ile 710 715 720 725			2275
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cgc acc cgc gaa atc gga atc ctc cgc gcc acc ggc gtc caa cga gga Arg Thr Arg Glu Ile Gly Ile Leu Arg Ala Thr Gly Val Gln Arg Gly 760 765 770			2419
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ggc gca atc cac gga ctc ctc cta ggt aca ttt atc ggc tgg gca atc 2515
 Gly Ala Ile His Gly Leu Leu Leu Gly Thr Phe Ile Gly Trp Ala Ile
 790 795 800 805

gtc agt tgt ctc cgc acc cga ggc atg gca ccc gtc gaa ttc ccc tgg 2563
 Val Ser Cys Leu Arg Thr Arg Gly Met Ala Pro Val Glu Phe Pro Trp
 810 815 820

acc caa atc gga tta atg ctc atc tcc gca atc atc atc gga ggc ata 2611
 Thr Gln Ile Gly Leu Met Leu Ile Ser Ala Ile Ile Ile Gly Gly Ile
 825 830 835

gca gcc ctc atc cca gcc aac cga gcc tcc cga atc tcc cct ttg gaa 2659
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<210> 2760

<211> 856

<212> PRT

<213> Corynebacterium glutamicum

<400> 2760

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Val Asp Ala Gly Val Glu Gly Val Asp Val Gly Val Ile Ala Gln Gln
 35 40 45

Asn Asn Pro Asp Gly Val Pro Phe Ser Val Ile Ala Glu Ile Glu Gln
 50 55 60

Tyr Pro Glu Val Arg Ala Val Asn Ile Ile Gly Asp Gly Pro Gly Met
 65 70 75 80

Pro Ser Gly Thr Thr Met Thr Gly Gln Ser Ala Leu Ile Leu Thr Asp
 85 90 95

Ser Asp Gly Asn Pro Leu Gln Ala Gly Ser Ser Gly Thr His Pro Leu
 100 105 110

Ala Ile Tyr Pro Gln Gly Glu Trp Val Ser Pro Glu Pro Thr Leu Ile
 115 120 125

Asp Gly His Phe Pro Thr Lys Pro Asp Glu Val Val Val Asn Ala Ser
 130 135 140

Ala Ala Lys Arg Gly Gly Leu Ser Leu Gly Asp His Leu Thr Ile Val
 145 150 155 160

Thr Pro Thr Glu Arg Ile Asp Ala Thr Leu Ser Gly Thr Phe Glu Ser
 165 170 175

Asn Thr Asp Val Ala Gly Trp Val Gly Val Gly Phe Thr Pro Gln Arg
 180 185 190
 Tyr Val Glu Leu Leu Thr Asn Gly Thr Asp Ala Ser Gln Ile Thr Ile
 195 200 205
 Ala Val Asn Asp Gly Ala Asp Pro Met Ala Val Arg Asn Arg Ile Gly
 210 215 220
 Lys Asn His Arg Asp Leu Leu Pro Leu Leu Pro Glu Gln Ile Ile Asp
 225 230 235 240
 Gln Thr Thr Gly Asp Thr Asp Arg Gln Leu Glu Phe Met Thr Tyr Val
 245 250 255
 Leu Leu Ala Phe Ala Ala Ile Ala Leu Ile Val Gly Ser Phe Ile Ile
 260 265 270
 Ala Asn Thr Phe Ala Met Ile Val Ala Gln Arg Thr Gly Glu Phe Ala
 275 280 285
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 Ile Met Glu Ala Val Phe Val Gly Leu Ile Gly Gly Phe Ile Gly Ile
 305 310 315 320
 Ala Val Gly Phe Gly Val Val Asn Ala Leu Val Gln Val Leu Asn Gln
 325 330 335
 Phe Gly Asp Thr Leu Ser Ser Ile Asp Ile Thr Tyr Asn Ala Gly Ser
 340 345 350
 Phe Ile Phe Pro Val Leu Phe Ala Val Thr Ala Thr Val Leu Ser Ser
 355 360 365
 Ile Ser Pro Ala His Arg Ala Gly Asn Leu Pro Pro Val Gln Ala Phe
 370 375 380
 Glu Ser Ser Asp Ala Arg Ser Asp Ala Leu Gly Arg Ile Arg Phe Leu
 385 390 395 400
 Val Ala Ala Val Met Leu Thr Leu Gly Ile Ser Leu Thr Ile Ala Gly
 405 410 415
 Ala Val Val Ser Ala Ile Asn Gly Asp Glu Phe Lys Thr Glu Thr Arg
 420 425 430
 Leu Ala Phe Ile Gly Ala Gly Leu Leu Leu Val Phe Phe Ser Leu Ser
 435 440 445
 Leu Ser Gly Pro Ala Leu Met Val Ala Thr Ser Gln Thr Leu Gly Val
 450 455 460
 Ala Ile Met Ser Pro Phe Arg Ala Val Gly Lys Leu Ala Gln Arg Asn
 465 470 475 480
 Thr Leu Arg Asn Pro Arg Arg Ser Ala Thr Thr Ala Leu Ala Val Thr
 485 490 495
 Leu Ser Val Gly Leu Val Ala Cys Val Gly Val Ile Gly Ala Thr Thr

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Gln Thr Arg Gly Val Gly Lys Val Gly Thr Leu Met Thr Gly Ser Val 565 570 575		
Gln Val Asn Gly Trp Asp Asn Glu Asn Thr Thr Ile Phe Asp Gly Asp 580 585 590		
Leu Ser Gln Phe Leu Asp Leu Ala Val Arg Ser Gly Asp Ala Phe Asp 595 600 605		
Asp Glu Thr Pro Gly Val Met Ile Ser Thr Thr Tyr Ala Asp Gln Ser 610 615 620		
Asp Leu Glu Val Gly Asp Thr Val Thr Val Asn Pro Tyr Gly Ser Asp 625 630 635 640		
Asp Gly Ile Arg Val Pro Ile Thr Gly Ile Tyr Ala Glu Thr Asn Leu 645 650 655		
Val Gly His Leu Met Val Asn Ala Ala Ala Thr Asn Arg Val Leu Thr 660 665 670		
Ser Ala Asp Thr Tyr His Arg Ser Gln Ile Phe Val Asn Gly Asp Gly 675 680 685		
Ser Thr Thr Asn Glu Glu Leu Arg Asp Ile Leu Val Asp Ala Val Ala 690 695 700		
Pro Phe Leu Ile Val Gln Val Lys Ser Lys Asp Glu Phe Arg Gly Ser 705 710 715 720		
Leu Gly Thr Gln Ile Asn Gln Leu Leu Gly Ile Ile Tyr Gly Leu Leu 725 730 735		
Ala Leu Ala Val Ile Ile Ala Val Leu Gly Ile Val Asn Thr Leu Phe 740 745 750		
Leu Ser Ile Ser Glu Arg Thr Arg Glu Ile Gly Ile Leu Arg Ala Thr 755 760 765		
Gly Val Gln Arg Gly Gln Ile Arg Arg Met Ile Thr Leu Glu Ser Val 770 775 780		
Ile Leu Ser Ile His Gly Ala Ile His Gly Leu Leu Leu Gly Thr Phe 785 790 795 800		
Ile Gly Trp Ala Ile Val Ser Cys Leu Arg Thr Arg Gly Met Ala Pro 805 810 815		
Val Glu Phe Pro Trp Thr Gln Ile Gly Leu Met Leu Ile Ser Ala Ile 820 825 830		

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Ile Ser Pro Leu Glu Ala Ile Asn
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<210> 2761

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(907)

<223> RXA02496

<400> 2761

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                                         Val Asn Arg Ser Asn
                                         1      5

tct tct tcg gta ttt tta ggt ttc ccc gag tct tcg cca gcg gcg gca 163
Ser Ser Ser Val Phe Leu Gly Phe Pro Glu Ser Ser Pro Ala Ala Ala
                10                15                20

tcg att cgt gct ggg gag gaa ctc cct ctt gat ttc cca cgt gaa tgg 211
Ser Ile Arg Ala Gly Glu Glu Leu Pro Leu Asp Phe Pro Arg Glu Trp
                25                30                35

tat gaa ttc acg gat cca act gat att gag cat gta ttt agc atc gat 259
Tyr Glu Phe Thr Asp Pro Thr Asp Ile Glu His Val Phe Ser Ile Asp
                40                45                50

tta acg tgg ctt gag tct aat tgg aat tgc acc ttt ggt acc ccc gat 307
Leu Thr Trp Leu Glu Ser Asn Trp Asn Cys Thr Phe Gly Thr Pro Asp
                55                60                65

tgt tta ggt att gat tcc gaa aac gcc gac gtg ggt tgt tgc ggc cac 355
Cys Leu Gly Ile Asp Ser Glu Asn Ala Asp Val Gly Cys Cys Gly His
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ggg gca ttc tta gca gat gag aca gat cga gat cag ctt tat gat gcc 403
Gly Ala Phe Leu Ala Asp Glu Thr Asp Arg Asp Gln Leu Tyr Asp Ala
                90                95                100

gtt gct cag atg ccc gct aag tat tgg cag cta cgc ccc gcc tcc acg 451
Val Ala Gln Met Pro Ala Lys Tyr Trp Gln Leu Arg Pro Ala Ser Thr
                105                110                115

gac tcg ttt tta gca tcc gat gac ggc acc gac att gag ccg tgg ctg 499
Asp Ser Phe Leu Ala Ser Asp Asp Gly Thr Asp Ile Glu Pro Trp Leu
                120                125                130

aca tgg gat gaa tta gat gat gaa gac ggc aat ccc gag ccc gct ttg 547
Thr Trp Asp Glu Leu Asp Asp Glu Asp Gly Asn Pro Glu Pro Ala Leu
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Lys Thr Thr Val Val Asn Gly Ala Cys Ile Phe Ala Asn Arg Ala Gly
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Trp Glu Thr Gly Ala Gly Cys Ala Leu His Gln Trp Gly Val Asn Ala
170 175 180

aat gag gat cta acc gtc gtc aag cct gaa gtt tgt tgg cag ctc ccg 691
Asn Glu Asp Leu Thr Val Val Lys Pro Glu Val Cys Trp Gln Leu Pro
185 190 195

ctg cgc cgc ctg gag gcc tgg gaa gag cgc ccc gac ggg caa gaa atc 739
Leu Arg Arg Leu Glu Ala Trp Glu Glu Arg Pro Asp Gly Gln Glu Ile
200 205 210

ttg cgc acc aca att act gaa tac aac cgg cgc ggc tgg ggc aac ggc 787
Leu Arg Thr Thr Ile Thr Glu Tyr Asn Arg Arg Gly Trp Gly Asn Gly
215 220 225

ggc gag gat ttc gac tgg tac tgc acc acc tct ccg cgc tgc cac acc 835
Gly Glu Asp Phe Asp Trp Tyr Cys Thr Thr Ser Pro Arg Cys His Thr
230 235 240 245

aat gcc gaa ccc atg tgg aaa aca cag gaa aca gaa ctc cgt gca ctc 883
Asn Ala Glu Pro Met Trp Lys Thr Gln Glu Thr Glu Leu Arg Ala Leu
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<210> 2762

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 2762

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20 25 30

Phe Pro Arg Glu Trp Tyr Glu Phe Thr Asp Pro Thr Asp Ile Glu His
35 40 45

Val Phe Ser Ile Asp Leu Thr Trp Leu Glu Ser Asn Trp Asn Cys Thr
50 55 60

Phe Gly Thr Pro Asp Cys Leu Gly Ile Asp Ser Glu Asn Ala Asp Val
65 70 75 80

Gly Cys Cys Gly His Gly Ala Phe Leu Ala Asp Glu Thr Asp Arg Asp
85 90 95

Gln Leu Tyr Asp Ala Val Ala Gln Met Pro Ala Lys Tyr Trp Gln Leu
100 105 110

Arg Pro Ala Ser Thr Asp Ser Phe Leu Ala Ser Asp Asp Gly Thr Asp

115	120	125
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Pro Glu Pro Ala Leu Lys Thr Thr Val Val Asn Gly Ala Cys Ile Phe 145 150 155 160		
Ala Asn Arg Ala Gly Trp Glu Thr Gly Ala Gly Cys Ala Leu His Gln 165 170 175		
Trp Gly Val Asn Ala Asn Glu Asp Leu Thr Val Val Lys Pro Glu Val 180 185 190		
Cys Trp Gln Leu Pro Leu Arg Arg Leu Glu Ala Trp Glu Glu Arg Pro 195 200 205		
Asp Gly Gln Glu Ile Leu Arg Thr Thr Ile Thr Glu Tyr Asn Arg Arg 210 215 220		
Gly Trp Gly Asn Gly Gly Glu Asp Phe Asp Trp Tyr Cys Thr Thr Ser 225 230 235 240		
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<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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<223> RXA02498

<400> 2763

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                                         1      5

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          10          15          20

acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211
Thr Asp Ala Pro Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly
          25          30          35

gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag 259
Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys
          40          45          50

ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa 307
Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu

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55	60	65	
cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa			355
Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu			
70	75	80	85
gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt			403
Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg			
	90	95	100
ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa			451
Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu			
	105	110	115
aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca			499
Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala			
	120	125	130
gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat			547
Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp			
	135	140	145
gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac			595
Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn			
	150	155	160
act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca			643
Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro			
	170	175	180
gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc			691
Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile			
	185	190	195
gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg			739
Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu			
	200	205	210
tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg			787
Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val			
	215	220	225
acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat			835
Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp			
	230	235	240
ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc			883
Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe			
	250	255	260
ggg ccg ctg gca atc gtc atg taatttgctg ttttgggccc ccg			927
Gly Pro Leu Ala Ile Val Met			
	265		

<210> 2764

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 2764

Met Ser Glu Glu Lys Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala
 1 5 10 15
 Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser
 20 25 30
 Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
 35 40 45
 Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
 50 55 60
 Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
 65 70 75 80
 Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
 85 90 95
 Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu
 100 105 110
 Arg Ile Val Asp Glu Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe
 115 120 125
 Pro Val Val Pro Ala Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala
 130 135 140
 Glu Lys Asp Ala Asp Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu
 145 150 155 160
 Val Glu Val Asp Asn Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu
 165 170 175
 Val Asp Glu Glu Pro Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile
 180 185 190
 Ile Met Met Ala Ile Val Gly Val Val Leu Gly Val Val Val Phe Leu
 195 200 205
 Gly Phe Glu Met Leu Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val
 210 215 220
 Leu Ala Val Gly Val Thr Leu Gly Met Val Gly Ile Ile His Ala Leu
 225 230 235 240
 Arg Thr Ser Arg Asp Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly
 245 250 255
 Leu Val Met Thr Phe Gly Pro Leu Ala Ile Val Met
 260 265

<210> 2765

<211> 222

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(199)

<223> RXA02500

<400> 2765

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ttttgtacgt acaacatcga tttaagcgag ggaaaccgta atg ggt tct gtc atc 115
                                         Met Gly Ser Val Ile
                                         1       5
aag aag cgc cgc aag cgc atg tcc aag aag aag cac cgc aag atg ctg 163
Lys Lys Arg Arg Lys Arg Met Ser Lys Lys Lys His Arg Lys Met Leu
              10              15              20
cgc cgt act cgt gtc cag cgt aga aaa ttg ggc aag taagccttca 209
Arg Arg Thr Arg Val Gln Arg Arg Lys Leu Gly Lys
              25              30
attgagcttc aaa 222

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<210> 2766

<211> 33

<212> PRT

<213> Corynebacterium glutamicum

<400> 2766

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Met Gly Ser Val Ile Lys Lys Arg Arg Lys Arg Met Ser Lys Lys Lys
 1             5             10             15
His Arg Lys Met Leu Arg Arg Thr Arg Val Gln Arg Arg Lys Leu Gly
      20             25             30
Lys

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<210> 2767

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA02506

<400> 2767

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cctttccctg aactctaagc aattgtgatc tatagtacaa atgcataaac attaacctgtg 60
atatccatct cttgcatacc ggccgaaagg tttagcacac atg cac ctc aat cag 115
                                         Met His Leu Asn Gln
                                         1       5
ctc gaa ttt ttc atc gca gta gcc caa cac gga cag atc aac cgc gcc 163
Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly Gln Ile Asn Arg Ala
              10              15              20
gcc gaa gaa ctc ctc att tcc caa ccc gct ctc agc cga cag atc tcc 211
Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu Ser Arg Gln Ile Ser
              25              30              35
gca ctt gaa aaa tcc gtc gga gct cca ctc ttc gaa cgc cat tcc cgc 259

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Ala	Leu	Glu	Lys	Ser	Val	Gly	Ala	Pro	Leu	Phe	Glu	Arg	His	Ser	Arg		
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ggt	gtc	tcc	ctc	aca	aag	gcc	gga	gaa	atc	ctc	cac	gaa	gaa	gcc	ctc	307	
Gly	Val	Ser	Leu	Thr	Lys	Ala	Gly	Glu	Ile	Leu	His	Glu	Glu	Ala	Leu		
	55					60					65						
cga	acg	ctt	agc	agg	atg	caa	tcg	gta	gtc	gat	gaa	atc	caa	tcc	ggt	355	
Arg	Thr	Leu	Ser	Arg	Met	Gln	Ser	Val	Val	Asp	Glu	Ile	Gln	Ser	Gly		
	70				75					80					85		
gag	cac	ctc	atc	acc	agc	atc	aac	atc	gga	gtt	ccc	cct	gga	atc	ccc	403	
Glu	His	Leu	Ile	Thr	Ser	Ile	Asn	Ile	Gly	Val	Pro	Pro	Gly	Ile	Pro		
				90					95					100			
atc	gac	tgg	ttg	cgc	tgc	caa	ctc	atc	gat	tta	ggc	ccc	gag	acc	cgc	451	
Ile	Asp	Trp	Leu	Arg	Cys	Gln	Leu	Ile	Asp	Leu	Gly	Pro	Glu	Thr	Arg		
			105					110					115				
att	tca	ctg	atc	gaa	tcc	ccc	acc	gat	gat	cag	cta	aaa	ctt	ctt	aaa	499	
Ile	Ser	Leu	Ile	Glu	Ser	Pro	Thr	Asp	Asp	Gln	Leu	Lys	Leu	Leu	Lys		
		120					125					130					
caa	cgc	gaa	ctc	gac	atc	gcc	ctt	tgt	cga	cgc	caa	agc	gag	gcc	ttt	547	
Gln	Arg	Glu	Leu	Asp	Ile	Ala	Leu	Cys	Arg	Arg	Gln	Ser	Glu	Ala	Phe		
	135					140					145						
gcc	acc	aca	ctt	gtc	cac	gaa	caa	gaa	ctg	gga	atc	gtc	gtc	cga	aaa	595	
Ala	Thr	Thr	Leu	Val	His	Glu	Gln	Glu	Leu	Gly	Ile	Val	Val	Arg	Lys		
	150				155					160					165		
aac	tcc	gaa	ctg	cac	caa	aaa	gtc	gca	gga	aaa	gac	aac	gcc	aca	ctc	643	
Asn	Ser	Glu	Leu	His	Gln	Lys	Val	Ala	Gly	Lys	Asp	Asn	Ala	Thr	Leu		
				170					175					180			
ttc	gat	ctt	gaa	ggg	ctt	cga	gtc	ctc	gca	cac	tcc	cgc	ggt	gaa	gta	691	
Phe	Asp	Leu	Glu	Gly	Leu	Arg	Val	Leu	Ala	His	Ser	Arg	Gly	Glu	Val		
			185					190					195				
aga	att	cag	gaa	gaa	atc	ctc	aaa	aac	gcc	atg	ctc	gcc	gca	gga	gtt	739	
Arg	Ile	Gln	Glu	Glu	Ile	Leu	Lys	Asn	Ala	Met	Leu	Ala	Ala	Gly	Val		
		200					205					210					
aat	gcc	acg	tgg	atc	ttc	cga	aaa	ttt	ggg	caa	tat	agc	tca	ctg	atc	787	
Asn	Ala	Thr	Trp	Ile	Phe	Arg	Lys	Phe	Gly	Gln	Tyr	Ser	Ser	Leu	Ile		
	215					220					225						
gca	gac	ctt	gtc	cag	gcc	gat	gtc	gca	ctc	aca	aca	gag	gaa	tcc	gcc	835	
Ala	Asp	Leu	Val	Gln	Ala	Asp	Val	Ala	Leu	Thr	Thr	Glu	Glu	Ser	Ala		
	230				235					240					245		
cgc	acc	aac	ttc	ccc	agc	tgg	caa	tgg	gtc	ccc	atc	gaa	ggc	gaa	gac	883	
Arg	Thr	Asn	Phe	Pro	Ser	Trp	Gln	Trp	Val	Pro	Ile	Glu	Gly	Glu	Asp		
				250					255					260			
gcc	tcc	gga	aat	gac	ctt	gtt	gtt	cgc	acc	tgg	atc	acc	tgg	aac	ccc	931	
Ala	Ser	Gly	Asn	Asp	Leu	Val	Val	Arg	Thr	Trp	Ile	Thr	Trp	Asn	Pro		
			265					270					275				
caa	ccc	acc	ccc	gcg	gtg	aag	gcc	ctg	atc	cag	aaa	ttt	att	gac	gga	979	
Gln	Pro	Thr	Pro	Ala	Val	Lys	Ala	Leu	Ile	Gln	Lys	Phe	Ile	Asp	Gly		

280

285

290

aac tgagttctaa acagccgccca tga
Asn

1005

<210> 2768

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 2768

Met His Leu Asn Gln Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly
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Gln Ile Asn Arg Ala Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu
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Ser Arg Gln Ile Ser Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe
35 40 45

Glu Arg His Ser Arg Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu
50 55 60

His Glu Glu Ala Leu Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp
65 70 75 80

Glu Ile Gln Ser Gly Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val
85 90 95

Pro Pro Gly Ile Pro Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu
100 105 110

Gly Pro Glu Thr Arg Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln
115 120 125

Leu Lys Leu Leu Lys Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg
130 135 140

Gln Ser Glu Ala Phe Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly
145 150 155 160

Ile Val Val Arg Lys Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys
165 170 175

Asp Asn Ala Thr Leu Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His
180 185 190

Ser Arg Gly Glu Val Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met
195 200 205

Leu Ala Ala Gly Val Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln
210 215 220

Tyr Ser Ser Leu Ile Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr
225 230 235 240

Thr Glu Glu Ser Ala Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro
245 250 255

Ile Glu Gly Glu Asp Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp
 260 265 270

Ile Thr Trp Asn Pro Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln
 275 280 285

Lys Phe Ile Asp Gly Asn
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<210> 2769

<211> 860

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(837)

<223> RXA02514

<400> 2769

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1 5 10 15	
gaa ggc gtt acc tct ttc ggc gca atc tcc atc gag gtt gaa gcg ggc	96
Glu Gly Val Thr Ser Phe Gly Ala Ile Ser Ile Glu Val Glu Ala Gly	
20 25 30	
gca gac gct atc gtc gca ctg cag tac gtc gga tcc ggc acc cac gct	144
Ala Asp Ala Ile Val Ala Leu Gln Tyr Val Gly Ser Gly Thr His Ala	
35 40 45	
gac aac gtc gaa ttc atc gtt ggc gac aac gca cgc ctg acc gtc atc	192
Asp Asn Val Glu Phe Ile Val Gly Asp Asn Ala Arg Leu Thr Val Ile	
50 55 60	
acg gac acc cac tgg aac gct gac gca gtt cac ctg agc aac cag ctt	240
Thr Asp Thr His Trp Asn Ala Asp Ala Val His Leu Ser Asn Gln Leu	
65 70 75 80	
gca cag ctg gga cgc gac gca act cta cgc cac acc gtg gca acc ttc	288
Ala Gln Leu Gly Arg Asp Ala Thr Leu Arg His Thr Val Ala Thr Phe	
85 90 95	
ggc gga gaa gta gtc cgc atc gtc cca cgc gtg cgt ttc acc gca cca	336
Gly Gly Glu Val Val Arg Ile Val Pro Arg Val Arg Phe Thr Ala Pro	
100 105 110	
ggc ggc gac gca gaa atg ctc ggc gtc tac ttc gca gat gat gga cag	384
Gly Gly Asp Ala Glu Met Leu Gly Val Tyr Phe Ala Asp Asp Gly Gln	
115 120 125	
tac ttc gag cag cgc ctg ctg gtt gac cac gct gta cca aac tgt cgc	432
Tyr Phe Glu Gln Arg Leu Leu Val Asp His Ala Val Pro Asn Cys Arg	
130 135 140	
tcc aac gtc ttg tac aag ggc gca ctt cag ggt gac aag aac tct gac	480
Ser Asn Val Leu Tyr Lys Gly Ala Leu Gln Gly Asp Lys Asn Ser Asp	
145 150 155 160	

aag cca gat gcc cgt acc tgc tgg gtt ggc gat gtg ctc atc cgc tca 528
Lys Pro Asp Ala Arg Thr Cys Trp Val Gly Asp Val Leu Ile Arg Ser
165 170 175

aac gcc cac ggc act gac acc tac gaa gct aac cgc tca ctc gtc ctc 576
Asn Ala His Gly Thr Asp Thr Tyr Glu Ala Asn Arg Ser Leu Val Leu
180 185 190

acc gag ggt gca cgc gca gac gct att cca aac ctc gag att gaa acc 624
Thr Glu Gly Ala Arg Ala Asp Ala Ile Pro Asn Leu Glu Ile Glu Thr
195 200 205

ggc cag atc gtt ggc gca gga cac gca gca acc gtc ggt cgt ttc gac 672
Gly Gln Ile Val Gly Ala Gly His Ala Ala Thr Val Gly Arg Phe Asp
210 215 220

gac gag cac gtg ttc tac ctc cag gcc cgt ggt att cct gca gag gaa 720
Asp Glu His Val Phe Tyr Leu Gln Ala Arg Gly Ile Pro Ala Glu Glu
225 230 235 240

gca cgc cgc ctc atc gtc cgc ggt ttc ttc aac gaa gtg atc aac aag 768
Ala Arg Arg Leu Ile Val Arg Gly Phe Phe Asn Glu Val Ile Asn Lys
245 250 255

gtc cca gtt gaa tcc atc cgc ggg gaa ttg gac aac cga gtc agc tcg 816
Val Pro Val Glu Ser Ile Arg Gly Glu Leu Asp Asn Arg Val Ser Ser
260 265 270

gaa ctc gca gtt ctt ggc atg taattaagcc aaagtaacta agc 860
Glu Leu Ala Val Leu Gly Met
275

<210> 2770

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 2770

Asn Ser His Asn Pro Thr Pro Val Thr Ile Thr Val Thr Gly Lys Gly
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Glu Gly Val Thr Ser Phe Gly Ala Ile Ser Ile Glu Val Glu Ala Gly
20 25 30

Ala Asp Ala Ile Val Ala Leu Gln Tyr Val Gly Ser Gly Thr His Ala
35 40 45

Asp Asn Val Glu Phe Ile Val Gly Asp Asn Ala Arg Leu Thr Val Ile
50 55 60

Thr Asp Thr His Trp Asn Ala Asp Ala Val His Leu Ser Asn Gln Leu
65 70 75 80

Ala Gln Leu Gly Arg Asp Ala Thr Leu Arg His Thr Val Ala Thr Phe
85 90 95

Gly Gly Glu Val Val Arg Ile Val Pro Arg Val Arg Phe Thr Ala Pro
100 105 110

Gly Gly Asp Ala Glu Met Leu Gly Val Tyr Phe Ala Asp Asp Gly Gln

115 120 125
 Tyr Phe Glu Gln Arg Leu Leu Val Asp His Ala Val Pro Asn Cys Arg
 130 135 140
 Ser Asn Val Leu Tyr Lys Gly Ala Leu Gln Gly Asp Lys Asn Ser Asp
 145 150 155 160
 Lys Pro Asp Ala Arg Thr Cys Trp Val Gly Asp Val Leu Ile Arg Ser
 165 170 175
 Asn Ala His Gly Thr Asp Thr Tyr Glu Ala Asn Arg Ser Leu Val Leu
 180 185 190
 Thr Glu Gly Ala Arg Ala Asp Ala Ile Pro Asn Leu Glu Ile Glu Thr
 195 200 205
 Gly Gln Ile Val Gly Ala Gly His Ala Ala Thr Val Gly Arg Phe Asp
 210 215 220
 Asp Glu His Val Phe Tyr Leu Gln Ala Arg Gly Ile Pro Ala Glu Glu
 225 230 235 240
 Ala Arg Arg Leu Ile Val Arg Gly Phe Phe Asn Glu Val Ile Asn Lys
 245 250 255
 Val Pro Val Glu Ser Ile Arg Gly Glu Leu Asp Asn Arg Val Ser Ser
 260 265 270
 Glu Leu Ala Val Leu Gly Met
 275

<210> 2771

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> RXA02518

<400> 2771

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gcgcacgcac attagccgc tgtattaatt ggaggaaacc atg agc gag cac acc 115
 Met Ser Glu His Thr
 1 5

gag aac acg aca gag gtt gaa gac cag aac gct tcc acc ttt gaa gca 163
 Glu Asn Thr Thr Glu Val Glu Asp Gln Asn Ala Ser Thr Phe Glu Ala
 10 15 20

caa agc tct gag cgc cca gag cag tcc gag gca gac ctg gct aag gcc 211
 Gln Ser Ser Glu Arg Pro Glu Gln Ser Glu Ala Asp Leu Ala Lys Ala
 25 30 35

agc gat gtt gag gag tac atg cgc gac gtt att gac cct gaa ctg ggc 259
 Ser Asp Val Glu Glu Tyr Met Arg Asp Val Ile Asp Pro Glu Leu Gly
 40 45 50

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att aac gtt gtt gac ctg ggc ctt gtc tac gat att tac atc atc aac 307
Ile Asn Val Val Asp Leu Gly Leu Val Tyr Asp Ile Tyr Ile Ile Asn
   55                60                65

ggc aac gaa gct cac atc gat atg act ctg act tca cca gct tgc ccg 355
Gly Asn Glu Ala His Ile Asp Met Thr Leu Thr Ser Pro Ala Cys Pro
   70                75                80                85

ctg act gac gtc atc gaa gat cag gca cgc acc gca atc gtc ggc aac 403
Leu Thr Asp Val Ile Glu Asp Gln Ala Arg Thr Ala Ile Val Gly Asn
                90                95                100

ggc att gca gag aag atg tcc ctg aac tgg gta tgg atg cca cct tgg 451
Gly Ile Ala Glu Lys Met Ser Leu Asn Trp Val Trp Met Pro Pro Trp
                105                110                115

ggt cca cac atg att acc gaa gag ggc cgc gct cag ctg cag gcc cta 499
Gly Pro His Met Ile Thr Glu Gly Arg Ala Gln Leu Gln Ala Leu
                120                125                130

gga ttc gcg gtt taaaaggctg cttatcgacg cca 534
Gly Phe Ala Val
   135

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<210> 2772

<211> 137

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2772

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Met Ser Glu His Thr Glu Asn Thr Thr Glu Val Glu Asp Gln Asn Ala
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Ser Thr Phe Glu Ala Gln Ser Ser Glu Arg Pro Glu Gln Ser Glu Ala
                20                25                30

Asp Leu Ala Lys Ala Ser Asp Val Glu Glu Tyr Met Arg Asp Val Ile
                35                40                45

Asp Pro Glu Leu Gly Ile Asn Val Val Asp Leu Gly Leu Val Tyr Asp
  50                55                60

Ile Tyr Ile Ile Asn Gly Asn Glu Ala His Ile Asp Met Thr Leu Thr
  65                70                75                80

Ser Pro Ala Cys Pro Leu Thr Asp Val Ile Glu Asp Gln Ala Arg Thr
                85                90                95

Ala Ile Val Gly Asn Gly Ile Ala Glu Lys Met Ser Leu Asn Trp Val
                100                105                110

Trp Met Pro Pro Trp Gly Pro His Met Ile Thr Glu Glu Gly Arg Ala
                115                120                125

Gln Leu Gln Ala Leu Gly Phe Ala Val
  130                135

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<210> 2773

<211> 1566

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1543)

<223> RXA02521

<400> 2773

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attgacaccc atcaaacact cctgatgaaa ggagcgggatc atg act tcg gca acg 115
                                     Met Thr Ser Ala Thr
                                     1 5
acg aac cca ggg gtt aac gag ccc ttg acc gat gac cag atc att gaa 163
Thr Asn Pro Gly Val Asn Glu Pro Leu Thr Asp Asp Gln Ile Ile Glu
          10          15          20
tcc atc ggt ccg tac aac tat ggt tgg cac gac tcc gac gac gct ggt 211
Ser Ile Gly Pro Tyr Asn Tyr Gly Trp His Asp Ser Asp Asp Ala Gly
          25          30          35
gca tcc gca cag cgt ggt ctc agc gag gat gtc gta cgc gac atc tct 259
Ala Ser Ala Gln Arg Gly Leu Ser Glu Asp Val Val Arg Asp Ile Ser
          40          45          50
gcg aag aag agc gag cca gaa tgg atg ctt cag cag cgc ctc aag gcc 307
Ala Lys Lys Ser Glu Pro Glu Trp Met Leu Gln Gln Arg Leu Lys Ala
          55          60          65
ctg agc att ttt gat aag aag cca gtt cca acc tgg ggt gca gac ctt 355
Leu Ser Ile Phe Asp Lys Lys Pro Val Pro Thr Trp Gly Ala Asp Leu
          70          75          80          85
tca ggc att gac ttc gac aac att aaa tac ttc gtc cgc tcc act gag 403
Ser Gly Ile Asp Phe Asp Asn Ile Lys Tyr Phe Val Arg Ser Thr Glu
          90          95          100
aag cag gca cag tcc tgg gag gat ctc cca gaa gac atc aag aat acc 451
Lys Gln Ala Gln Ser Trp Glu Asp Leu Pro Glu Asp Ile Lys Asn Thr
          105          110          115
tac gac aag ctg ggt att cct gag gcc gag aag cag cgc ctc gtt gca 499
Tyr Asp Lys Leu Gly Ile Pro Glu Ala Glu Lys Gln Arg Leu Val Ala
          120          125          130
ggt gtt gca gct cag tac gag tct gag gtt gtc tac cac cag atc cgc 547
Gly Val Ala Ala Gln Tyr Glu Ser Glu Val Val Tyr His Gln Ile Arg
          135          140          145
gag gac ctg gag gaa aag gga gtt atc ttc ctt gac acc gat acc gca 595
Glu Asp Leu Glu Glu Lys Gly Val Ile Phe Leu Asp Thr Asp Thr Ala
          150          155          160          165
ctg aaa gag cac cct gag atc ttc cag gag tac ttc ggc acc gtc att 643
Leu Lys Glu His Pro Glu Ile Phe Gln Glu Tyr Phe Gly Thr Val Ile
          170          175          180
cca gca ggc gac aac aag ttc tcc gca ctg aac tcc gct gtc tgg tcc 691

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Pro	Ala	Gly	Asp	Asn	Lys	Phe	Ser	Ala	Leu	Asn	Ser	Ala	Val	Trp	Ser			
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ggt	gga	tct	ttc	atc	tac	gtg	cca	aag	ggt	gtc	cac	gtg	gac	att	cct		739	
Gly	Gly	Ser	Phe	Ile	Tyr	Val	Pro	Lys	Gly	Val	His	Val	Asp	Ile	Pro			
		200					205					210						
ctg	cag	gct	tac	ttc	cgc	atc	aac	acc	gag	aac	atg	ggt	cag	ttc	gaa		787	
Leu	Gln	Ala	Tyr	Phe	Arg	Ile	Asn	Thr	Glu	Asn	Met	Gly	Gln	Phe	Glu			
	215					220					225							
cgc	acc	ctg	atc	atc	gtt	gat	gag	gat	gcc	tac	gtt	cac	tac	gtt	gag		835	
Arg	Thr	Leu	Ile	Ile	Val	Asp	Glu	Asp	Ala	Tyr	Val	His	Tyr	Val	Glu			
230					235					240					245			
ggc	tgt	acc	gca	cct	att	tac	aag	tcc	gac	tcc	ctg	cac	tcc	gca	gtc		883	
Gly	Cys	Thr	Ala	Pro	Ile	Tyr	Lys	Ser	Asp	Ser	Leu	His	Ser	Ala	Val			
				250					255					260				
gtt	gag	atc	atc	gtg	aag	aag	ggt	gga	cgc	tgc	cgc	tac	acc	acc	att		931	
Val	Glu	Ile	Ile	Val	Lys	Lys	Gly	Gly	Arg	Cys	Arg	Tyr	Thr	Thr	Ile			
			265					270						275				
cag	aac	tgg	tcc	aac	aac	gtc	tac	aac	ctg	gtg	acc	aag	cgc	acc	aag		979	
Gln	Asn	Trp	Ser	Asn	Asn	Val	Tyr	Asn	Leu	Val	Thr	Lys	Arg	Thr	Lys			
		280					285					290						
gtt	gaa	gag	ggc	ggc	acc	atg	gaa	tgg	gtc	gat	ggc	aac	atc	ggc	tcc		1027	
Val	Glu	Glu	Gly	Gly	Thr	Met	Glu	Trp	Val	Asp	Gly	Asn	Ile	Gly	Ser			
	295					300					305							
aag	gtc	acc	atg	aag	tac	cca	gct	gtc	tgg	atg	act	ggc	cca	cac	gca		1075	
Lys	Val	Thr	Met	Lys	Tyr	Pro	Ala	Val	Trp	Met	Thr	Gly	Pro	His	Ala			
310					315					320					325			
aag	ggc	gaa	gtt	ctc	tcc	gtc	gct	ttc	gca	ggt	gag	gga	cag	ttc	cag		1123	
Lys	Gly	Glu	Val	Leu	Ser	Val	Ala	Phe	Ala	Gly	Glu	Gly	Gln	Phe	Gln			
				330					335					340				
gac	acc	ggc	gcc	aag	atg	acc	cac	atg	gct	cct	tac	act	tcc	tcc	aac		1171	
Asp	Thr	Gly	Ala	Lys	Met	Thr	His	Met	Ala	Pro	Tyr	Thr	Ser	Ser	Asn			
			345					350					355					
atc	gtg	tcc	aag	tct	gtg	gca	cgt	ggc	ggt	gga	cgt	gcg	gct	tac	cgt		1219	
Ile	Val	Ser	Lys	Ser	Val	Ala	Arg	Gly	Gly	Gly	Arg	Ala	Ala	Tyr	Arg			
		360					365					370						
ggt	ctg	gtt	cag	atc	aac	gca	aac	gct	cac	cac	tca	acc	tcc	aac	gtt		1267	
Gly	Leu	Val	Gln	Ile	Asn	Ala	Asn	Ala	His	His	Ser	Thr	Ser	Ser	Val			
		375				380					385							
gag	tgt	gac	gca	ctg	ctg	gtc	gat	gac	atc	tcc	cgt	tct	gac	acc	tac		1315	
Glu	Cys	Asp	Ala	Leu	Leu	Val	Asp	Asp	Ile	Ser	Arg	Ser	Asp	Thr	Tyr			
390					395					400					405			
cca	tac	aac	gac	atc	cgt	aac	gat	cac	gtg	tca	ctc	ggc	cac	gag	gca		1363	
Pro	Tyr	Asn	Asp	Ile	Arg	Asn	Asp	His	Val	Ser	Leu	Gly	His	Glu	Ala			
				410					415					420				
act	gtt	tcc	cag	gtt	tct	gaa	gag	cag	ctg	ttc	tac	ctc	atg	agc	cgc		1411	
Thr	Val	Ser	Gln	Val	Ser	Glu	Glu	Gln	Leu	Phe	Tyr	Leu	Met	Ser	Arg			

425 430 435
 gga ctt gcg gaa gaa gaa gca atg gca atg atc gtt cgt ggc ttc gtt 1459
 Gly Leu Ala Glu Glu Glu Ala Met Ala Met Ile Val Arg Gly Phe Val
 440 445 450
 gag cca atc gct aag gaa ctc cca atg gag tac gcc ctt gag ctc aac 1507
 Glu Pro Ile Ala Lys Glu Leu Pro Met Glu Tyr Ala Leu Glu Leu Asn
 455 460 465
 cga ctg atc gaa ctg cag atg gaa gga tcg gtg ggc taagcccaat 1553
 Arg Leu Ile Glu Leu Gln Met Glu Gly Ser Val Gly
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 gactgaagta gca 1566

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 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 2774
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 Asp Gln Ile Ile Glu Ser Ile Gly Pro Tyr Asn Tyr Gly Trp His Asp
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 Ser Asp Asp Ala Gly Ala Ser Ala Gln Arg Gly Leu Ser Glu Asp Val
 35 40 45
 Val Arg Asp Ile Ser Ala Lys Lys Ser Glu Pro Glu Trp Met Leu Gln
 50 55 60
 Gln Arg Leu Lys Ala Leu Ser Ile Phe Asp Lys Lys Pro Val Pro Thr
 65 70 75 80
 Trp Gly Ala Asp Leu Ser Gly Ile Asp Phe Asp Asn Ile Lys Tyr Phe
 85 90 95
 Val Arg Ser Thr Glu Lys Gln Ala Gln Ser Trp Glu Asp Leu Pro Glu
 100 105 110
 Asp Ile Lys Asn Thr Tyr Asp Lys Leu Gly Ile Pro Glu Ala Glu Lys
 115 120 125
 Gln Arg Leu Val Ala Gly Val Ala Ala Gln Tyr Glu Ser Glu Val Val
 130 135 140
 Tyr His Gln Ile Arg Glu Asp Leu Glu Glu Lys Gly Val Ile Phe Leu
 145 150 155 160
 Asp Thr Asp Thr Ala Leu Lys Glu His Pro Glu Ile Phe Gln Glu Tyr
 165 170 175
 Phe Gly Thr Val Ile Pro Ala Gly Asp Asn Lys Phe Ser Ala Leu Asn
 180 185 190
 Ser Ala Val Trp Ser Gly Gly Ser Phe Ile Tyr Val Pro Lys Gly Val
 195 200 205

His Val Asp Ile Pro Leu Gln Ala Tyr Phe Arg Ile Asn Thr Glu Asn
 210 215 220
 Met Gly Gln Phe Glu Arg Thr Leu Ile Ile Val Asp Glu Asp Ala Tyr
 225 230 235 240
 Val His Tyr Val Glu Gly Cys Thr Ala Pro Ile Tyr Lys Ser Asp Ser
 245 250 255
 Leu His Ser Ala Val Val Glu Ile Ile Val Lys Lys Gly Gly Arg Cys
 260 265 270
 Arg Tyr Thr Thr Ile Gln Asn Trp Ser Asn Asn Val Tyr Asn Leu Val
 275 280 285
 Thr Lys Arg Thr Lys Val Glu Gly Gly Thr Met Glu Trp Val Asp
 290 295 300
 Gly Asn Ile Gly Ser Lys Val Thr Met Lys Tyr Pro Ala Val Trp Met
 305 310 315 320
 Thr Gly Pro His Ala Lys Gly Glu Val Leu Ser Val Ala Phe Ala Gly
 325 330 335
 Glu Gly Gln Phe Gln Asp Thr Gly Ala Lys Met Thr His Met Ala Pro
 340 345 350
 Tyr Thr Ser Ser Asn Ile Val Ser Lys Ser Val Ala Arg Gly Gly Gly
 355 360 365
 Arg Ala Ala Tyr Arg Gly Leu Val Gln Ile Asn Ala Asn Ala His His
 370 375 380
 Ser Thr Ser Asn Val Glu Cys Asp Ala Leu Leu Val Asp Asp Ile Ser
 385 390 395 400
 Arg Ser Asp Thr Tyr Pro Tyr Asn Asp Ile Arg Asn Asp His Val Ser
 405 410 415
 Leu Gly His Glu Ala Thr Val Ser Gln Val Ser Glu Glu Gln Leu Phe
 420 425 430
 Tyr Leu Met Ser Arg Gly Leu Ala Glu Glu Glu Ala Met Ala Met Ile
 435 440 445
 Val Arg Gly Phe Val Glu Pro Ile Ala Lys Glu Leu Pro Met Glu Tyr
 450 455 460
 Ala Leu Glu Leu Asn Arg Leu Ile Glu Leu Gln Met Glu Gly Ser Val
 465 470 475 480
 Gly

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<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXA02524

<400> 2775

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tctctgatcc caccgacctc aaagtattgg gactggacaa atg aca gag acc aca 115
                                         Met Thr Glu Thr Thr
                                         1           5

cct caa ccc cca aag cca gag ccc gag ctc ccg aaa ttt ctc agc aac 163
Pro Gln Pro Pro Lys Pro Glu Pro Glu Leu Pro Lys Phe Leu Ser Asn
                        10                        15                        20

cca gaa cgc gcc gac atc att ttg ttc atc gca ctc att gtg atg ggc 211
Pro Glu Arg Ala Asp Ile Ile Leu Phe Ile Ala Leu Ile Val Met Gly
                        25                        30                        35

att ttc tcc ctc tgc atg atc cca ctg cgc gcc tgg atg ctc acc caa 259
Ile Phe Ser Leu Cys Met Ile Pro Leu Arg Ala Trp Met Leu Thr Gln
                        40                        45                        50

cct ctg gcc tac acc ctc atc gtc ggt ggt tac acc agt gca gtc gtg 307
Pro Leu Ala Tyr Thr Leu Ile Val Gly Gly Tyr Thr Ser Ala Val Val
                        55                        60                        65

ggc ggc gcg aac gct tcg gta gaa aac ggc atc tgg tgg gtc tac tgg 355
Gly Gly Ala Asn Ala Ser Val Glu Asn Gly Ile Trp Trp Val Tyr Trp
70                        75                        80                        85

ctc tgc acc ctg atc ggc gcg ctg aag ttc atg ccc gtc tat tgg ctg 403
Leu Cys Thr Leu Ile Gly Ala Leu Lys Phe Met Pro Val Tyr Trp Leu
                        90                        95                        100

atg ggt aag cgc tgg ggc atg gaa ttt atc gac atg tcc ctc caa tac 451
Met Gly Lys Arg Trp Gly Met Glu Phe Ile Asp Met Ser Leu Gln Tyr
                        105                        110                        115

atg ccc cgc ttc cac cgc atg ttc aaa aaa tcc gtc gac tcc gaa tcc 499
Met Pro Arg Phe His Arg Met Phe Lys Lys Ser Val Asp Ser Glu Ser
                        120                        125                        130

acc cgc ctc tac gcc tgg atc atc ggc ctc att cca ctc gca tac ctc 547
Thr Arg Leu Tyr Ala Trp Ile Ile Gly Leu Ile Pro Leu Ala Tyr Leu
                        135                        140                        145

cca gga cca gtg ccg gga acc atc ctt aac gca gtg gct ggg ctg gtg 595
Pro Gly Pro Val Pro Gly Thr Ile Leu Asn Ala Val Ala Gly Leu Val
150                        155                        160                        165

aaa atc ccc ttc tgg atc atc atg gcc tgg aat gcg atc tgc gta cta 643
Lys Ile Pro Phe Trp Ile Ile Met Ala Trp Asn Ala Ile Cys Val Leu
                        170                        175                        180

tcg gtc aac gga cta ttc atg tgg ctg gga tac acc ttc ggc gaa caa 691
Ser Val Asn Gly Leu Phe Met Trp Leu Gly Tyr Thr Phe Gly Glu Gln
                        185                        190                        195

gtc ctc gac atc gtc aac gtg gtc aac cgc tac atg ctt tgg ata acc 739

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Val Leu Asp Ile Val Asn Val Val Asn Arg Tyr Met Leu Trp Ile Thr
 200 205 210

tta gga ttg ctg gcg ctg atg ttt ttc cgc gca cgg aag caa ttt gcc 787
 Leu Gly Leu Leu Ala Leu Met Phe Phe Arg Ala Arg Lys Gln Phe Ala
 215 220 225

aag taaatggttg aaaggaatat gac 813
 Lys
 230

<210> 2776

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 2776

Met Thr Glu Thr Thr Pro Gln Pro Pro Lys Pro Glu Pro Glu Leu Pro
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Lys Phe Leu Ser Asn Pro Glu Arg Ala Asp Ile Ile Leu Phe Ile Ala
 20 25 30

Leu Ile Val Met Gly Ile Phe Ser Leu Cys Met Ile Pro Leu Arg Ala
 35 40 45

Trp Met Leu Thr Gln Pro Leu Ala Tyr Thr Leu Ile Val Gly Gly Tyr
 50 55 60

Thr Ser Ala Val Val Gly Gly Ala Asn Ala Ser Val Glu Asn Gly Ile
 65 70 75 80

Trp Trp Val Tyr Trp Leu Cys Thr Leu Ile Gly Ala Leu Lys Phe Met
 85 90 95

Pro Val Tyr Trp Leu Met Gly Lys Arg Trp Gly Met Glu Phe Ile Asp
 100 105 110

Met Ser Leu Gln Tyr Met Pro Arg Phe His Arg Met Phe Lys Lys Ser
 115 120 125

Val Asp Ser Glu Ser Thr Arg Leu Tyr Ala Trp Ile Ile Gly Leu Ile
 130 135 140

Pro Leu Ala Tyr Leu Pro Gly Pro Val Pro Gly Thr Ile Leu Asn Ala
 145 150 155 160

Val Ala Gly Leu Val Lys Ile Pro Phe Trp Ile Ile Met Ala Trp Asn
 165 170 175

Ala Ile Cys Val Leu Ser Val Asn Gly Leu Phe Met Trp Leu Gly Tyr
 180 185 190

Thr Phe Gly Glu Gln Val Leu Asp Ile Val Asn Val Val Asn Arg Tyr
 195 200 205

Met Leu Trp Ile Thr Leu Gly Leu Leu Ala Leu Met Phe Phe Arg Ala
 210 215 220

Arg Lys Gln Phe Ala Lys

225

230

<210> 2777

<211> 501

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXA02525

<400> 2777

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cgcacggaag caatttgcca agtaaattggt tgaaaggaat atg acc acc atg cga 115
Met Thr Thr Met Arg
1 5

gaa gtt tca acc gac ctc aac atc ctc atc gtc ccc agc gaa tgg gaa 163
Glu Val Ser Thr Asp Leu Asn Ile Leu Ile Val Pro Ser Glu Trp Glu
10 15 20

aaa gta cta gaa aac cta cca gcg aca ttg agt gag tcc gga ttc gta 211
Lys Val Leu Glu Asn Leu Pro Ala Thr Leu Ser Glu Ser Gly Phe Val
25 30 35

gcc tct gaa atc cac tcc cag atc gtc gac ctc acc tgc gaa ccc gac 259
Ala Ser Glu Ile His Ser Gln Ile Val Asp Leu Thr Cys Glu Pro Asp
40 45 50

aac atg ctt gtc acc cag ttc tcc cag cta gag ggc cac cca cca att 307
Asn Met Leu Val Thr Gln Phe Ser Gln Leu Glu Gly His Pro Pro Ile
55 60 65

gtg gaa gtg ctc cac cgc cta gta att aac ggc tcc tcc gac ctg gag 355
Val Glu Val Leu His Arg Leu Val Ile Asn Gly Ser Ser Asp Leu Glu
70 75 80 85

ctt aaa gac ctc acc aaa aag gtg gtg ggg gcg ttg cct cag ggg acc 403
Leu Lys Asp Leu Thr Lys Lys Val Val Gly Ala Leu Pro Gln Gly Thr
90 95 100

tac tgg tat gga act tcc ctt gaa ggt gcg acc gaa cct ggc gtt aac 451
Tyr Trp Tyr Gly Thr Ser Leu Glu Gly Ala Thr Glu Pro Gly Val Asn
105 110 115

gca tca tgc gcg tgg cag cat cgg ggc tagttttccg cgtttagtca 498
Ala Ser Cys Ala Trp Gln His Arg Gly
120 125

gtt 501

<210> 2778

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 2778

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 20 25 30
 Glu Ser Gly Phe Val Ala Ser Glu Ile His Ser Gln Ile Val Asp Leu
 35 40 45
 Thr Cys Glu Pro Asp Asn Met Leu Val Thr Gln Phe Ser Gln Leu Glu
 50 55 60
 Gly His Pro Pro Ile Val Glu Val Leu His Arg Leu Val Ile Asn Gly
 65 70 75 80
 Ser Ser Asp Leu Glu Leu Lys Asp Leu Thr Lys Lys Val Val Gly Ala
 85 90 95
 Leu Pro Gln Gly Thr Tyr Trp Tyr Gly Thr Ser Leu Glu Gly Ala Thr
 100 105 110
 Glu Pro Gly Val Asn Ala Ser Cys Ala Trp Gln His Arg Gly
 115 120 125

<210> 2779

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> RXA02540

<400> 2779

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aaccgctaga cggttctcttt gagaaaggag gtgacgaaac atg gca tcc aca ccg 115
 Met Ala Ser Thr Pro
 1 5

aaa aaa tcc aac gat gaa ggt cag ttt gac cgt gtc gat ttt caa ggg 163
 Lys Lys Ser Asn Asp Glu Gly Gln Phe Asp Arg Val Asp Phe Gln Gly
 10 15 20

gaa gtc ttc gtt atc tct gtc gca gcc gag ctt gcc ggc atg cat gcc 211
 Glu Val Phe Val Ile Ser Val Ala Ala Glu Leu Ala Gly Met His Ala
 25 30 35

caa act ttg cga acc tac gat cgc atg ggt ttg gtc acc ccg ata cgc 259
 Gln Thr Leu Arg Thr Tyr Asp Arg Met Gly Leu Val Thr Pro Ile Arg
 40 45 50

act cgc gga ggc ggt cgc cgt tac tcc cgc gct gac gtg gaa tta ctc 307
 Thr Arg Gly Gly Gly Arg Arg Tyr Ser Arg Ala Asp Val Glu Leu Leu
 55 60 65

cga gaa att cag cac ctc agc cag gag gaa ggc gta aac ctc gcc gga 355
 Arg Glu Ile Gln His Leu Ser Gln Glu Glu Gly Val Asn Leu Ala Gly
 70 75 80 85

atc aag gcg atc atc gag ctc ggc gaa gaa aac cga aac ctc aaa gaa 403
 Ile Lys Ala Ile Ile Glu Leu Gly Glu Glu Asn Arg Asn Leu Lys Glu
 90 95 100

tcc ctg cgt aag gtc aca gct gag aat gag cag ctc aaa gat caa tta 451
 Ser Leu Arg Lys Val Thr Ala Glu Asn Glu Gln Leu Lys Asp Gln Leu
 105 110 115

cgc agc ggg cgt ccg cgt ggc gag ctg gtg cac gtg ccc cgc tcc acc 499
 Arg Ser Gly Arg Pro Arg Gly Glu Leu Val His Val Pro Arg Ser Thr
 120 125 130

gcg gtg gtc atg tgg gaa cgc cgc aag ggg cgt tcc aag taaaaacatg 548
 Ala Val Val Met Trp Glu Arg Arg Lys Gly Arg Ser Lys
 135 140 145

cttgctgacg cca 561

<210> 2780

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 2780

Met Ala Ser Thr Pro Lys Lys Ser Asn Asp Glu Gly Gln Phe Asp Arg
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Val Asp Phe Gln Gly Glu Val Phe Val Ile Ser Val Ala Ala Glu Leu
 20 25 30

Ala Gly Met His Ala Gln Thr Leu Arg Thr Tyr Asp Arg Met Gly Leu
 35 40 45

Val Thr Pro Ile Arg Thr Arg Gly Gly Gly Arg Arg Tyr Ser Arg Ala
 50 55 60

Asp Val Glu Leu Leu Arg Glu Ile Gln His Leu Ser Gln Glu Glu Gly
 65 70 75 80

Val Asn Leu Ala Gly Ile Lys Ala Ile Ile Glu Leu Gly Glu Glu Asn
 85 90 95

Arg Asn Leu Lys Glu Ser Leu Arg Lys Val Thr Ala Glu Asn Glu Gln
 100 105 110

Leu Lys Asp Gln Leu Arg Ser Gly Arg Pro Arg Gly Glu Leu Val His
 115 120 125

Val Pro Arg Ser Thr Ala Val Val Met Trp Glu Arg Arg Lys Gly Arg
 130 135 140

Ser Lys
 145

<210> 2781

<211> 1551

<212> DNA

<213> Corynebacterium glutamicum

<223> RXA02544

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ggc ata gtg att ttt gtg agc aca gaa tca gga aac acc cca aaa agg 163
Gly Ile Val Ile Phe Val Ser Thr Glu Ser Gly Asn Thr Pro Lys Arg
10 15 20

gat gat gca aaa agc acc atc cct ccg aaa gat ttg cct gac acc gtc 211
Asp Asp Ala Lys Ser Thr Ile Pro Pro Lys Asp Leu Pro Asp Thr Val
25 30 35

tta gac gcg att gaa ggc aat ttt gag cca ccg cta aat acc cag aag 259
Leu Asp Ala Ile Glu Gly Asn Phe Glu Pro Pro Leu Asn Thr Gln Lys
40 45 50

tcg gcg gtt ccc cct aat gcc gaa gca act gtc gag gct gat tct gaa 307
Ser Ala Val Pro Pro Asn Ala Glu Ala Thr Val Glu Ala Asp Ser Glu
55 60 65

gga act acc gac cgc tct gtc att ttg ggc agg gac ggc cgc tgg ctg 355
Gly Thr Thr Asp Arg Ser Val Ile Leu Gly Arg Asp Gly Arg Trp Leu
70 75 80 85

tcc gga tgg gca ttg cgc ttc atc gtg ctg gtt atc gcc ggc gtc att 403
Ser Gly Trp Ala Leu Arg Phe Ile Val Leu Val Ile Ala Gly Val Ile
90 95 100

gca ctt cgt atg ctg ggc ttc atc tgg gtt ggc atc ctc cca gtc gtc 451
Ala Leu Arg Met Leu Gly Phe Ile Trp Val Gly Ile Leu Pro Val Val
105 110 115

ctc gca ctt cta gtc tgc acc gtg cta tgg cca cca gtg aaa tgg ctg 499
Leu Ala Leu Leu Val Cys Thr Val Leu Trp Pro Pro Val Lys Trp Leu
120 125 130

cgc gag cat aag att ccc acg gcg ctc gcc gtt gtc atc aca att ttg 547
Arg Glu His Lys Ile Pro Thr Ala Leu Ala Val Val Ile Thr Ile Leu
135 140 145

ggt ttc ttc gcc ctc atc ggc gga gtt ttt gca gcc atc gcg cca agc 595
Gly Phe Phe Ala Leu Ile Gly Gly Val Phe Ala Ala Ile Ala Pro Ser
150 155 160 165

gtg tct tcc cag aca aag caa gtg gta gac caa gca act gtt ggt atc 643
Val Ser Ser Gln Thr Lys Gln Val Val Asp Gln Ala Thr Val Gly Ile
170 175 180

gaa gat cta atg gat tgg gtt cag ggc cca cct ttt aac tta gat atc 691
Glu Asp Leu Met Asp Trp Val Gln Gly Pro Pro Phe Asn Leu Asp Ile
185 190 195

tca cag ttt gaa ggc gcg ctc aat gac cta aca tcc atg ctg caa tca	739
Ser Gln Phe Glu Gly Ala Leu Asn Asp Leu Thr Ser Met Leu Gln Ser	
200 205 210	
cag tct tcc acc att gct tct ggt gtg ttc tct gga ctg tca acg gca	787
Gln Ser Ser Thr Ile Ala Ser Gly Val Phe Ser Gly Leu Ser Thr Ala	
215 220 225	
tca tcc atc gtt gtc aca cta gca gtg atg ctg gtg ttg acc ttc ttc	835
Ser Ser Ile Val Val Thr Leu Ala Val Met Leu Val Leu Thr Phe Phe	
230 235 240 245	
ttc ctc aaa gac ggt cct cgt ttc ctg cca tgg atg cgc ggc ttc act	883
Phe Leu Lys Asp Gly Pro Arg Phe Leu Pro Trp Met Arg Gly Phe Thr	
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Gly Glu Asn Ala Gly Trp His Leu Thr Glu Val Leu Thr Arg Thr Trp	
265 270 275	
aat acc ttg gcc gga ttc atc cgt gct cag gca ttg gtg tcc atg gtt	979
Asn Thr Leu Ala Gly Phe Ile Arg Ala Gln Ala Leu Val Ser Met Val	
280 285 290	
gac gca ata ttc att ggt atc gga ttg ctg ctt ctt ggc gtc cca atg	1027
Asp Ala Ile Phe Ile Gly Ile Gly Leu Leu Leu Leu Gly Val Pro Met	
295 300 305	
gcc ctc gcg ctc gcg gtc atc aca ttc ttc gcg ggc ttc atc ccc atc	1075
Ala Leu Ala Leu Ala Val Ile Thr Phe Phe Ala Gly Phe Ile Pro Ile	
310 315 320 325	
gtc ggt gcg gtg tct gca ggc gcc ctg gct gtc atc atc gcg cta gtt	1123
Val Gly Ala Val Ser Ala Gly Ala Leu Ala Val Ile Ile Ala Leu Val	
330 335 340	
acc aac ggc gtg acc aat gcg ctt ttg gta ctt gta ttg atc ctg gcg	1171
Thr Asn Gly Val Thr Asn Ala Leu Leu Val Leu Val Leu Ile Leu Ala	
345 350 355	
gtt cag cag atc gag ggc aat atc ttg tcc cca ttc ctg cag tcc aag	1219
Val Gln Gln Ile Glu Gly Asn Ile Leu Ser Pro Phe Leu Gln Ser Lys	
360 365 370	
gct atg aac ctg cac gca gcg gtt gtt ttg cta tcc gtc acc gtc ggc	1267
Ala Met Asn Leu His Ala Ala Val Val Leu Leu Ser Val Thr Val Gly	
375 380 385	
tcc acc atg ttc ggc atc atc ggc gca ttc ttg gct gtt cca gta gcc	1315
Ser Thr Met Phe Gly Ile Ile Gly Ala Phe Leu Ala Val Pro Val Ala	
390 395 400 405	
gcg acg ttg gct gtc tgg gtg cgc tac cac tct gaa atg gtt gct ttg	1363
Ala Thr Leu Ala Val Trp Val Arg Tyr His Ser Glu Met Val Ala Leu	
410 415 420	
cgc gcc ggt gag atc acc agt gat gac att gag atc gcc acg acg aaa	1411
Arg Ala Gly Glu Ile Thr Ser Asp Asp Ile Glu Ile Ala Thr Thr Lys	
425 430 435	
ggt tcc cca acc agc ctc aat ggc caa gaa acc ctt gct gcc att cga	1459

Gly Ser Pro Thr Ser Leu Asn Gly Gln Glu Thr Leu Ala Ala Ile Arg
 440 445 450

agc aga ttc gcc atc ctt ggc cgc aag aag ccg aca tct gcc act gca 1507
 Ser Arg Phe Ala Ile Leu Gly Arg Lys Lys Pro Thr Ser Ala Thr Ala
 455 460 465

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<210> 2782

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 2782

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Asn Thr Pro Lys Arg Asp Asp Ala Lys Ser Thr Ile Pro Pro Lys Asp
 20 25 30

Leu Pro Asp Thr Val Leu Asp Ala Ile Glu Gly Asn Phe Glu Pro Pro
 35 40 45

Leu Asn Thr Gln Lys Ser Ala Val Pro Pro Asn Ala Glu Ala Thr Val
 50 55 60

Glu Ala Asp Ser Glu Gly Thr Thr Asp Arg Ser Val Ile Leu Gly Arg
 65 70 75 80

Asp Gly Arg Trp Leu Ser Gly Trp Ala Leu Arg Phe Ile Val Leu Val
 85 90 95

Ile Ala Gly Val Ile Ala Leu Arg Met Leu Gly Phe Ile Trp Val Gly
 100 105 110

Ile Leu Pro Val Val Leu Ala Leu Leu Val Cys Thr Val Leu Trp Pro
 115 120 125

Pro Val Lys Trp Leu Arg Glu His Lys Ile Pro Thr Ala Leu Ala Val
 130 135 140

Val Ile Thr Ile Leu Gly Phe Phe Ala Leu Ile Gly Gly Val Phe Ala
 145 150 155 160

Ala Ile Ala Pro Ser Val Ser Ser Gln Thr Lys Gln Val Val Asp Gln
 165 170 175

Ala Thr Val Gly Ile Glu Asp Leu Met Asp Trp Val Gln Gly Pro Pro
 180 185 190

Phe Asn Leu Asp Ile Ser Gln Phe Glu Gly Ala Leu Asn Asp Leu Thr
 195 200 205

Ser Met Leu Gln Ser Gln Ser Ser Thr Ile Ala Ser Gly Val Phe Ser
 210 215 220

Gly Leu Ser Thr Ala Ser Ser Ile Val Val Thr Leu Ala Val Met Leu

ctcagcctgt aacctcttgg tcgttctatg cttgggtcacc atg act gag act ctt 115
Met Thr Glu Thr Leu
1 5

ttt gta tcc gcc aca act gag gaa gcg gtg tat ctt cca gat gga atc 163
Phe Val Ser Ala Thr Thr Glu Glu Ala Val Tyr Leu Pro Asp Gly Ile
10 15 20

gac ttg ctg gtg act ggc atc gga acg acc gca gca acg atg att ttg 211
Asp Leu Leu Val Thr Gly Ile Gly Thr Thr Ala Ala Thr Met Ile Leu
25 30 35

act aag gag ttg gct act cgg gag gtg ctt cct gcc cga att gtc aat 259
Thr Lys Glu Leu Ala Thr Arg Glu Val Leu Pro Ala Arg Ile Val Asn
40 45 50

att ggt acg gcg gga gct ttg gtg gat gga ttg gct ggc gta tac gag 307
Ile Gly Thr Ala Gly Ala Leu Val Asp Gly Leu Ala Gly Val Tyr Glu
55 60 65

atc gaa tac gtt ctg cag cat gat ttc agt agc gag tta atc gct gaa 355
Ile Glu Tyr Val Leu Gln His Asp Phe Ser Ser Glu Leu Ile Ala Glu
70 75 80 85

atg aca gga aag cca tgc tca aat ggt tca act ttg gcc acg agt ggg 403
Met Thr Gly Lys Pro Cys Ser Asn Gly Ser Thr Leu Ala Thr Ser Gly
90 95 100

cac ttc cca gta gcg agt ttg gca aca gga aac tca ttt att gca gat 451
His Phe Pro Val Ala Ser Leu Ala Thr Gly Asn Ser Phe Ile Ala Asp
105 110 115

tca gaa acc cgc aac cac ctg gcc acc cgg gcc tcc ctc tgc gat atg 499
Ser Glu Thr Arg Asn His Leu Ala Thr Arg Ala Ser Leu Cys Asp Met
120 125 130

gag ggc gcg gcg ctg gtg ggc gtc gca aag cat ttt ggt gtt ccg att 547
Glu Gly Ala Ala Leu Val Gly Val Ala Lys His Phe Gly Val Pro Ile
135 140 145

acg ctg ctg aag cag gtt agt gac agc gcg gat gag gag gct tcg ggg 595
Thr Leu Leu Lys Gln Val Ser Asp Ser Ala Asp Glu Glu Ala Ser Gly
150 155 160 165

tcg tgg ttt gat gcg gtc gat gcg ggc gca cga cag ttg gcg gag gct 643
Ser Trp Phe Asp Ala Val Asp Ala Gly Ala Arg Gln Leu Ala Glu Ala
170 175 180

gtg aag gag ttt aaa taacaaaaaac ccgatgcctg gcg 681
Val Lys Glu Phe Lys
185

<210> 2784

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 2784

Met Thr Glu Thr Leu Phe Val Ser Ala Thr Thr Glu Glu Ala Val Tyr
1 5 10 15

Leu Pro Asp Gly Ile Asp Leu Leu Val Thr Gly Ile Gly Thr Thr Ala
 20 25 30
 Ala Thr Met Ile Leu Thr Lys Glu Leu Ala Thr Arg Glu Val Leu Pro
 35 40 45
 Ala Arg Ile Val Asn Ile Gly Thr Ala Gly Ala Leu Val Asp Gly Leu
 50 55 60
 Ala Gly Val Tyr Glu Ile Glu Tyr Val Leu Gln His Asp Phe Ser Ser
 65 70 75 80
 Glu Leu Ile Ala Glu Met Thr Gly Lys Pro Cys Ser Asn Gly Ser Thr
 85 90 95
 Leu Ala Thr Ser Gly His Phe Pro Val Ala Ser Leu Ala Thr Gly Asn
 100 105 110
 Ser Phe Ile Ala Asp Ser Glu Thr Arg Asn His Leu Ala Thr Arg Ala
 115 120 125
 Ser Leu Cys Asp Met Glu Gly Ala Ala Leu Val Gly Val Ala Lys His
 130 135 140
 Phe Gly Val Pro Ile Thr Leu Leu Lys Gln Val Ser Asp Ser Ala Asp
 145 150 155 160
 Glu Glu Ala Ser Gly Ser Trp Phe Asp Ala Val Asp Ala Gly Ala Arg
 165 170 175
 Gln Leu Ala Glu Ala Val Lys Glu Phe Lys
 180 185

<210> 2785

<211> 1227

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1204)

<223> RXA02546

<400> 2785

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attcagggca attccagttt ctctaggatc gagaaataac atg cca ttg ttt atc 115
 Met Pro Leu Phe Ile
 1 5

gac gac gcc ctc cac cgc agc aaa aaa tac ttc cac gcg cac tta agc 163
 Asp Asp Ala Leu His Arg Ser Lys Lys Tyr Phe His Ala His Leu Ser
 10 15 20

gag ctg ctc ctc ggc gaa ttt gca ggc ctc agc ctg ccc ctg cac cca 211
 Glu Leu Leu Leu Gly Glu Phe Ala Gly Leu Ser Leu Pro Leu His Pro
 25 30 35

ccg acg gca gct aaa gcc gcc gcc gat att gat gcc acg agg gaa ttt 259

Pro Thr Ala Ala Lys Ala Ala Ala Asp Ile Asp Ala Thr Arg Glu Phe	
40 45 50	
atc cgc caa tgg gag ggg cgt gat gat gtg gaa tat gcc att cga aac	307
Ile Arg Gln Trp Glu Gly Arg Asp Asp Val Glu Tyr Ala Ile Arg Asn	
55 60 65	
tgg tct cct gtg ggc tta ggt aaa act gaa gta ccc gtt agg ctg acg	355
Trp Ser Pro Val Gly Leu Gly Lys Thr Glu Val Pro Val Arg Leu Thr	
70 75 80 85	
ttg aac acg act gag gaa tta gtt gtg ttt gcg cag gta gag gat gaa	403
Leu Asn Thr Thr Glu Glu Leu Val Val Phe Ala Gln Val Glu Asp Glu	
90 95 100	
tgg tct tca ctt cac gag agg ttt tca cag ctg tct ggt ttt aca gcg	451
Trp Ser Ser Leu His Glu Arg Phe Ser Gln Leu Ser Gly Phe Thr Ala	
105 110 115	
gag gtg gtg gcg aaa cat gtg tgc ctg tgg cgt tgc ctg tct aac gat	499
Glu Val Val Ala Lys His Val Ser Leu Trp Arg Ser Leu Ser Asn Asp	
120 125 130	
gat ctc tct aag gca gtg tta gtt gtg gat tgg ttt ttg aaa cac cct	547
Asp Leu Ser Lys Ala Val Leu Val Val Asp Trp Phe Leu Lys His Pro	
135 140 145	
aac tct ggc ctg ctg aaa cgc gcc gtc gca gtt gaa ggc gtg cat acc	595
Asn Ser Gly Leu Leu Lys Arg Ala Val Ala Val Glu Gly Val His Thr	
150 155 160 165	
aaa tgg ctc gaa aac cac cgc gta ctc att gaa acg tta gtg gcc gac	643
Lys Trp Leu Glu Asn His Arg Val Leu Ile Glu Thr Leu Val Ala Asp	
170 175 180	
aaa cgt ggt gaa cct ggt cgt gcc gat ctt gga ctt ggt gac gcc gaa	691
Lys Arg Gly Glu Pro Gly Arg Ala Asp Leu Gly Leu Gly Asp Ala Glu	
185 190 195	
gct cgc gtc cgg ctc cgc ttc cat tcc gta gat gct ccc gct ggg ctc	739
Ala Arg Val Arg Leu Arg Phe His Ser Val Asp Ala Pro Ala Gly Leu	
200 205 210	
aca gac att gaa gta ccg ctt tcc aac ctg tgt gaa tta caa gaa ccg	787
Thr Asp Ile Glu Val Pro Leu Ser Asn Leu Cys Glu Leu Gln Glu Pro	
215 220 225	
caa gta att ctg atg gtg gaa aac ctc gat tca ttt ctc gct tta ccc	835
Gln Val Ile Leu Met Val Glu Asn Leu Asp Ser Phe Leu Ala Leu Pro	
230 235 240 245	
act tgg ccg ggc gta aca att gct tgg ggt gcg ggc tac cgt gca gta	883
Thr Trp Pro Gly Val Thr Ile Ala Trp Gly Ala Gly Tyr Arg Ala Val	
250 255 260	
gac att gtt cga gga ccc tac ttt tct aat ggt cgg ttg ctg tac tgg	931
Asp Ile Val Arg Gly Pro Tyr Phe Ser Asn Gly Arg Leu Leu Tyr Trp	
265 270 275	
ggt gac ctt gac ctg gac ggt ttc aaa att ctc gac ggc gtc cgc agc	979
Gly Asp Leu Asp Leu Asp Gly Phe Lys Ile Leu Asp Gly Val Arg Ser	

280	285	290	
cat gtt cct cac acc gaa tcc gtg ctg atg aac tct gaa acc gtc tcc			1027
His Val Pro His Thr Glu Ser Val Leu Met Asn Ser Glu Thr Val Ser			
295	300	305	
cgc tgg cgc tac ctt ggc gtt gcc gac cga gaa ttc aag gca gag agc			1075
Arg Trp Arg Tyr Leu Gly Val Ala Asp Arg Glu Phe Lys Ala Glu Ser			
310	315	320	325
ttt gac aac ctt cat gat ttt gaa tct gac gca ctt gac cta ctc att			1123
Phe Asp Asn Leu His Asp Phe Glu Ser Asp Ala Leu Asp Leu Leu Ile			
330	335		340
aca gac ggt gag ctc cgc att gaa caa gaa cgc atc cgc ctc gat gtt			1171
Thr Asp Gly Glu Leu Arg Ile Glu Gln Glu Arg Ile Arg Leu Asp Val			
345	350		355
gct gtt gaa gaa atc gag aaa gta att cgt ggg tgaagttggt tcagagttgt			1224
Ala Val Glu Glu Ile Glu Lys Val Ile Arg Gly			
360	365		
ttt			1227

<210> 2786

<211> 368

<212> PRT

<213> Corynebacterium glutamicum

<400> 2786

Met	Pro	Leu	Phe	Ile	Asp	Asp	Ala	Leu	His	Arg	Ser	Lys	Lys	Tyr	Phe
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His	Ala	His	Leu	Ser	Glu	Leu	Leu	Leu	Gly	Glu	Phe	Ala	Gly	Leu	Ser
			20					25					30		

Leu	Pro	Leu	His	Pro	Pro	Thr	Ala	Ala	Lys	Ala	Ala	Ala	Asp	Ile	Asp
		35					40					45			

Ala	Thr	Arg	Glu	Phe	Ile	Arg	Gln	Trp	Glu	Gly	Arg	Asp	Asp	Val	Glu
	50					55					60				

Tyr	Ala	Ile	Arg	Asn	Trp	Ser	Pro	Val	Gly	Leu	Gly	Lys	Thr	Glu	Val
65					70					75					80

Pro	Val	Arg	Leu	Thr	Leu	Asn	Thr	Thr	Glu	Glu	Leu	Val	Val	Phe	Ala
				85					90					95	

Gln	Val	Glu	Asp	Glu	Trp	Ser	Ser	Leu	His	Glu	Arg	Phe	Ser	Gln	Leu
			100					105					110		

Ser	Gly	Phe	Thr	Ala	Glu	Val	Val	Ala	Lys	His	Val	Ser	Leu	Trp	Arg
	115						120					125			

Ser	Leu	Ser	Asn	Asp	Asp	Leu	Ser	Lys	Ala	Val	Leu	Val	Val	Asp	Trp
	130					135					140				

Phe	Leu	Lys	His	Pro	Asn	Ser	Gly	Leu	Leu	Lys	Arg	Ala	Val	Ala	Val
145					150					155					160

Glu Gly Val His Thr Lys Trp Leu Glu Asn His Arg Val Leu Ile Glu
 165 170 175
 Thr Leu Val Ala Asp Lys Arg Gly Glu Pro Gly Arg Ala Asp Leu Gly
 180 185 190
 Leu Gly Asp Ala Glu Ala Arg Val Arg Leu Arg Phe His Ser Val Asp
 195 200 205
 Ala Pro Ala Gly Leu Thr Asp Ile Glu Val Pro Leu Ser Asn Leu Cys
 210 215 220
 Glu Leu Gln Glu Pro Gln Val Ile Leu Met Val Glu Asn Leu Asp Ser
 225 230 235 240
 Phe Leu Ala Leu Pro Thr Trp Pro Gly Val Thr Ile Ala Trp Gly Ala
 245 250 255
 Gly Tyr Arg Ala Val Asp Ile Val Arg Gly Pro Tyr Phe Ser Asn Gly
 260 265 270
 Arg Leu Leu Tyr Trp Gly Asp Leu Asp Leu Asp Gly Phe Lys Ile Leu
 275 280 285
 Asp Gly Val Arg Ser His Val Pro His Thr Glu Ser Val Leu Met Asn
 290 295 300
 Ser Glu Thr Val Ser Arg Trp Arg Tyr Leu Gly Val Ala Asp Arg Glu
 305 310 315 320
 Phe Lys Ala Glu Ser Phe Asp Asn Leu His Asp Phe Glu Ser Asp Ala
 325 330 335
 Leu Asp Leu Leu Ile Thr Asp Gly Glu Leu Arg Ile Glu Gln Glu Arg
 340 345 350
 Ile Arg Leu Asp Val Ala Val Glu Glu Ile Glu Lys Val Ile Arg Gly
 355 360 365

<210> 2787

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1326)

<223> RXA02549

<400> 2787

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 Thr Leu Thr Ala Ile Ser Ser Glu Thr Trp Pro Ile Met Leu Ala Pro
 1 5 10 15
 tgg gta tgt ctg cct ctg ctt tcg cga aat gtg gat gca cgg gcc atc 96
 Trp Val Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile
 20 25 30
 gcg ttg tcc tta ctt ccc gcg gca tgc atg ggt gca gtt aat gcc acc 144
 Ala Leu Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr

35	40	45	
gcc acg atg gca gca ctc atc ccg gca gcg ctg atc ttg ctg tat aga Ala Thr Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg 50 55 60			192
ggg ctc ttc tta agg ctg ctt ctg tgg gga atg ggc gtt ctc gct gtt Gly Leu Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val 65 70 75 80			240
aat tca tgg tgg atc gga cct ttg ttg gtg ctt ggc aaa tac gcc ccg Asn Ser Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro 85 90 95			288
ccc ttc acc gaa ttc atc gaa agt tcc tcc gtc acc act tcc tgg ctc Pro Phe Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu 100 105 110			336
aac cca gta gaa ata ctc cgc gga acc acc agt tgg aca ccc ttc gta Asn Pro Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val 115 120 125			384
gac act gaa cga caa gcc gga tat ctc ctg gtc aac gat gct ctc ttt Asp Thr Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe 130 135 140			432
gtc acc ctc agc gtt ctc gtc gca gcc ctc ggc ttg atc ggc ctc acc Val Thr Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr 145 150 155 160			480
ttg atg aaa cac cgt gga ctg tgg gca ttc atg ctg gcc atc gga ctc Leu Met Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu 165 170 175			528
ctc atc ctc ggc agc gcc cac cta acg gct gtt caa gaa ttc ctc gac Leu Ile Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp 180 185 190			576
ggc cca ggc gca gca ctt cga aac atc cac aaa ttt gat cta tta gtc Gly Pro Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val 195 200 205			624
cgc atg ccg ttg atg gtg ggc gtt gcc gca ttg ggg tcg cat atc agt Arg Met Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser 210 215 220			672
ctg ccc ttg ctt ggg acg act gca ttg acc agc gga caa ggc aaa cac Leu Pro Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His 225 230 235 240			720
cac acc atc ccg ctg cct ctc caa aaa cgc caa gcc gca gga ctc ctc His Thr Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu 245 250 255			768
gtg gtg atc atc gct gtc ggt gct ctt gct ccc gca tgg tcg gca cgg Val Val Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg 260 265 270			816
ctg cta cct cag gga acg tgg gat gaa gtg cct gac tac tgg tac gaa Leu Leu Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu 275 280 285			864

gcc aca gaa ttc ctc aac caa aac gcc aca ggc acc cgc acg ttg att 912
 Ala Thr Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile
 290 295 300

tgg cct agc tcg ccg ttt gcc cgc cag gac tgg gga tgg act cgg gat 960
 Trp Pro Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp
 305 310 315 320

gaa cca gct caa cca ctt ctt gat gtt ccg tgg gct gtc cgc gat gcc 1008
 Glu Pro Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala
 325 330 335

att cct ttg gtt ccc ccg gag gcg att cgc gga tta gat ggt ctc gac 1056
 Ile Pro Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp
 340 345 350

gac cta ggc act cta ggc acc ggt cta aac gac gag gct tta aaa cgt 1104
 Asp Leu Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg
 355 360 365

cta ggc atc ggc gca gta ctg gtg agg cat gat ctg gaa gcc gac cca 1152
 Leu Gly Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro
 370 375 380

gat att gag gtg gat ctg cct ggg gaa aag cac act ttt ggc tcc caa 1200
 Asp Ile Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln
 385 390 395 400

ggc caa gta gac gtc tac ctc acc gac ccc gac cgc aat atg tgg atc 1248
 Gly Gln Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile
 405 410 415

act tcc ggc aca tcc aag cag ctg ccc acc gtc gct ggc ggc ggc gaa 1296
 Thr Ser Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu
 420 425 430

atc ctc tcg ctc cta gac acc atc aac ggc 1326
 Ile Leu Ser Leu Leu Asp Thr Ile Asn Gly
 435 440

<210> 2788

<211> 442

<212> PRT

<213> Corynebacterium glutamicum

<400> 2788

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Trp Val Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile
 20 25 30

Ala Leu Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr
 35 40 45

Ala Thr Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg
 50 55 60

Gly Leu Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val

65	70	75	80
Asn Ser Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro	85	90	95
Pro Phe Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu	100	105	110
Asn Pro Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val	115	120	125
Asp Thr Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe	130	135	140
Val Thr Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr	145	150	155
Leu Met Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu	165	170	175
Leu Ile Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp	180	185	190
Gly Pro Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val	195	200	205
Arg Met Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser	210	215	220
Leu Pro Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His	225	230	235
His Thr Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu	245	250	255
Val Val Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg	260	265	270
Leu Leu Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu	275	280	285
Ala Thr Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile	290	295	300
Trp Pro Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp	305	310	315
Glu Pro Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala	325	330	335
Ile Pro Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp	340	345	350
Asp Leu Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg	355	360	365
Leu Gly Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro	370	375	380
Asp Ile Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln	385	390	395
			400

Gly Gln Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile
 405 410 415

Thr Ser Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu
 420 425 430

Ile Leu Ser Leu Leu Asp Thr Ile Asn Gly
 435 440

<210> 2789

<211> 918

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(895)

<223> RXA02552

<400> 2789

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tatgcctgaa acttgagcat ggcaacagca aggagacacc gtg gga aaa cat gca 115
 Val Gly Lys His Ala
 1 5

gct gaa aca tcg gaa ccg aag aaa aat tca ccg tgg cgc att ggt ttg 163
 Ala Glu Thr Ser Glu Pro Lys Lys Asn Ser Pro Trp Arg Ile Gly Leu
 10 15 20

ttg acg ttt ttg att tct tca gtt gtc gtg acg ctg gtg ggc atg gtg 211
 Leu Thr Phe Leu Ile Ser Ser Val Val Val Thr Leu Val Gly Met Val
 25 30 35

atg ctg tgg ccg gat tct gat gat gtg gtg ttg gcg gat aac ttt tcg 259
 Met Leu Trp Pro Asp Ser Asp Asp Val Val Leu Ala Asp Asn Phe Ser
 40 45 50

cag acg ttt gcg gga aat cat gag cag gtg gat gga acg atc acg ctc 307
 Gln Thr Phe Ala Gly Asn His Glu Gln Val Asp Gly Thr Ile Thr Leu
 55 60 65

gtt gat aat tct gcg tgt aat tcg cca gac acc ggc cga gtt ttt gcg 355
 Val Asp Asn Ser Ala Cys Asn Ser Pro Asp Thr Gly Arg Val Phe Ala
 70 75 80 85

gaa agc ccc acg att tct gcg gag ccg gca acg ttg gag tgc gtg cgt 403
 Glu Ser Pro Thr Ile Ser Ala Glu Pro Ala Thr Leu Glu Cys Val Arg
 90 95 100

gca ctc gta gac atc aca tcg ggt gcc aat gag ggg cag aaa act cag 451
 Ala Leu Val Asp Ile Thr Ser Gly Ala Asn Glu Gly Gln Lys Thr Gln
 105 110 115

ctg atc act tac gcg caa cct ggt gat ccg gag ttt tcc gag ggc gac 499
 Leu Ile Thr Tyr Ala Gln Pro Gly Asp Pro Glu Phe Ser Glu Gly Asp
 120 125 130

aag atc cgc atg gtg gaa aca ccg gat aca aat ggc gag atc atc tac 547

Lys Ile Arg Met Val Glu Thr Pro Asp Thr Asn Gly Glu Ile Ile Tyr
 135 140 145
 acc ttt gct gat tac cag cgc gga ccg gcg ttg atc att tgg ggt gtg 595
 Thr Phe Ala Asp Tyr Gln Arg Gly Pro Ala Leu Ile Ile Trp Gly Val
 150 155 160 165
 gtt ctc att gtg gcg atg gga gct ttc gcg gcg tgg cga ggt gtg cgt 643
 Val Leu Ile Val Ala Met Gly Ala Phe Ala Ala Trp Arg Gly Val Arg
 170 175 180
 gcg ctg gtt ggt ttg gtc gtc acc ttg gga att gtt ggt att ttc ttg 691
 Ala Leu Val Gly Leu Val Val Thr Leu Gly Ile Val Gly Ile Phe Leu
 185 190 195
 ctg cca gga ttg gcc agc ggg cac gat gcg atg tgg ttg gcg ctg gtg 739
 Leu Pro Gly Leu Ala Ser Gly His Asp Ala Met Trp Leu Ala Leu Val
 200 205 210
 tgt ggc gcg gcg atc ttg ttg att gtg gtg ccg atg gtt cac gga atc 787
 Cys Gly Ala Ala Ile Leu Leu Ile Val Val Pro Met Val His Gly Ile
 215 220 225
 aac tgg aaa tcg gca gct gcg ttg gcg ggc acg ctg gtg gca ttg ttg 835
 Asn Trp Lys Ser Ala Ala Ala Leu Ala Gly Thr Leu Val Ala Leu Leu
 230 235 240 245
 ttg tcg gcg gtg ttg tcg tgg gcg tcg atc gtc acc act gaa ttt gcg 883
 Leu Ser Ala Val Leu Ser Trp Ala Ser Ile Val Thr Thr Glu Phe Ala
 250 255 260
 cgg act ggg cga tgagaatcat ctgaagatca tca 918
 Arg Thr Gly Arg
 265

<210> 2790

<211> 265

<212> PRT

<213> Corynebacterium glutamicum

<400> 2790

Val Gly Lys His Ala Ala Glu Thr Ser Glu Pro Lys Lys Asn Ser Pro
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 20 25 30
 Leu Val Gly Met Val Met Leu Trp Pro Asp Ser Asp Asp Val Val Leu
 35 40 45
 Ala Asp Asn Phe Ser Gln Thr Phe Ala Gly Asn His Glu Gln Val Asp
 50 55 60
 Gly Thr Ile Thr Leu Val Asp Asn Ser Ala Cys Asn Ser Pro Asp Thr
 65 70 75 80
 Gly Arg Val Phe Ala Glu Ser Pro Thr Ile Ser Ala Glu Pro Ala Thr
 85 90 95
 Leu Glu Cys Val Arg Ala Leu Val Asp Ile Thr Ser Gly Ala Asn Glu

100					105					110					
Gly	Gln	Lys	Thr	Gln	Leu	Ile	Thr	Tyr	Ala	Gln	Pro	Gly	Asp	Pro	Glu
		115					120					125			
Phe	Ser	Glu	Gly	Asp	Lys	Ile	Arg	Met	Val	Glu	Thr	Pro	Asp	Thr	Asn
	130					135					140				
Gly	Glu	Ile	Ile	Tyr	Thr	Phe	Ala	Asp	Tyr	Gln	Arg	Gly	Pro	Ala	Leu
145					150					155					160
Ile	Ile	Trp	Gly	Val	Val	Leu	Ile	Val	Ala	Met	Gly	Ala	Phe	Ala	Ala
				165					170					175	
Trp	Arg	Gly	Val	Arg	Ala	Leu	Val	Gly	Leu	Val	Val	Thr	Leu	Gly	Ile
		180						185					190		
Val	Gly	Ile	Phe	Leu	Leu	Pro	Gly	Leu	Ala	Ser	Gly	His	Asp	Ala	Met
	195						200					205			
Trp	Leu	Ala	Leu	Val	Cys	Gly	Ala	Ala	Ile	Leu	Leu	Ile	Val	Val	Pro
	210					215					220				
Met	Val	His	Gly	Ile	Asn	Trp	Lys	Ser	Ala	Ala	Ala	Leu	Ala	Gly	Thr
225					230				235						240
Leu	Val	Ala	Leu	Leu	Leu	Ser	Ala	Val	Leu	Ser	Trp	Ala	Ser	Ile	Val
			245						250					255	
Thr	Thr	Glu	Phe	Ala	Arg	Thr	Gly	Arg							
		260						265							

<210> 2791

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXA02554

<400> 2791

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ggataggctc	cataaaaata	accaaaggcg	gaaaatttca	atg	tca	cac	act	aag	115
				Met	Ser	His	Thr	Lys	
				1				5	

cca	tcc	att	gcc	atc	ctc	ggt	gct	ggc	cga	gtg	ggt	tct	tca	ctt	gcc	163
Pro	Ser	Ile	Ala	Ile	Leu	Gly	Ala	Gly	Arg	Val	Gly	Ser	Ser	Leu	Ala	
			10					15						20		

agg	tca	gcg	gtc	gcc	gca	ggc	tat	gag	gta	aag	gtt	gct	ggt	tca	ggt	211
Arg	Ser	Ala	Val	Ala	Ala	Gly	Tyr	Glu	Val	Lys	Val	Ala	Gly	Ser	Gly	
			25					30					35			

gct	gtg	gac	aaa	atc	gct	ctt	acc	gct	gag	atc	ctt	atg	ccc	ggc	gcg	259
Ala	Val	Asp	Lys	Ile	Ala	Leu	Thr	Ala	Glu	Ile	Leu	Met	Pro	Gly	Ala	
		40					45					50				

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307
 Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
 55 60 65
 ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355
 Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
 70 75 80 85
 gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403
 Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
 90 95 100
 ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451
 Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
 105 110 115
 att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499
 Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
 120 125 130
 att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547
 Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
 135 140 145
 gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
 Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
 150 155 160 165
 att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
 Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
 170 175 180
 ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691
 Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
 185 190 195
 aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
 Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
 200 205
 aac 747

<210> 2792

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 2792

Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val
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 Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
 20 25 30
 Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
 35 40 45
 Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
 50 55 60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
65 70 75 80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
85 90 95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
100 105 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
115 120 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
130 135 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
145 150 155 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
165 170 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
180 185 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
195 200 205

<210> 2793

<211> 854

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (82)..(831)

<223> RXA02569

<400> 2793

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acgatctgca tggggattac t atg tca cgc tca tct aaa att tcg gtc gcg 111
Met Ser Arg Ser Ser Lys Ile Ser Val Ala
1 5 10

ttt ggt ggc cta ctc atc gct gct acc tgg ctg tat ttg gtc ttg gtc 159
Phe Gly Gly Leu Leu Ile Ala Ala Thr Trp Leu Tyr Leu Val Leu Val
15 20 25

agg cct acc gat tgg gaa tca gtg ggt ggt tcc acg gaa gcg ttg atc 207
Arg Pro Thr Asp Trp Glu Ser Val Gly Gly Ser Thr Glu Ala Leu Ile
30 35 40

acg ttg gtg ggc tat gtt gcc ggc acg atc gcg ttg ttg gtt ggt gtg 255
Thr Leu Val Gly Tyr Val Ala Gly Thr Ile Ala Leu Leu Val Gly Val
45 50 55

ctg cct acg ctt cca gcc agg acc att gcg atc att cct gtg gct ttg 303
Leu Pro Thr Leu Pro Ala Arg Thr Ile Ala Ile Ile Pro Val Ala Leu
60 65 70

gtg ctc aat att ttg tta ggc caa gtc act ggt tct ttt gtc att ccg 351
 Val Leu Asn Ile Leu Leu Gly Gln Val Thr Gly Ser Phe Val Ile Pro 90
 75 80 85

ctg tat tta gat gcg gtg ggc aca gtg ctg gtc gca gct ctt gct ggt 399
 Leu Tyr Leu Asp Ala Val Gly Thr Val Leu Val Ala Ala Leu Ala Gly 105
 95 100

cct agt gct ggt ttg gca aca ggt gct tta agt tct gtg gtg tgg gcg 447
 Pro Ser Ala Gly Leu Ala Thr Gly Ala Leu Ser Ser Val Val Trp Ala 120
 110 115

ttg ttc aat ccg ctg gct ttg ccg ttt gct gca ggt tcc gcg ctg act 495
 Leu Phe Asn Pro Leu Ala Leu Pro Phe Ala Ala Gly Ser Ala Leu Thr 135
 125 130

ggt tgg ttg acc ggt gtg gtg att aaa aag ggt gcg ttt aag aat atc 543
 Gly Trp Leu Thr Gly Val Val Ile Lys Lys Gly Ala Phe Lys Asn Ile 150
 140 145

ttc gcc acc atc atc tct ggt gcg gtc att ggt ttg atc acg ggt gct 591
 Phe Ala Thr Ile Ile Ser Gly Ala Val Ile Gly Leu Ile Thr Gly Ala 170
 155 160 165

gtc gct gcc ccg gtt gcg gcg ttt gtt tat ggc gga acc gcc ggt gtg 639
 Val Ala Ala Pro Val Ala Ala Phe Val Tyr Gly Gly Thr Ala Gly Val 185
 175 180

gga act ggt gcg gtg gtt agc ctc ttc cgc gaa atg ggt aac tct ttg 687
 Gly Thr Gly Ala Val Val Ser Leu Phe Arg Glu Met Gly Asn Ser Leu 200
 190 195

ctc gca tcg gta acc tgg cag tcg ttt att tcc gat cct ttg gat aag 735
 Leu Ala Ser Val Thr Trp Gln Ser Phe Ile Ser Asp Pro Leu Asp Lys 215
 205 210

gcc att gtt atg ctc att gtg ttt gtg gtg gtc aag tcg cta ccc aag 783
 Ala Ile Val Met Leu Ile Val Phe Val Val Val Lys Ser Leu Pro Lys 230
 220 225

cgc acc act agg gca ttg gtt ccg cag cgg gtt ccg gag gac gtc gct 831
 Arg Thr Thr Arg Ala Leu Val Pro Gln Arg Val Pro Glu Asp Val Ala 250
 235 240 245

taaacatgaa tcctttgaca tgg 854

<210> 2794

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 2794

Met Ser Arg Ser Ser Lys Ile Ser Val Ala Phe Gly Gly Leu Leu Ile
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Ala Ala Thr Trp Leu Tyr Leu Val Leu Val Arg Pro Thr Asp Trp Glu
 20 25 30

Ser Val Gly Gly Ser Thr Glu Ala Leu Ile Thr Leu Val Gly Tyr Val

35	40	45
Ala Gly Thr Ile Ala Leu Leu Val Gly Val Leu Pro Thr Leu Pro Ala 50 55 60		
Arg Thr Ile Ala Ile Ile Pro Val Ala Leu Val Leu Asn Ile Leu Leu 65 70 75 80		
Gly Gln Val Thr Gly Ser Phe Val Ile Pro Leu Tyr Leu Asp Ala Val 85 90 95		
Gly Thr Val Leu Val Ala Ala Leu Ala Gly Pro Ser Ala Gly Leu Ala 100 105 110		
Thr Gly Ala Leu Ser Ser Val Val Trp Ala Leu Phe Asn Pro Leu Ala 115 120 125		
Leu Pro Phe Ala Ala Gly Ser Ala Leu Thr Gly Trp Leu Thr Gly Val 130 135 140		
Val Ile Lys Lys Gly Ala Phe Lys Asn Ile Phe Ala Thr Ile Ile Ser 145 150 155 160		
Gly Ala Val Ile Gly Leu Ile Thr Gly Ala Val Ala Ala Pro Val Ala 165 170 175		
Ala Phe Val Tyr Gly Gly Thr Ala Gly Val Gly Thr Gly Ala Val Val 180 185 190		
Ser Leu Phe Arg Glu Met Gly Asn Ser Leu Leu Ala Ser Val Thr Trp 195 200 205		
Gln Ser Phe Ile Ser Asp Pro Leu Asp Lys Ala Ile Val Met Leu Ile 210 215 220		
Val Phe Val Val Val Lys Ser Leu Pro Lys Arg Thr Thr Arg Ala Leu 225 230 235 240		
Val Pro Gln Arg Val Pro Glu Asp Val Ala 245 250		

<210> 2795

<211> 765

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(742)

<223> RXA02570

<400> 2795

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cattggttcc gcagcggggt ccggaggacg tcgcttaa	atg aat cct ttg aca	115
	Met Asn Pro Leu Thr	
	1 5	

tgg atc att ggc gca ttc agc atg tgg atc gtg gtg ctg ggc gtt aat	163
Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val Val Leu Gly Val Asn	

10										15					20					
aag	ctt	ggt	tta	agc	atc	gca	gtg	atc	atc	atc	gcg	cag	gtc	gtg	gcg	211				
Lys	Leu	Gly	Leu	Ser	Ile	Ala	Val	Ile	Ile	Ile	Ala	Gln	Val	Val	Ala					
25				30				35												
atg	att	cgg	gtg	cgc	aat	gta	tct	gtg	ttg	gct	tca	aca	gca	ttg	tta	259				
Met	Ile	Arg	Val	Arg	Asn	Val	Ser	Val	Leu	Ala	Ser	Thr	Ala	Leu	Leu					
40				45				50												
tcg	gtt	cct	gca	ttg	gcc	tcg	atg	gcg	ctg	att	cac	atg	ccg	tat	tct	307				
Ser	Val	Pro	Ala	Leu	Ala	Ser	Met	Ala	Leu	Ile	His	Met	Pro	Tyr	Ser					
55				60				65												
tcc	gac	ggc	tgg	ttg	att	gct	ctt	acc	ttg	acg	gct	cgt	ttt	agt	gcg	355				
Ser	Asp	Gly	Trp	Leu	Ile	Ala	Leu	Thr	Leu	Thr	Ala	Arg	Phe	Ser	Ala					
70				75				80				85								
ttg	atg	tct	att	ttc	ctc	ctt	gca	gca	aca	gcg	att	act	att	cct	gag	403				
Leu	Met	Ser	Ile	Phe	Leu	Leu	Ala	Ala	Thr	Ala	Ile	Thr	Ile	Pro	Glu					
90				95				100												
ctg	gtg	aaa	tcc	cta	tat	cgt	tgg	ccc	aag	ctg	gcg	tat	atc	gtg	ggt	451				
Leu	Val	Lys	Ser	Leu	Tyr	Arg	Trp	Pro	Lys	Leu	Ala	Tyr	Ile	Val	Gly					
105				110				115												
tct	gca	ttg	cag	atg	att	ccg	cag	ggt	aaa	cag	acc	ttg	gcg	ttg	gtt	499				
Ser	Ala	Leu	Gln	Met	Ile	Pro	Gln	Gly	Lys	Gln	Thr	Leu	Ala	Leu	Val					
120				125				130												
cgt	gat	gcc	aat	gct	ttg	cgc	ggg	cgc	agc	ggt	aaa	ggt	ccc	gtg	cgc	547				
Arg	Asp	Ala	Asn	Ala	Leu	Arg	Gly	Arg	Ser	Val	Lys	Gly	Pro	Val	Arg					
135				140				145												
gcg	gtg	aaa	tat	gtg	ggt	ttg	ccc	ctg	att	aca	cat	tta	ctt	agt	gca	595				
Ala	Val	Lys	Tyr	Val	Gly	Leu	Pro	Leu	Ile	Thr	His	Leu	Leu	Ser	Ala					
150				155				160				165								
ggt	gcc	gcg	cga	gcg	att	ccc	ttg	gag	gtc	gca	ggc	ctg	gac	agg	ccg	643				
Gly	Ala	Ala	Arg	Ala	Ile	Pro	Leu	Glu	Val	Ala	Gly	Leu	Asp	Arg	Pro					
170				175				180												
ggg	ccg	cgt	acg	gtg	ttg	gtt	gag	gtg	gtg	gag	ggg	cgc	gtc	gaa	aag	691				
Gly	Pro	Arg	Thr	Val	Leu	Val	Glu	Val	Val	Glu	Gly	Arg	Val	Glu	Lys					
185				190				195												
cat	tgt	cgc	tgg	ttg	ttg	ccg	ctt	ttg	gca	gtc	ggg	atg	gcg	tgg	tgg	739				
His	Cys	Arg	Trp	Leu	Leu	Pro	Leu	Leu	Ala	Val	Gly	Met	Ala	Trp	Trp					
200				205				210												
ctc taactcaa at cgtcggaccg tcc															765					
Leu																				

<210> 2796

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 2796

Met Asn Pro Leu Thr Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val
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 Val Leu Gly Val Asn Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile
 20 25 30
 Ala Gln Val Val Ala Met Ile Arg Val Arg Asn Val Ser Val Leu Ala
 35 40 45
 Ser Thr Ala Leu Leu Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile
 50 55 60
 His Met Pro Tyr Ser Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr
 65 70 75 80
 Ala Arg Phe Ser Ala Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala
 85 90 95
 Ile Thr Ile Pro Glu Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu
 100 105 110
 Ala Tyr Ile Val Gly Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln
 115 120 125
 Thr Leu Ala Leu Val Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val
 130 135 140
 Lys Gly Pro Val Arg Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr
 145 150 155 160
 His Leu Leu Ser Ala Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala
 165 170 175
 Gly Leu Asp Arg Pro Gly Pro Arg Thr Val Leu Val Glu Val Val Glu
 180 185 190
 Gly Arg Val Glu Lys His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val
 195 200 205
 Gly Met Ala Trp Trp Leu
 210

<210> 2797

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA02573

<400> 2797

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gaagtgaagt actttccgaa agattcacag ggagcatgca atg acg aac aaa acc 115
 Met Thr Asn Lys Thr
 1 5

atg ctg gtt gct ttt gat ggc tca ccg gaa tcc cgg cgc gct ttg gaa 163

Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser Arg Arg Ala Leu Glu
10 15 20

tat gcg gcg aaa ttg ttg cag ccg cgc acc gtg gaa att tta act gcg 211
Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val Glu Ile Leu Thr Ala
25 30 35

tgg gag cca ttg cat cgg caa gct gcg cgc tcg gtt tcg ttg atc acc 259
Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser Val Ser Leu Ile Thr
40 45 50

ttg ggg gtg gaa ccc gaa gac ccc gcc cat tcc gct gca cta aaa acc 307
Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser Ala Ala Leu Lys Thr
55 60 65

tgc cag gaa ggc gta gag cta gcc caa tct cta ggt ctg gaa gcg cga 355
Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu Gly Leu Glu Ala Arg
70 75 80 85

gcc cac atg gtg gaa tcc gca acg gcc gtg tgg agc gcc atc gtt gat 403
Ala His Met Val Glu Ser Ala Thr Ala Val Trp Ser Ala Ile Val Asp
90 95 100

gct gct gac gag ctc cgc ccc gac gtg att gtc acc ggc acc cgc ggg 451
Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val Thr Gly Thr Arg Gly
105 110 115

atc tcc gga tgg aaa tcc ctg tgg caa tcc tcc acc tca gac agc gtg 499
Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser Thr Ser Asp Ser Val
120 125 130

ctc cac cac gcc gac gta cca gtt ttt gtc gtt cca ccc ctg gac 544
Leu His His Ala Asp Val Pro Val Phe Val Val Pro Pro Leu Asp
135 140 145

taaaaccgag acgagaacca aga 567

<210> 2798

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 2798

Met Thr Asn Lys Thr Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser
1 5 10 15

Arg Arg Ala Leu Glu Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val
20 25 30

Glu Ile Leu Thr Ala Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser
35 40 45

Val Ser Leu Ile Thr Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser
50 55 60

Ala Ala Leu Lys Thr Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu
65 70 75 80

Gly Leu Glu Ala Arg Ala His Met Val Glu Ser Ala Thr Ala Val Trp
85 90 95

Ser Ala Ile Val Asp Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val
 100 105 110

Thr Gly Thr Arg Gly Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser
 115 120 125

Thr Ser Asp Ser Val Leu His His Ala Asp Val Pro Val Phe Val Val
 130 135 140

Pro Pro Leu Asp
 145

<210> 2799
 <211> 1258
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1258)
 <223> RXA02575

<400> 2799
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tgagtaggaa tttcgcacatca gtgcaactag ccttttcaggt gtg aag aac tct ggg 115
 Val Lys Asn Ser Gly
 1 5

aaa aat tcg gca aag aat cgg acc aaa ggg atc cta atc ggg gtt ctc 163
 Lys Asn Ser Ala Lys Asn Arg Thr Lys Gly Ile Leu Ile Gly Val Leu
 10 15 20

gtt ggt ctg att gcc att ttt gca ggc atc tat gcg gtc gat gtt ttc 211
 Val Gly Leu Ile Ala Ile Phe Ala Gly Ile Tyr Ala Val Asp Val Phe
 25 30 35

ctc aac aag gac aac atc cct cgt gga aca acc gtc ggt ggc gtc agt 259
 Leu Asn Lys Asp Asn Ile Pro Arg Gly Thr Thr Val Gly Gly Val Ser
 40 45 50

att tcc aac ctc agt gca caa gaa gcc cgc aca aag ttg gaa acc gaa 307
 Ile Ser Asn Leu Ser Ala Gln Glu Ala Arg Thr Lys Leu Glu Thr Glu
 55 60 65

ctg gcc aat gat gtg gtg cag ccc gtc acc gtg acg gca ggg gag cag 355
 Leu Ala Asn Asp Val Val Gln Pro Val Thr Val Thr Ala Gly Glu Gln
 70 75 80 85

agc acc act ttt gat cca gtt gcc tcc ggc gtc ggc atc gat tgg gac 403
 Ser Thr Thr Phe Asp Pro Val Ala Ser Gly Val Gly Ile Asp Trp Asp
 90 95 100

gca acc atc gaa ggc acc ggc gag cag tct tgg aac ccc att acc cgc 451
 Ala Thr Ile Glu Gly Thr Gly Glu Gln Ser Trp Asn Pro Ile Thr Arg
 105 110 115

ttc gtg gcg ctg ttc aaa gaa tcc gaa tct ccc atc gtg agc acc gtc 499
 Phe Val Ala Leu Phe Lys Glu Ser Glu Ser Pro Ile Val Ser Thr Val

120	125	130	
gat ccc gca gcc ttc ggc ccg acc ctt gat cgc atg gtc ggc gaa ctc Asp Pro Ala Ala Phe Gly Pro Thr Leu Asp Arg Met Val Gly Glu Leu 135 140 145			547
tat cga gat ccc att tcc gga aac ctg cat atc gac gcc ggc acc ctc Tyr Arg Asp Pro Ile Ser Gly Asn Leu His Ile Asp Ala Gly Thr Leu 150 155 160 165			595
gtg gtc aac gac acc atc gac gga caa gcc gta gac cgc acc att ttg Val Val Asn Asp Thr Ile Asp Gly Gln Ala Val Asp Arg Thr Ile Leu 170 175 180			643
gaa caa gca gtc aca gaa aac tgg ctc aac cca gag ggc gta aaa gcc Glu Gln Ala Val Thr Glu Asn Trp Leu Asn Pro Glu Gly Val Lys Ala 185 190 195			691
gag cca tac gtt gtt ccc gct gcg atc agc caa gac acc atc gat aaa Glu Pro Tyr Val Val Pro Ala Ala Ile Ser Gln Asp Thr Ile Asp Lys 200 205 210			739
ctt gca gaa ggc gcc gga gct aaa gca gta tct agc cct ttc gtc gtc Leu Ala Glu Gly Ala Gly Ala Lys Ala Val Ser Ser Pro Phe Val Val 215 220 225			787
cga ggc gat gac gga att gaa ggc acc atc ccc gtc gag cgc atg ggt Arg Gly Asp Asp Gly Ile Glu Gly Thr Ile Pro Val Glu Arg Met Gly 230 235 240 245			835
gaa gtg gtg agt ttc cca gaa gaa aac ggc acc atc cgc gtc gac atc Glu Val Val Ser Phe Pro Glu Glu Asn Gly Thr Ile Arg Val Asp Ile 250 255 260			883
aat gca gaa gca gca aca gca atg ctg gcc gaa ggt ctc aaa gaa aca Asn Ala Glu Ala Ala Thr Ala Met Leu Ala Glu Gly Leu Lys Glu Thr 265 270 275			931
gag atc gag ccc acc aac gct caa atc agt ttc tcc tca ggc tcc cgc Glu Ile Glu Pro Thr Asn Ala Gln Ile Ser Phe Ser Ser Gly Ser Arg 280 285 290			979
gta gtc acc cca gaa gtc acc gga cac gga atc aac tgg gaa gaa acc Val Val Thr Pro Glu Val Thr Gly His Gly Ile Asn Trp Glu Glu Thr 295 300 305			1027
ctg gcc gat ctg ccc aac aac ctc acc ggc gat ggc ccc cgc acc atc Leu Ala Asp Leu Pro Asn Asn Leu Thr Gly Asp Gly Pro Arg Thr Ile 310 315 320 325			1075
gac gca atc tac gag gac acc cca gca aca ttc acc gcc acc gac gcc Asp Ala Ile Tyr Glu Asp Thr Pro Ala Thr Phe Thr Ala Thr Asp Ala 330 335 340			1123
caa aac gct acc ttc aat gag gtc atg ggc gag ttc acc acc ggc ggc Gln Asn Ala Thr Phe Asn Glu Val Met Gly Glu Phe Thr Thr Gly Gly 345 350 355			1171
ttc tct gct gcc tcc gga aca aac atc cgc ctc acc gcg caa atg gtc Phe Ser Ala Ala Ser Gly Thr Asn Ile Arg Leu Thr Ala Gln Met Val 360 365 370			1219

gac ggc gca gtc gtt tca cct ggc gat aca ttc tcc ctc
 Asp Gly Ala Val Val Ser Pro Gly Asp Thr Phe Ser Leu
 375 380 385

1258

<210> 2800

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 2800

Val Lys Asn Ser Gly Lys Asn Ser Ala Lys Asn Arg Thr Lys Gly Ile
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Leu Ile Gly Val Leu Val Gly Leu Ile Ala Ile Phe Ala Gly Ile Tyr
 20 25 30

Ala Val Asp Val Phe Leu Asn Lys Asp Asn Ile Pro Arg Gly Thr Thr
 35 40 45

Val Gly Gly Val Ser Ile Ser Asn Leu Ser Ala Gln Glu Ala Arg Thr
 50 55 60

Lys Leu Glu Thr Glu Leu Ala Asn Asp Val Val Gln Pro Val Thr Val
 65 70 75 80

Thr Ala Gly Glu Gln Ser Thr Thr Phe Asp Pro Val Ala Ser Gly Val
 85 90 95

Gly Ile Asp Trp Asp Ala Thr Ile Glu Gly Thr Gly Glu Gln Ser Trp
 100 105 110

Asn Pro Ile Thr Arg Phe Val Ala Leu Phe Lys Glu Ser Glu Ser Pro
 115 120 125

Ile Val Ser Thr Val Asp Pro Ala Ala Phe Gly Pro Thr Leu Asp Arg
 130 135 140

Met Val Gly Glu Leu Tyr Arg Asp Pro Ile Ser Gly Asn Leu His Ile
 145 150 155 160

Asp Ala Gly Thr Leu Val Val Asn Asp Thr Ile Asp Gly Gln Ala Val
 165 170 175

Asp Arg Thr Ile Leu Glu Gln Ala Val Thr Glu Asn Trp Leu Asn Pro
 180 185 190

Glu Gly Val Lys Ala Glu Pro Tyr Val Val Pro Ala Ala Ile Ser Gln
 195 200 205

Asp Thr Ile Asp Lys Leu Ala Glu Gly Ala Gly Ala Lys Ala Val Ser
 210 215 220

Ser Pro Phe Val Val Arg Gly Asp Asp Gly Ile Glu Gly Thr Ile Pro
 225 230 235 240

Val Glu Arg Met Gly Glu Val Val Ser Phe Pro Glu Glu Asn Gly Thr
 245 250 255

Ile Arg Val Asp Ile Asn Ala Glu Ala Ala Thr Ala Met Leu Ala Glu

Leu 70	Pro	Val	Ser	Trp	Ile 75	Val	Arg	Thr	Met	Leu 80	Leu	Val	Ala	Gly	Phe 85	
gcg	ggc	gcg	tgg	ggt	gcg	atg	cgc	ctt	ggg	cct	tcc	aag	ttt	ttg	gcc	403
Ala	Gly	Ala	Trp	Gly	Ala	Met	Arg	Leu	Gly	Pro	Ser	Lys	Phe	Leu	Ala	
				90					95					100		
ggt	acc	gtg	gcg	att	tac	aat	ccc	ttc	gtg	gtg	gag	cgt	ctg	ctg	cag	451
Val	Thr	Val	Ala	Ile	Tyr	Asn	Pro	Phe	Val	Val	Glu	Arg	Leu	Leu	Gln	
			105					110					115			
ggc	cat	tgg	tgc	ttg	gtg	atg	gcg	gtg	tgg	ctg	ttc	ccg	ctg	gtt	gtg	499
Gly	His	Trp	Ser	Leu	Val	Met	Ala	Val	Trp	Leu	Phe	Pro	Leu	Val	Val	
		120					125					130				
gcg	ctg	cgc	agg	cat	ccg	cgt	tgg	cag	gtt	gtg	gcg	atc	tgg	gcg	gcg	547
Ala	Leu	Arg	Arg	His	Pro	Arg	Trp	Gln	Val	Val	Ala	Ile	Trp	Ala	Ala	
	135					140					145					
tgc	ttg	acg	ccc	acg	ggt	gcg	gtg	gtt	gcg	gcg	gtc	acg	ggc	gtg	gcg	595
Ser	Leu	Thr	Pro	Thr	Gly	Ala	Val	Val	Ala	Ala	Val	Thr	Gly	Val	Ala	
150					155				160					165		
agt	tct	aaa	aga	aaa	cgc	ttt	acg	acg	cta	tgt	tcc	ttc	ctt	tgc	tgg	643
Ser	Ser	Lys	Arg	Lys	Arg	Phe	Thr	Thr	Leu	Cys	Ser	Phe	Leu	Ser	Trp	
				170					175					180		
ctt	cct	tgg	cta	ata	cct	gcg	ctt	ctt	gcc	acc	ccc	act	tgc	gga	ggt	691
Leu	Pro	Trp	Leu	Ile	Pro	Ala	Leu	Leu	Ala	Thr	Pro	Thr	Ser	Gly	Gly	
			185					190					195			
gcg	ctg	acc	ttc	gcc	att	cgt	tct	gaa	aca	tat	gca	gga	acg	ttg	gga	739
Ala	Leu	Thr	Phe	Ala	Ile	Arg	Ser	Glu	Thr	Tyr	Ala	Gly	Thr	Leu	Gly	
		200					205					210				
act	gcg	ctg	ggc	ctg	ggt	gga	att	tgg	aac	gcg	ggg	gcc	gtg	ccg	gcc	787
Thr	Ala	Leu	Gly	Leu	Gly	Gly	Ile	Trp	Asn	Ala	Gly	Ala	Val	Pro	Ala	
	215					220					225					
tca	cgc	gaa	ctg	ggt	ttc	gcg	gtt	gct	gga	att	ttg	tta	ttt	gcg	att	835
Ser	Arg	Glu	Leu	Gly	Phe	Ala	Val	Ala	Gly	Ile	Leu	Leu	Phe	Ala	Ile	
230					235				240					245		
ctg	ctg	gcg	ggt	ttc	aaa	aac	tgt	ccg	tgg	gtt	ctc	gca	ctg	ctg	gcg	883
Leu	Leu	Ala	Gly	Phe	Lys	Asn	Cys	Pro	Trp	Val	Leu	Ala	Leu	Leu	Ala	
			250					255					260			
gtc	gta	ggt	ttt	atg	ggg	gcg	atc	ggt	ccg	tgg	ctg	atg	ccg	aat	ctg	931
Val	Val	Gly	Phe	Met	Gly	Ala	Ile	Gly	Pro	Trp	Leu	Met	Pro	Asn	Leu	
			265					270					275			
ttc	acg	tgg	acc	atc	gca	tat	gtt	cca	ggc	gcc	gcg	ctg	ttt	agg	gat	979
Phe	Thr	Trp	Thr	Ile	Ala	Tyr	Val	Pro	Gly	Ala	Ala	Leu	Phe	Arg	Asp	
		280					285					290				
tct	caa	aaa	ctc	ctc	atg	ctg	gct	atc	cct	gcc	tat	gtg	tgt	ttg	gcc	1027
Ser	Gln	Lys	Leu	Leu	Met	Leu	Ala	Ile	Pro	Ala	Tyr	Val	Cys	Leu	Ala	
	295					300					305					
gcc	ggg	gtg	aaa	agc	cca	ctg	tgc	tgg	gtg	gct	acc	ggt	ttg	gcg	ttg	1075
Ala	Gly	Val	Lys	Ser	Pro	Leu	Ser	Trp	Val	Ala	Thr	Gly	Leu	Ala	Leu	

310	315	320	325	
ctc cag att cct gat gca cca cgt gag gtt tcc gtg ata cgc cca agt				1123
Leu Gln Ile Pro Asp Ala Pro Arg Glu Val Ser Val Ile Arg Pro Ser	330	335	340	
tca gcg cat gtg gaa tca gtg gaa gca ctg gca gaa atc gct gat ggc				1171
Ser Ala His Val Glu Ser Val Glu Ala Leu Ala Glu Ile Ala Asp Gly	345	350	355	
cgc gac atc tta atc atc ggc caa ggc ccc ttg gtg acc cgc gag gat				1219
Arg Asp Ile Leu Ile Ile Gly Gln Gly Pro Leu Val Thr Arg Glu Asp	360	365	370	
ggg atc ccg gtt gtc gat ccc aaa acc aaa gcc ctc tcc gtg gtg gaa				1267
Gly Ile Pro Val Val Asp Pro Lys Thr Lys Ala Leu Ser Val Val Glu	375	380	385	
tcc ggc gaa ctg cgt gtg gac gga atc atc acc gac gcg ccc tca cag				1315
Ser Gly Glu Leu Arg Val Asp Gly Ile Ile Thr Asp Ala Pro Ser Gln	395	400	405	
cgg tgg acc gaa gca acg cag gca tgg gcg gcc ggg gat atc gag cgc				1363
Arg Trp Thr Glu Ala Thr Gln Ala Trp Ala Ala Gly Asp Ile Glu Arg	410	415	420	
ctt gaa gaa ctt ggc gtt ggt gtc gtg gtg gat gga gat acg atc aca				1411
Leu Glu Glu Leu Gly Val Gly Val Val Val Asp Gly Asp Thr Ile Thr	425	430	435	
gaa act ggc gca cca ccg cag cat ggc tgg aaa tac tac ctc ggt gtg				1459
Glu Thr Gly Ala Pro Pro Gln His Gly Trp Lys Tyr Tyr Leu Gly Val	440	445	450	
ggc ctg acc gtg ctg tgg atg gcg ttg ccg ctg gga cta ctt ttt cga				1507
Gly Leu Thr Val Leu Trp Met Ala Leu Pro Leu Gly Leu Leu Phe Arg	455	460	465	
cgc aag acc aag aag tagttcctcg aactgcgctc ccg				1545
Arg Lys Thr Lys Lys				
470				

<210> 2802

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 2802

Met Thr Pro Thr Arg Arg Ile Leu Leu Trp Ala Trp Thr Thr Val Leu			
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Leu Gly Ser Leu Leu Trp Pro Leu Ala Ala Pro Gly Glu Leu Leu Leu			
20	25	30	

Arg Asp Met Ser Val Val Asp His Pro Ala Leu Ser Leu Asn Ala Leu			
35	40	45	

Gly Phe Gly Asp Leu Pro Ser Arg Asn Ala Pro Gln Asp Gly Val Leu			
50	55	60	

Ala Leu Leu Gly Phe Leu Pro Val Ser Trp Ile Val Arg Thr Met Leu
65 70 75 80

Leu Val Ala Gly Phe Ala Gly Ala Trp Gly Ala Met Arg Leu Gly Pro
85 90 95

Ser Lys Phe Leu Ala Val Thr Val Ala Ile Tyr Asn Pro Phe Val Val
100 105 110

Glu Arg Leu Leu Gln Gly His Trp Ser Leu Val Met Ala Val Trp Leu
115 120 125

Phe Pro Leu Val Val Ala Leu Arg Arg His Pro Arg Trp Gln Val Val
130 135 140

Ala Ile Trp Ala Ala Ser Leu Thr Pro Thr Gly Ala Val Val Ala Ala
145 150 155 160

Val Thr Gly Val Ala Ser Ser Lys Arg Lys Arg Phe Thr Thr Leu Cys
165 170 175

Ser Phe Leu Ser Trp Leu Pro Trp Leu Ile Pro Ala Leu Leu Ala Thr
180 185 190

Pro Thr Ser Gly Gly Ala Leu Thr Phe Ala Ile Arg Ser Glu Thr Tyr
195 200 205

Ala Gly Thr Leu Gly Thr Ala Leu Gly Leu Gly Gly Ile Trp Asn Ala
210 215 220

Gly Ala Val Pro Ala Ser Arg Glu Leu Gly Phe Ala Val Ala Gly Ile
225 230 235 240

Leu Leu Phe Ala Ile Leu Leu Ala Gly Phe Lys Asn Cys Pro Trp Val
245 250 255

Leu Ala Leu Leu Ala Val Val Gly Phe Met Gly Ala Ile Gly Pro Trp
260 265 270

Leu Met Pro Asn Leu Phe Thr Trp Thr Ile Ala Tyr Val Pro Gly Ala
275 280 285

Ala Leu Phe Arg Asp Ser Gln Lys Leu Leu Met Leu Ala Ile Pro Ala
290 295 300

Tyr Val Cys Leu Ala Ala Gly Val Lys Ser Pro Leu Ser Trp Val Ala
305 310 315 320

Thr Gly Leu Ala Leu Leu Gln Ile Pro Asp Ala Pro Arg Glu Val Ser
325 330 335

Val Ile Arg Pro Ser Ser Ala His Val Glu Ser Val Glu Ala Leu Ala
340 345 350

Glu Ile Ala Asp Gly Arg Asp Ile Leu Ile Ile Gly Gln Gly Pro Leu
355 360 365

Val Thr Arg Glu Asp Gly Ile Pro Val Val Asp Pro Lys Thr Lys Ala
370 375 380

Leu Ser Val Val Glu Ser Gly Glu Leu Arg Val Asp Gly Ile Ile Thr

385		390		395		400
Asp Ala Pro Ser Gln Arg Trp Thr Glu Ala Thr Gln Ala Trp Ala Ala						
	405			410		415
Gly Asp Ile Glu Arg Leu Glu Glu Leu Gly Val Gly Val Val Val Asp						
	420		425			430
Gly Asp Thr Ile Thr Glu Thr Gly Ala Pro Pro Gln His Gly Trp Lys						
	435		440		445	
Tyr Tyr Leu Gly Val Gly Leu Thr Val Leu Trp Met Ala Leu Pro Leu						
	450		455		460	
Gly Leu Leu Phe Arg Arg Lys Thr Lys Lys						
465		470				

<210> 2803

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> RXA02577

<400> 2803

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ggggtcgacg gaggtttgga atgcaacgtg ggtcgccaag actcccaggg aggcgattgc 60

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gcgtagtccc tcgagtgcgc tgatgaatcc gcgatggcgg atg ggt gca tat gat 115
                               Met Gly Ala Tyr Asp
                               1                               5

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tgg gta gac att att tca aca tgc gag ttt agc gga aag gtg tgg gct 163
Trp Val Asp Ile Ile Ser Thr Cys Glu Phe Ser Gly Lys Val Trp Ala
                10                15                20

```

```

gtt ttt atg aag cga tct gca acg gtc ctc att att gcg ggc gtg ctg 211
Val Phe Met Lys Arg Ser Ala Thr Val Leu Ile Ile Ala Gly Val Leu
                25                30                35

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```

ttc ctc att ttt gcc ttc acg gta ccg ccg tat gtg act ggt cag gcg 259
Phe Leu Ile Phe Ala Phe Thr Val Pro Pro Tyr Val Thr Gly Gln Ala
                40                45                50

```

```

cgg acg att ccg aag gat ttg gat ctg acg ttg gtg agc gaa agt ccg 307
Arg Thr Ile Pro Lys Asp Leu Asp Leu Thr Leu Val Ser Glu Ser Pro
                55                60                65

```

```

cag ggg ttt gtg cgc act gaa cat att gtg act gct ccg acg gaa aag 355
Gln Gly Phe Val Arg Thr Glu His Ile Val Thr Ala Pro Thr Glu Lys
                70                75                80                85

```

```

gtc gat gag atc gcg acg cat gtg gat cag aca gtt acg gat gtg cag 403
Val Asp Glu Ile Ala Thr His Val Asp Gln Thr Val Thr Asp Val Gln
                90                95                100

```

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ggg aaa act gtt gcg gaa att tcg gat gat gtg gtg ttg att gga cac 451
Gly Lys Thr Val Ala Glu Ile Ser Asp Asp Val Val Leu Ile Gly His

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105	110	115	
tct cgt tat ccg gtg att aag ccg act gcc acc att tcg ggt tcg ccg Ser Arg Tyr Pro Val Ile Lys Pro Thr Ala Thr Ile Ser Gly Ser Pro 120 125 130			499
gcg gat agt agc aat gtg gtg cgg gag ggg ttg cat tac ttc ttc ccg Ala Asp Ser Ser Asn Val Val Arg Glu Gly Leu His Tyr Phe Phe Pro 135 140 145			547
gct aat acg ttg cgg aat tct tat ccc tat tat gac atc gta ttg ggt Ala Asn Thr Leu Arg Asn Ser Tyr Pro Tyr Tyr Asp Ile Val Leu Gly 150 155 160 165			595
gag gat tcc ccg gtg gat tat gtc tcg cgc gag ggc aat act tat acc Glu Asp Ser Pro Val Asp Tyr Val Ser Arg Glu Gly Asn Thr Tyr Thr 170 175 180			643
ttc tac cag cat ctt cgt tat gtt cca ttg gat gat tct cac acc tat Phe Tyr Gln His Leu Arg Tyr Val Pro Leu Asp Asp Ser His Thr Tyr 185 190 195			691
tcg gtg gag cgg acc ctg aaa gtg gat cgt ttt tcc ggc atc att gtg Ser Val Glu Arg Thr Leu Lys Val Asp Arg Phe Ser Gly Ile Ile Val 200 205 210			739
gct aaa gat gag gcg atg acg ttt cat ggc cca gac ggc gat gac aca Ala Lys Asp Glu Ala Met Thr Phe His Gly Pro Asp Gly Asp Asp Thr 215 220 225			787
gta gaa ttc act tat act gcg gat acg ttg aag ctt ctg cag gat cat Val Glu Phe Thr Tyr Thr Ala Asp Thr Leu Lys Leu Leu Gln Asp His 230 235 240 245			835
gcg cat gat att gat cag cgg ttg tcg tgg gct aag ggg ttt gat ttc Ala His Asp Ile Asp Gln Arg Leu Ser Trp Ala Lys Gly Phe Asp Phe 250 255 260			883
ttt tct aaa ttc tta ggc ctg tcg ttg ctt gcg att ggt gtg ttc ctc Phe Ser Lys Phe Leu Gly Leu Ser Leu Leu Ala Ile Gly Val Phe Leu 265 270 275			931
acg gga att ttc aag cgc ggc cag ctg atg agc act gtg aat aaa ctc Thr Gly Ile Phe Lys Arg Gly Gln Leu Met Ser Thr Val Asn Lys Leu 280 285 290			979
agg agt taaatcctta tgaccccgac ccg Arg Ser 295			1008

<210> 2804

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 2804

Met	Gly	Ala	Tyr	Asp	Trp	Val	Asp	Ile	Ile	Ser	Thr	Cys	Glu	Phe	Ser
1				5				10						15	

Gly Lys Val Trp Ala Val Phe Met Lys Arg Ser Ala Thr Val Leu Ile

20	25	30
Ile Ala Gly Val Leu Phe Leu	Ile Phe Ala Phe Thr Val	Pro Pro Tyr
35	40	45
Val Thr Gly Gln Ala Arg Thr	Ile Pro Lys Asp Leu Asp	Leu Thr Leu
50	55	60
Val Ser Glu Ser Pro Gln Gly Phe	Val Arg Thr Glu His Ile	Val Thr
65	70	75
Ala Pro Thr Glu Lys Val Asp Glu	Ile Ala Thr His Val Asp	Gln Thr
85	90	95
Val Thr Asp Val Gln Gly Lys Thr	Val Ala Glu Ile Ser Asp	Asp Val
100	105	110
Val Leu Ile Gly His Ser Arg Tyr	Pro Val Ile Lys Pro Thr	Ala Thr
115	120	125
Ile Ser Gly Ser Pro Ala Asp Ser	Ser Asn Val Val Arg Glu Gly	Leu
130	135	140
His Tyr Phe Phe Pro Ala Asn Thr	Leu Arg Asn Ser Tyr Pro Tyr	Tyr
145	150	155
Asp Ile Val Leu Gly Glu Asp Ser	Pro Val Asp Tyr Val Ser Arg	Glu
165	170	175
Gly Asn Thr Tyr Thr Phe Tyr Gln	His Leu Arg Tyr Val Pro	Leu Asp
180	185	190
Asp Ser His Thr Tyr Ser Val Glu	Arg Thr Leu Lys Val Asp	Arg Phe
195	200	205
Ser Gly Ile Ile Val Ala Lys Asp	Glu Ala Met Thr Phe His Gly	Pro
210	215	220
Asp Gly Asp Asp Thr Val Glu Phe	Thr Tyr Thr Ala Asp Thr	Leu Lys
225	230	235
Leu Leu Gln Asp His Ala His Asp	Ile Asp Gln Arg Leu Ser Trp	Ala
245	250	255
Lys Gly Phe Asp Phe Phe Ser Lys	Phe Leu Gly Leu Ser Leu	Leu Ala
260	265	270
Ile Gly Val Phe Leu Thr Gly Ile	Phe Lys Arg Gly Gln Leu Met	Ser
275	280	285
Thr Val Asn Lys Leu Arg Ser		
290	295	

<210> 2805

<211> 474

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(451)

<223> RXA02584

<400> 2805

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gacagtccgc aattgaaagg ccagatacgt gaaccgctgg atg tcc ttg ctg tgt 115
 Met Ser Leu Leu Cys
 1 5

gat tcc atc gcc atc ggt ctc ttc gca ctc ttc gcc cgc gtc gcc cac 163
 Asp Ser Ile Ala Ile Gly Leu Phe Ala Leu Phe Ala Arg Val Ala His
 10 15 20

caa agc gcc gac atg cca cta aat gtg cag ggc tgg ttt ttc aca tgg 211
 Gln Ser Ala Asp Met Pro Leu Asn Val Gln Gly Trp Phe Phe Thr Trp
 25 30 35

ctg cca ttc ctc gca ggt gtg ttc atc gcc tac ctg gtg gca atc ctc 259
 Leu Pro Phe Leu Ala Gly Val Phe Ile Ala Tyr Leu Val Ala Ile Leu
 40 45 50

cct gcg aag ctt ccc agc gaa cgc atc cgc ccc gct ggc ctg acc gtg 307
 Pro Ala Lys Leu Pro Ser Glu Arg Ile Arg Pro Ala Gly Leu Thr Val
 55 60 65

tgg ata ctc gcg gta att gtg gga ctt gtg att tgg ggc ttc aac aat 355
 Trp Ile Leu Ala Val Ile Val Gly Leu Val Ile Trp Gly Phe Asn Asn
 70 75 80 85

ggg ggt gtt cca cac tgg tcc ttc atg att gtc gca acg acc gcc tcc 403
 Gly Gly Val Pro His Trp Ser Phe Met Ile Val Ala Thr Thr Ala Ser
 90 95 100

gcc att ttg gtt ctc ggc tgg cga gcg ttg ttt aag gtg aca atg cgc 451
 Ala Ile Leu Val Leu Gly Trp Arg Ala Leu Phe Lys Val Thr Met Arg
 105 110 115

taagtgtttt taaaaaatgg gag 474

<210> 2806

<211> 117

<212> PRT

<213> Corynebacterium glutamicum

<400> 2806

Met Ser Leu Leu Cys Asp Ser Ile Ala Ile Gly Leu Phe Ala Leu Phe
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Ala Arg Val Ala His Gln Ser Ala Asp Met Pro Leu Asn Val Gln Gly
 20 25 30

Trp Phe Phe Thr Trp Leu Pro Phe Leu Ala Gly Val Phe Ile Ala Tyr
 35 40 45

Leu Val Ala Ile Leu Pro Ala Lys Leu Pro Ser Glu Arg Ile Arg Pro
 50 55 60

Ala Gly Leu Thr Val Trp Ile Leu Ala Val Ile Val Gly Leu Val Ile
 65 70 75 80

Trp Gly Phe Asn Asn Gly Gly Val Pro His Trp Ser Phe Met Ile Val
85 90 95

Ala Thr Thr Ala Ser Ala Ile Leu Val Leu Gly Trp Arg Ala Leu Phe
100 105 110

Lys Val Thr Met Arg
115

<210> 2807

<211> 1104

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1081)

<223> RXA02585

<400> 2807

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gatcctatttt ttcctgaggg atcagctgga tttcctcaaa atg ggc atc caa caa 115
Met Gly Ile Gln Gln
1 5

atc cgc cac gtc agc ccc gta ggc gtt gcc ctc acc atg gtg gcg ttg 163
Ile Arg His Val Ser Pro Val Gly Val Ala Leu Thr Met Val Ala Leu
10 15 20

gtg ttg tca ttc gtt gcg atg gcc aga gtc atg cag atc atg ttg aaa 211
Val Leu Ser Phe Val Ala Met Ala Arg Val Met Gln Ile Met Leu Lys
25 30 35

gcc gga ggt agt cct gcg act ctc aaa gcc acc acg gct tta act ttt 259
Ala Gly Gly Ser Pro Ala Thr Leu Lys Ala Thr Thr Ala Leu Thr Phe
40 45 50

gcg gct aac tcc tgg tcc gcg acc ctt cct ggc ggc ccg gcg ttt tcc 307
Ala Ala Asn Ser Trp Ser Ala Thr Leu Pro Gly Gly Pro Ala Phe Ser
55 60 65

gcg att ctc acc tat aaa gtg cag cgc agc tgg ggt gcc agc gcc gtg 355
Ala Ile Leu Thr Tyr Lys Val Gln Arg Ser Trp Gly Ala Ser Ala Val
70 75 80 85

ctg tgt tcg tgg ttt ttc ctg ctc tcc agt gcc cta tcg acc gtc tgg 403
Leu Cys Ser Trp Phe Phe Leu Leu Ser Ser Ala Leu Ser Thr Val Trp
90 95 100

ttg gtt gct ctc ggt gtc atc gcc gtg ttt tat atg ggc gca tcg ctg 451
Leu Val Ala Leu Gly Val Ile Ala Val Phe Tyr Met Gly Ala Ser Leu
105 110 115

aac tta tgg tca ctg atc gcc aca ttc atc gcc atg gtc ggg ctg tct 499
Asn Leu Trp Ser Leu Ile Ala Thr Phe Ile Ala Met Val Gly Leu Ser
120 125 130

ggc gcc gtt tat tgg gca gcc aac aac ccc gac tcc ttg gct cgg tgg 547

Gly	Ala	Val	Tyr	Trp	Ala	Ala	Asn	Asn	Pro	Asp	Ser	Leu	Ala	Arg	Trp		
135						140					145						
gtg	cga	aaa	ttg	acg	aaa	aac	agg	gag	tgg	ggc	ttc	gtc	gaa	aag	ctt	595	
Val	Arg	Lys	Leu	Thr	Lys	Asn	Arg	Glu	Trp	Gly	Phe	Val	Glu	Lys	Leu		
150					155					160					165		
ctt	gga	agc	att	gag	cag	ctg	cgc	tgc	gtc	tgc	ctc	acc	ggg	ccg	caa	643	
Leu	Gly	Ser	Ile	Glu	Gln	Leu	Arg	Ser	Val	Ser	Leu	Thr	Gly	Pro	Gln		
				170					175					180			
ttc	gcg	gcc	agc	acc	gcg	tgg	tct	tta	ggc	aat	agg	ctt	ttc	gac	gcc	691	
Phe	Ala	Ala	Ser	Thr	Ala	Trp	Ser	Leu	Gly	Asn	Arg	Leu	Phe	Asp	Ala		
			185					190					195				
atc	tcc	ctc	tgg	att	tgc	atc	tgg	gcg	gtc	acc	ggc	act	gcc	ccg	atg	739	
Ile	Ser	Leu	Trp	Ile	Cys	Ile	Trp	Ala	Val	Thr	Gly	Thr	Ala	Pro	Met		
		200					205					210					
ttt	gaa	cca	gaa	ccc	aac	aac	acc	acc	atc	gca	ggc	gta	ctg	ttg	gcg	787	
Phe	Glu	Pro	Glu	Pro	Asn	Asn	Thr	Thr	Ile	Ala	Gly	Val	Leu	Leu	Ala		
	215					220					225						
tac	acc	acc	gca	aaa	atc	gca	ggc	tca	atc	caa	gcc	acc	cca	ggc	gga	835	
Tyr	Thr	Thr	Ala	Lys	Ile	Ala	Gly	Ser	Ile	Gln	Ala	Thr	Pro	Gly	Gly		
230					235					240					245		
atc	ggc	ccc	atc	gaa	gcc	gcc	tac	atc	gca	gcc	ctc	gta	gcc	acc	ggt	883	
Ile	Gly	Pro	Ile	Glu	Ala	Ala	Tyr	Ile	Ala	Ala	Leu	Val	Ala	Thr	Gly		
				250					255					260			
atg	acc	gca	gtg	gaa	gcc	gcc	gga	gct	gtc	ata	atc	tac	cgt	tta	tgc	931	
Met	Thr	Ala	Val	Glu	Ala	Ala	Gly	Ala	Val	Ile	Ile	Tyr	Arg	Leu	Cys		
			265					270					275				
tca	ttt	atc	atc	atg	gcg	att	gtc	gga	tgg	gtc	atc	tat	ttt	atc	tat	979	
Ser	Phe	Ile	Ile	Met	Ala	Ile	Val	Gly	Trp	Val	Ile	Tyr	Phe	Ile	Tyr		
		280					285					290					
ttc	acc	ccc	cag	gga	ctc	aag	gcc	aat	gaa	tcc	ctg	gat	gtg	gaa	cag	1027	
Phe	Thr	Pro	Gln	Gly	Leu	Lys	Ala	Asn	Glu	Ser	Leu	Asp	Val	Glu	Gln		
	295					300					305						
gat	acg	att	aac	tca	gac	tct	aac	cga	cag	tcc	gca	att	gaa	agg	cca	1075	
Asp	Thr	Ile	Asn	Ser	Asp	Ser	Asn	Arg	Gln	Ser	Ala	Ile	Glu	Arg	Pro		
310					315					320					325		
gat	acg	tga	acc	gctg	gat	gtc	cttg	ctg								1104	
Asp	Thr																

<210> 2808

<211> 327

<212> PRT

<213> Corynebacterium glutamicum

<400> 2808

Met	Gly	Ile	Gln	Gln	Ile	Arg	His	Val	Ser	Pro	Val	Gly	Val	Ala	Leu
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Thr Met Val Ala Leu Val Leu Ser Phe Val Ala Met Ala Arg Val Met
 20 25 30
 Gln Ile Met Leu Lys Ala Gly Gly Ser Pro Ala Thr Leu Lys Ala Thr
 35 40 45
 Thr Ala Leu Thr Phe Ala Ala Asn Ser Trp Ser Ala Thr Leu Pro Gly
 50 55 60
 Gly Pro Ala Phe Ser Ala Ile Leu Thr Tyr Lys Val Gln Arg Ser Trp
 65 70 75 80
 Gly Ala Ser Ala Val Leu Cys Ser Trp Phe Phe Leu Leu Ser Ser Ala
 85 90 95
 Leu Ser Thr Val Trp Leu Val Ala Leu Gly Val Ile Ala Val Phe Tyr
 100 105 110
 Met Gly Ala Ser Leu Asn Leu Trp Ser Leu Ile Ala Thr Phe Ile Ala
 115 120 125
 Met Val Gly Leu Ser Gly Ala Val Tyr Trp Ala Ala Asn Asn Pro Asp
 130 135 140
 Ser Leu Ala Arg Trp Val Arg Lys Leu Thr Lys Asn Arg Glu Trp Gly
 145 150 155 160
 Phe Val Glu Lys Leu Leu Gly Ser Ile Glu Gln Leu Arg Ser Val Ser
 165 170 175
 Leu Thr Gly Pro Gln Phe Ala Ala Ser Thr Ala Trp Ser Leu Gly Asn
 180 185 190
 Arg Leu Phe Asp Ala Ile Ser Leu Trp Ile Cys Ile Trp Ala Val Thr
 195 200 205
 Gly Thr Ala Pro Met Phe Glu Pro Glu Pro Asn Asn Thr Thr Ile Ala
 210 215 220
 Gly Val Leu Leu Ala Tyr Thr Thr Ala Lys Ile Ala Gly Ser Ile Gln
 225 230 235 240
 Ala Thr Pro Gly Gly Ile Gly Pro Ile Glu Ala Ala Tyr Ile Ala Ala
 245 250 255
 Leu Val Ala Thr Gly Met Thr Ala Val Glu Ala Ala Gly Ala Val Ile
 260 265 270
 Ile Tyr Arg Leu Cys Ser Phe Ile Ile Met Ala Ile Val Gly Trp Val
 275 280 285
 Ile Tyr Phe Ile Tyr Phe Thr Pro Gln Gly Leu Lys Ala Asn Glu Ser
 290 295 300
 Leu Asp Val Glu Gln Asp Thr Ile Asn Ser Asp Ser Asn Arg Gln Ser
 305 310 315 320
 Ala Ile Glu Arg Pro Asp Thr
 325

<210> 2809
 <211> 807
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(784)
 <223> RXA02588

<400> 2809

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                                         Met Ser Asp Val His
                                         1 5

gag gtc att cat agc tac aat ccc act gac aaa gaa ggc cct gaa agt 163
Glu Val Ile His Ser Tyr Asn Pro Thr Asp Lys Glu Gly Pro Glu Ser
                        10 15 20

gtc ctt cta gtg tgg gac gct ccc aac cta gat atg ggt ttg ggc gct 211
Val Leu Leu Val Trp Asp Ala Pro Asn Leu Asp Met Gly Leu Gly Ala
                        25 30 35

att ttg ggt ggt cgc cca acc gct gcg tac cga cct cgc ttt gat gcc 259
Ile Leu Gly Gly Arg Pro Thr Ala Ala Tyr Arg Pro Arg Phe Asp Ala
                        40 45 50

atc ggt cgg tgg ttg ctt gct cgc gca ggt cgc agg gca cat gag ttg 307
Ile Gly Arg Trp Leu Leu Ala Arg Ala Gly Arg Arg Ala His Glu Leu
                        55 60 65

ggc cgc cac att gag cct gag gca acg gtg ttt gcc aac atc acc cca 355
Gly Arg His Ile Glu Pro Glu Ala Thr Val Phe Ala Asn Ile Thr Pro
                        70 75 80 85

ggg ggc tct gat gtt gtt cga cct tgg gtg gaa gcg ctg cgt aac gtt 403
Gly Gly Ser Asp Val Val Arg Pro Trp Val Glu Ala Leu Arg Asn Val
                        90 95 100

ggg ttc gcg gtc ttc gct aag cct aag atc ggc gag gat tcc gat gtc 451
Gly Phe Ala Val Phe Ala Lys Pro Lys Ile Gly Glu Asp Ser Asp Val
                        105 110 115

gat ccg gac atg att gat cac att cgc agg cgc tat gaa gaa ggc gtg 499
Asp Pro Asp Met Ile Asp His Ile Arg Arg Arg Tyr Glu Glu Gly Val
                        120 125 130

ctg cgg ggt gtc atc gtg gcc agt gca gat ggt cag aac ttc cgt gag 547
Leu Arg Gly Val Ile Val Ala Ser Ala Asp Gly Gln Asn Phe Arg Glu
                        135 140 145

act ctc gag gag ctc gtt gca gag ggc att cct gcc acg gtc att ggt 595
Thr Leu Glu Glu Leu Val Ala Glu Gly Ile Pro Ala Thr Val Ile Gly
                        150 155 160 165

ttc cac gag cac gcg tca tgg gct gta gct cat gac acc atc gag ttt 643
Phe His Glu His Ala Ser Trp Ala Val Ala His Asp Thr Ile Glu Phe
                        170 175 180
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gtt gat ctg gag gaa atc ccc ggc gtc ttc cgt gag ccg ctt cct cgc 691
Val Asp Leu Glu Glu Ile Pro Gly Val Phe Arg Glu Pro Leu Pro Arg
185 190 195

gtc agc ctg gat aac ctg cca gac ggt ggc gca tgg ctg cag ccg ttc 739
Val Ser Leu Asp Asn Leu Pro Asp Gly Gly Ala Trp Leu Gln Pro Phe
200 205 210

cgc cct ctg act gcc ttg tta tcc aac cgc cac aat tcc cag gag 784
Arg Pro Leu Thr Ala Leu Ser Asn Arg His Asn Ser Gln Glu
215 220 225

taatccaccc gtgttttcta aat 807

<210> 2810

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 2810

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Glu Gly Pro Glu Ser Val Leu Leu Val Trp Asp Ala Pro Asn Leu Asp
20 25 30

Met Gly Leu Gly Ala Ile Leu Gly Gly Arg Pro Thr Ala Ala Tyr Arg
35 40 45

Pro Arg Phe Asp Ala Ile Gly Arg Trp Leu Leu Ala Arg Ala Gly Arg
50 55 60

Arg Ala His Glu Leu Gly Arg His Ile Glu Pro Glu Ala Thr Val Phe
65 70 75 80

Ala Asn Ile Thr Pro Gly Gly Ser Asp Val Val Arg Pro Trp Val Glu
85 90 95

Ala Leu Arg Asn Val Gly Phe Ala Val Phe Ala Lys Pro Lys Ile Gly
100 105 110

Glu Asp Ser Asp Val Asp Pro Asp Met Ile Asp His Ile Arg Arg Arg
115 120 125

Tyr Glu Glu Gly Val Leu Arg Gly Val Ile Val Ala Ser Ala Asp Gly
130 135 140

Gln Asn Phe Arg Glu Thr Leu Glu Glu Leu Val Ala Glu Gly Ile Pro
145 150 155 160

Ala Thr Val Ile Gly Phe His Glu His Ala Ser Trp Ala Val Ala His
165 170 175

Asp Thr Ile Glu Phe Val Asp Leu Glu Glu Ile Pro Gly Val Phe Arg
180 185 190

Glu Pro Leu Pro Arg Val Ser Leu Asp Asn Leu Pro Asp Gly Gly Ala
195 200 205

Trp Leu Gln Pro Phe Arg Pro Leu Thr Ala Leu Leu Ser Asn Arg His

210

215

220

Asn Ser Gln Glu
225

<210> 2811

<211> 1953

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1930)

<223> RXA02591

<400> 2811

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ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca 115
Met Thr Thr Ala Ala
1 5

atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg 163
Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu
10 15 20

aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg 211
Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val
25 30 35

ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt 259
Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu
40 45 50

gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac 307
Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn
55 60 65

agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc 355
Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser
70 75 80 85

cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac 403
Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn
90 95 100

aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac 451
Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr
105 110 115

gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg 499
Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met
120 125 130

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac 547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp
135 140 145

tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att 595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile

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gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu 170 175 180				643
cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp 185 190 195				691
cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu 200 205 210				739
att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys 215 220 225				787
aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly 230 235 240 245				835
tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly 250 255 260				883
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr 265 270 275				931
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val 280 285 290				979
gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr 295 300 305				1027
gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn 310 315 320 325				1075
tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr 330 335 340				1123
ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu 345 350 355				1171
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn 360 365 370				1219
gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg 375 380 385				1267
tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn 390 395 400 405				1315

gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc 1363
 Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg
 410 415 420

gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc 1411
 Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly
 425 430 435

acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca 1459
 Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala
 440 445 450

gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca 1507
 Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro
 455 460 465

ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg 1555
 Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met
 470 475 480 485

ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg 1603
 Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp
 490 495 500

ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac 1651
 Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp
 505 510 515

aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt 1699
 Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val
 520 525 530

ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc 1747
 Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu
 535 540 545

gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg 1795
 Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu
 550 555 560 565

acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag 1843
 Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu
 570 575 580

tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag 1891
 Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln
 585 590 595

ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac 1940
 Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala
 600 605 610

gcttaagaac tgc 1953

<210> 2812

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 2812

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 Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
 35 40 45
 Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
 50 55 60
 Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65 70 75 80
 Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
 85 90 95
 Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
 100 105 110
 Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
 115 120 125
 Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
 130 135 140
 Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
 145 150 155 160
 Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
 165 170 175
 Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
 180 185 190
 Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
 195 200 205
 Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
 210 215 220
 Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
 225 230 235 240
 Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
 245 250 255
 Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
 260 265 270
 Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
 275 280 285
 Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
 290 295 300
 Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
 305 310 315 320

Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
325 330 335

Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
340 345 350

Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
355 360 365

Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
370 375 380

His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
385 390 395 400

Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
405 410 415

Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
420 425 430

Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
435 440 445

Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
450 455 460

Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
465 470 475 480

Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
485 490 495

Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
500 505 510

Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
515 520 525

Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
530 535 540

Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
545 550 555 560

Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
565 570 575

Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
580 585 590

Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
595 600 605

His Ala
610

<210> 2813

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXA02598

<400> 2813

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                                     Val Thr Thr Asp Gln
                                     1 5
aac aaa aga agt ctc agt gag ctt gcg gcc aga atc gtt agt gaa atc 163
Asn Lys Arg Ser Leu Ser Glu Leu Ala Ala Arg Ile Val Ser Glu Ile
                10                15                20
tgt gca ccg tgg gta ctc aac atc gga ttt ttc ctc atc ctg ggc ggc 211
Cys Ala Pro Trp Val Leu Asn Ile Gly Phe Phe Leu Ile Leu Gly Gly
                25                30                35
gta aca ggc gcc tgg acg cta gga att gtg gcg gca atc gga acc gga 259
Val Thr Gly Ala Trp Thr Leu Gly Ile Val Ala Ala Ile Gly Thr Gly
                40                45                50
atc gtt ccg atg atc tta att ttg ggc ttg atg aag ctc ggc agg gta 307
Ile Val Pro Met Ile Leu Ile Leu Gly Leu Met Lys Leu Gly Arg Val
                55                60                65
gga aac cac cat gtg acg acc cga aat cag cgc ggc ctt gtg ttt gtg 355
Gly Asn His His Val Thr Thr Arg Asn Gln Arg Gly Leu Val Phe Val
                70                75                80                85
ggc atc att gtt tgt gtc atc att ttg att ttt atc ctc aga gcc ctt 403
Gly Ile Ile Val Cys Val Ile Ile Leu Ile Phe Ile Leu Arg Ala Leu
                90                95                100
gaa gca cct cag ctg att tgg gat ggc atg ttc tca gca ctg att ttc 451
Glu Ala Pro Gln Leu Ile Trp Asp Gly Met Phe Ser Ala Leu Ile Phe
                105                110                115
tta gtt ctg ttt gca caa gtg acg ttg aaa att aaa gcc tca gtt cat 499
Leu Val Leu Phe Ala Gln Val Thr Leu Lys Ile Lys Ala Ser Val His
                120                125                130
gtt ggg ctg tgg gtg tgt tta gtg atg ttc ctc ggt ctg acg gtt tct 547
Val Gly Leu Trp Val Cys Leu Val Met Phe Leu Gly Leu Thr Val Ser
                135                140                145
tcg tgg tgg tta ctc ggg ttg ctg ttt acc cca gtc acc gcg tgg gca 595
Ser Trp Trp Leu Leu Gly Leu Leu Phe Thr Pro Val Thr Ala Trp Ala
                150                155                160                165
cgt atg cgg atc aag cat cat acg atg tcg gag att gtg gcg ggc gtt 643
Arg Met Arg Ile Lys His His Thr Met Ser Glu Ile Val Ala Gly Val
                170                175                180
gtt aca gga gca gtt gca acc ggc att tgt tat gca ctc cta ctt gcg 691
Val Thr Gly Ala Val Ala Thr Gly Ile Cys Tyr Ala Leu Leu Leu Ala
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<210> 2814

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 2814

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Leu Ile Leu Gly Gly Val Thr Gly Ala Trp Thr Leu Gly Ile Val Ala
35 40 45

Ala Ile Gly Thr Gly Ile Val Pro Met Ile Leu Ile Leu Gly Leu Met
50 55 60

Lys Leu Gly Arg Val Gly Asn His His Val Thr Thr Arg Asn Gln Arg
65 70 75 80

Gly Leu Val Phe Val Gly Ile Ile Val Cys Val Ile Ile Leu Ile Phe
85 90 95

Ile Leu Arg Ala Leu Glu Ala Pro Gln Leu Ile Trp Asp Gly Met Phe
100 105 110

Ser Ala Leu Ile Phe Leu Val Leu Phe Ala Gln Val Thr Leu Lys Ile
115 120 125

Lys Ala Ser Val His Val Gly Leu Trp Val Cys Leu Val Met Phe Leu
130 135 140

Gly Leu Thr Val Ser Ser Trp Trp Leu Leu Gly Leu Leu Phe Thr Pro
145 150 155 160

Val Thr Ala Trp Ala Arg Met Arg Ile Lys His His Thr Met Ser Glu
165 170 175

Ile Val Ala Gly Val Val Thr Gly Ala Val Ala Thr Gly Ile Cys Tyr
180 185 190

Ala Leu Leu Leu Ala
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<210> 2815

<211> 1521

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1498)

<223> RXA02600

<400> 2815

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ctg tcc tta acc aac agc tcc gtc gct ggt att gca gcg gga gcg ttg	Leu Ser Leu Thr Asn Ser Ser Val Ala Gly Ile Ala Ala Gly Ala Leu	163													
ctg ttt ctc tcc gtc cct ttc gca tcg cct gtt cac gcg caa acc ata Leu Phe Leu Ser Val Pro Phe Ala Ser Pro Val His Ala Gln Thr Ile 10 15 20 25 30 35															211
ctg caa gac acc ctt gaa gtg act gtg ttg gat aat gcc gac gag ctc	Leu Gln Asp Thr Leu Glu Val Thr Val Leu Asp Asn Ala Asp Glu Leu 40 45 50	259													
gct cca gag gat gag gat ttc ctc agc acg gaa aca ccc aag att gat	Ala Pro Glu Asp Glu Asp Phe Leu Ser Thr Glu Thr Pro Lys Ile Asp 55 60 65	307													
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act gac aaa atc aat gat gac gtt gaa aat tac ctg cgc gcc gaa cac	Thr Asp Lys Ile Asn Asp Asp Val Glu Asn Tyr Leu Arg Ala Glu His 90 95 100	403													
ccc gag tgg atc caa aca aac tct ttc gcc cct ggt gaa gtg atc atc	Pro Glu Trp Ile Gln Thr Asn Ser Phe Ala Pro Gly Glu Val Ile Ile 105 110 115	451													
gca gtc ggt ttc gac ccc aac acc atg ggt gcc tac gcg ggt aac gat	Ala Val Gly Phe Asp Pro Asn Thr Met Gly Ala Tyr Ala Gly Asn Asp 120 125 130	499													
gtg gcc gca gag act ggg atc gca gaa caa gac cgc atc gac ggc acc	Val Ala Ala Glu Thr Gly Ile Ala Glu Gln Asp Arg Ile Asp Gly Thr 135 140 145	547													
acc gat gcg atg cgc cca tta ctc caa gac ggt cgc att gcc cta ggc	Thr Asp Ala Met Arg Pro Leu Leu Gln Asp Gly Arg Ile Ala Leu Gly 150 155 160 165	595													
atg ttg gag ggt gca aaa tcg gtt gct gat acc tct gtc gtt cgg gaa	Met Leu Glu Gly Ala Lys Ser Val Ala Asp Thr Ser Val Val Arg Glu 170 175 180	643													
agc tca gct cca agt ggt gga gta atc gcc gct att ttg ggt ggc atc	Ser Ser Ala Pro Ser Gly Gly Val Ile Ala Ala Ile Leu Gly Gly Ile 185 190 195	691													
gct gct ctc gtg gca att att gtc gcg tgg gct acg agt tac gcg aat	Ala Ala Leu Val Ala Ile Ile Val Ala Trp Ala Thr Ser Tyr Ala Asn 200 205 210	739													
aag aag aag gca gaa aag gct cgt gag cag ttt gat tat gca tca cgc	Lys Lys Lys Ala Glu Lys Ala Arg Glu Gln Phe Asp Tyr Ala Ser Arg 215 220 225	787													

cat tat ggt gag gtc gcc cag caa ctc gac ggt atc aac gtg cga gcg His Tyr Gly Glu Val Ala Gln Gln Leu Asp Gly Ile Asn Val Arg Ala 230 235 240 245	835
cac tcg cta act tcc cca ctg gct gat gat gag ctc cgc agg caa tgg His Ser Leu Thr Ser Pro Leu Ala Asp Asp Glu Leu Arg Arg Gln Trp 250 255 260	883
gac gat gta aat tct cgt ttt ctt gaa gtc aat gat att ttt ggc agg Asp Asp Val Asn Ser Arg Phe Leu Glu Val Asn Asp Ile Phe Gly Arg 265 270 275	931
ctc gaa ggt ttg acc tcg acc tca gaa aac aag gca ttt cga aaa gcc Leu Glu Gly Leu Thr Ser Thr Ser Glu Asn Lys Ala Phe Arg Lys Ala 280 285 290	979
ttg cca gat att gaa aaa gct cat act gcc gtg act caa atg gag atc Leu Pro Asp Ile Glu Lys Ala His Thr Ala Val Thr Gln Met Glu Ile 295 300 305	1027
gca cag aaa aac att gac acg ctc tac gat atg gag cac ggc cat gaa Ala Gln Lys Asn Ile Asp Thr Leu Tyr Asp Met Glu His Gly His Glu 310 315 320 325	1075
gac acc cgt cgc agg gaa tta act agg ctg cgt gcc gat atg cag gaa Asp Thr Arg Arg Arg Glu Leu Thr Arg Leu Arg Ala Asp Met Gln Glu 330 335 340	1123
gcc cgt caa gat atc aac gat aaa gat gca gtt gtt gac gat att ctc Ala Arg Gln Asp Ile Asn Asp Lys Asp Ala Val Val Asp Asp Ile Leu 345 350 355	1171
cgc acg ctg atc cag cgc acg gaa act atc gca ccg tcc gca cct gat Arg Thr Leu Ile Gln Arg Thr Glu Thr Ile Ala Pro Ser Ala Pro Asp 360 365 370	1219
ttc atg gac caa tac gcc cgc ttg atc cgt gat tat gcc gtg gcg ctt Phe Met Asp Gln Tyr Ala Arg Leu Ile Arg Asp Tyr Ala Val Ala Leu 375 380 385	1267
caa ggt gtg gaa aag aac ctc gag cag gtt aaa cag acc acc gag cgc Gln Gly Val Glu Lys Asn Leu Glu Gln Val Lys Gln Thr Thr Glu Arg 390 395 400 405	1315
aat gct cca gcc atc tac gac gac aat tgg cgc gtg ggc act ggc tac Asn Ala Pro Ala Ile Tyr Asp Asp Asn Trp Arg Val Gly Thr Gly Tyr 410 415 420	1363
aac tcg tgg gtc ccg tac tac atg atc agt tct tgg cac gca gct gat Asn Ser Trp Val Pro Tyr Tyr Met Ile Ser Ser Trp His Ala Ala Asp 425 430 435	1411
gtc agt gct gca tcg tca gct tct tcc agt tca gca aat acc act ttc Val Ser Ala Ala Ser Ser Ala Ser Ser Ser Ala Asn Thr Thr Phe 440 445 450	1459
agc agt ggt ttc agc ggc gct gga gga ggt tcc agc tgg taaacaccac Ser Ser Gly Phe Ser Gly Ala Gly Gly Gly Ser Ser Trp 455 460 465	1508

cactgaagtc aac

1521

<210> 2816

<211> 466

<212> PRT

<213> Corynebacterium glutamicum

<400> 2816

Met Gln Pro Phe Pro Leu Ser Leu Thr Asn Ser Ser Val Ala Gly Ile
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Ala Ala Gly Ala Leu Leu Phe Leu Ser Val Pro Phe Ala Ser Pro Val
20 25 30
His Ala Gln Thr Ile Leu Gln Asp Thr Leu Glu Val Thr Val Leu Asp
35 40 45
Asn Ala Asp Glu Leu Ala Pro Glu Asp Glu Asp Phe Leu Ser Thr Glu
50 55 60
Thr Pro Lys Ile Asp Phe Pro Asp Ser Val Thr Ala Val Arg Tyr Ile
65 70 75 80
Thr Leu Thr Asp Asn Thr Asp Lys Ile Asn Asp Asp Val Glu Asn Tyr
85 90 95
Leu Arg Ala Glu His Pro Glu Trp Ile Gln Thr Asn Ser Phe Ala Pro
100 105 110
Gly Glu Val Ile Ile Ala Val Gly Phe Asp Pro Asn Thr Met Gly Ala
115 120 125
Tyr Ala Gly Asn Asp Val Ala Ala Glu Thr Gly Ile Ala Glu Gln Asp
130 135 140
Arg Ile Asp Gly Thr Thr Asp Ala Met Arg Pro Leu Leu Gln Asp Gly
145 150 155 160
Arg Ile Ala Leu Gly Met Leu Glu Gly Ala Lys Ser Val Ala Asp Thr
165 170 175
Ser Val Val Arg Glu Ser Ser Ala Pro Ser Gly Gly Val Ile Ala Ala
180 185 190
Ile Leu Gly Gly Ile Ala Ala Leu Val Ala Ile Ile Val Ala Trp Ala
195 200 205
Thr Ser Tyr Ala Asn Lys Lys Lys Ala Glu Lys Ala Arg Glu Gln Phe
210 215 220
Asp Tyr Ala Ser Arg His Tyr Gly Glu Val Ala Gln Gln Leu Asp Gly
225 230 235 240
Ile Asn Val Arg Ala His Ser Leu Thr Ser Pro Leu Ala Asp Asp Glu
245 250 255
Leu Arg Arg Gln Trp Asp Asp Val Asn Ser Arg Phe Leu Glu Val Asn
260 265 270
Asp Ile Phe Gly Arg Leu Glu Gly Leu Thr Ser Thr Ser Glu Asn Lys

275	280	285
Ala Phe Arg Lys Ala Leu Pro Asp Ile Glu Lys 290	Ala His Thr Ala Val 300	
Thr Gln Met Glu Ile Ala Gln Lys Asn Ile Asp Thr Leu Tyr Asp Met 305	310	315 320
Glu His Gly His Glu Asp Thr Arg Arg Arg Glu Leu Thr Arg Leu Arg 325	330	335
Ala Asp Met Gln Glu Ala Arg Gln Asp Ile Asn Asp Lys Asp Ala Val 340	345	350
Val Asp Asp Ile Leu Arg Thr Leu Ile Gln Arg Thr Glu Thr Ile Ala 355	360	365
Pro Ser Ala Pro Asp Phe Met Asp Gln Tyr Ala Arg Leu Ile Arg Asp 370	375	380
Tyr Ala Val Ala Leu Gln Gly Val Glu Lys Asn Leu Glu Gln Val Lys 385	390	395 400
Gln Thr Thr Glu Arg Asn Ala Pro Ala Ile Tyr Asp Asp Asn Trp Arg 405	410	415
Val Gly Thr Gly Tyr Asn Ser Trp Val Pro Tyr Tyr Met Ile Ser Ser 420	425	430
Trp His Ala Ala Asp Val Ser Ala Ala Ser Ser Ala Ser Ser Ser Ser 435	440	445
Ala Asn Thr Thr Phe Ser Ser Gly Phe Ser Gly Ala Gly Gly Gly Ser 450	455	460
Ser Trp 465		

<210> 2817
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2089)
 <223> RXA02601

<400> 2817
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 Met Lys Gly Glu Asp
 1 5
 acg tca atg agc gca aca aac ctg gcg gtt gag cag cta cag cga gtg 163
 Thr Ser Met Ser Ala Thr Asn Leu Ala Val Glu Gln Leu Gln Arg Val
 10 15 20
 ctc ctg ccg agg cgc ggc gag cca gca gat gtc agg tcg ttg tac ctg 211

Leu	Leu	Pro	Arg	Arg	Gly	Glu	Pro	Ala	Asp	Val	Arg	Ser	Leu	Tyr	Leu		
			25					30					35				
ttg	gaa	gca	gaa	agt	aat	aag	gaa	cgc	ctg	gaa	tgg	gaa	gat	cgt	ttt	259	
Leu	Glu	Ala	Glu	Ser	Asn	Lys	Glu	Arg	Leu	Glu	Trp	Glu	Asp	Arg	Phe		
		40					45					50					
agc	gtt	tcc	gtc	ccc	gct	ggc	gcc	gag	gtg	tct	ttt	cag	acc	tac	ttc	307	
Ser	Val	Ser	Val	Pro	Ala	Gly	Ala	Glu	Val	Ser	Phe	Gln	Thr	Tyr	Phe		
	55					60					65						
aat	gca	ttt	cct	gca	agc	tac	tgg	cgt	cgc	tgg	tca	cag	cta	gat	tct	355	
Asn	Ala	Phe	Pro	Ala	Ser	Tyr	Trp	Arg	Arg	Trp	Ser	Gln	Leu	Asp	Ser		
70					75					80					85		
gtc	gta	ctg	aaa	ctg	aaa	gtt	tcc	ggc	gaa	gcg	cgc	gtc	gac	ctc	tac	403	
Val	Val	Leu	Lys	Leu	Lys	Val	Ser	Gly	Glu	Ala	Arg	Val	Asp	Leu	Tyr		
			90						95					100			
cga	tcc	aag	atc	gat	gga	gca	cgc	atc	gga	att	acc	ggg	tcc	gta	gtc	451	
Arg	Ser	Lys	Ile	Asp	Gly	Ala	Arg	Ile	Gly	Ile	Thr	Gly	Ser	Val	Val		
			105					110					115				
aaa	gat	gac	ttc	atc	gaa	ttt	gaa	gtt	tca	tta	gcc	cca	ttc	gaa	gac	499	
Lys	Asp	Asp	Phe	Ile	Glu	Phe	Glu	Val	Ser	Leu	Ala	Pro	Phe	Glu	Asp		
		120					125					130					
ggc	ggc	tgg	atc	tgg	ttc	gac	ctc	acc	gct	gaa	acc	gac	gca	acc	gtc	547	
Gly	Gly	Trp	Ile	Trp	Phe	Asp	Leu	Thr	Ala	Glu	Thr	Asp	Ala	Thr	Val		
	135					140					145						
gaa	gaa	gca	ggc	tgg	tac	gct	cca	cac	gcg	cca	aaa	gcc	cag	atc	atg	595	
Glu	Glu	Ala	Gly	Trp	Tyr	Ala	Pro	His	Ala	Pro	Lys	Ala	Gln	Ile	Met		
150					155				160						165		
cca	gat	gga	tct	gaa	gtc	ggc	cca	ttt	gaa	gcc	cgt	gca	acc	gtc	gga	643	
Pro	Asp	Gly	Ser	Glu	Val	Gly	Pro	Phe	Glu	Ala	Arg	Ala	Thr	Val	Gly		
				170					175					180			
atc	ccg	acc	ttc	aac	cgc	cca	gct	gat	gca	gtt	gca	gca	ctg	gaa	gca	691	
Ile	Pro	Thr	Phe	Asn	Arg	Pro	Ala	Asp	Ala	Val	Ala	Ala	Leu	Glu	Ala		
			185					190					195				
ctt	gcc	tcc	gac	cca	gca	gtt	gac	gcc	gtc	att	gat	acc	gtc	atc	atg	739	
Leu	Ala	Ser	Asp	Pro	Ala	Val	Asp	Ala	Val	Ile	Asp	Thr	Val	Ile	Met		
		200					205					210					
cct	gat	caa	ggc	aac	aag	cac	cct	gcc	gac	gag	cca	ggg	tac	aag	gca	787	
Pro	Asp	Gln	Gly	Asn	Lys	His	Pro	Ala	Asp	Glu	Pro	Gly	Tyr	Lys	Ala		
	215					220					225						
gct	gtt	gag	cac	ttc	ggc	gac	cgc	ttc	ttc	gaa	ttc	cgc	cag	ggc	aac	835	
Ala	Val	Glu	His	Phe	Gly	Asp	Arg	Phe	Phe	Glu	Phe	Arg	Gln	Gly	Asn		
230					235					240					245		
ctc	ggc	gga	tcc	ggc	ggg	tac	tcc	cgc	atc	atg	ttc	gaa	gcc	ctt	ggc	883	
Leu	Gly	Gly	Ser	Gly	Gly	Tyr	Ser	Arg	Ile	Met	Phe	Glu	Ala	Leu	Gly		
				250					255					260			
gga	gtc	gac	ggc	aag	ggc	gaa	gca	ggc	gct	gcc	aag	agc	cca	tac	atc	931	
Gly	Val	Asp	Gly	Lys	Gly	Glu	Ala	Gly	Ala	Ala	Lys	Ser	Pro	Tyr	Ile		

265	270	275	
ctg tac atg gat gac gac att gct att gag cca gac tca gtg ctg cgt Leu Tyr Met Asp Asp Asp Ile Ala Ile Glu Pro Asp Ser Val Leu Arg 280 285 290			979
gcg ctt cag gta gcc cgc tac gca aaa tcc ccc atc ctc gtt ggc gga Ala Leu Gln Val Ala Arg Tyr Ala Lys Ser Pro Ile Leu Val Gly Gly 295 300 305			1027
caa atg ctc aac ctg caa gag cgc agc cac ctt cac acc atg ggc gaa Gln Met Leu Asn Leu Gln Glu Arg Ser His Leu His Thr Met Gly Glu 310 315 320 325			1075
gta gtt ggc gga cac gac ttc atg tgg acc gcc gca cca cac gtg cac Val Val Gly Gly His Asp Phe Met Trp Thr Ala Ala Pro His Val His 330 335 340			1123
tac gac cac gac ttc tct gca cac cca cta cat gat cgc ggt aaa ttc Tyr Asp His Asp Phe Ser Ala His Pro Leu His Asp Arg Gly Lys Phe 345 350 355			1171
gac gac aag cca gac gca cca aac tcc cgc gac ctg cac cgc cgc atc Asp Asp Lys Pro Asp Ala Pro Asn Ser Arg Asp Leu His Arg Arg Ile 360 365 370			1219
gac gtt gac ttc aac ggc tgg tgg atg tgc atg atc cca cgc gtt gtc Asp Val Asp Phe Asn Gly Trp Trp Met Cys Met Ile Pro Arg Val Val 375 380 385			1267
gcc gaa cag atc ggc caa cca ctc cca ctc ttt atc aag tgg gac gac Ala Glu Gln Ile Gly Gln Pro Leu Pro Leu Phe Ile Lys Trp Asp Asp 390 395 400 405			1315
gcc gaa tac ggt cta cgc gca cgc aaa gct gga ttc ccc aca gca acc Ala Glu Tyr Gly Leu Arg Ala Arg Lys Ala Gly Phe Pro Thr Ala Thr 410 415 420			1363
tgg cca gga atc gca atc tgg cac atg gcc tgg tcc gac aaa gac gac Trp Pro Gly Ile Ala Ile Trp His Met Ala Trp Ser Asp Lys Asp Asp 425 430 435			1411
gcc atc gac tgg cag gcc tac ttc cac ctc cgc aac cgc ctc gtg gtt Ala Ile Asp Trp Gln Ala Tyr Phe His Leu Arg Asn Arg Leu Val Val 440 445 450			1459
gcc gcg atg tac cac caa ggc agc gtc gac ggc att gtc cga tcg atg Ala Ala Met Tyr His Gln Gly Ser Val Asp Gly Ile Val Arg Ser Met 455 460 465			1507
caa aaa gcc acc ttc aag cac ctg ctg tgc ctg gaa tac tcc acc gtg Gln Lys Ala Thr Phe Lys His Leu Leu Cys Leu Glu Tyr Ser Thr Val 470 475 480 485			1555
gca atc caa aac gaa gca atg aag gac ttc ctt gca gga cca gat cag Ala Ile Gln Asn Glu Ala Met Lys Asp Phe Leu Ala Gly Pro Asp Gln 490 495 500			1603
ctc ttc tcg atc ctg gac acc tca cta cct cga att gca gcg att cgc Leu Phe Ser Ile Leu Asp Thr Ser Leu Pro Arg Ile Ala Ala Ile Arg 505 510 515			1651

aaa acc tat cca gac gcc gtt gtg ctg cca agc gcc acc gaa ctg cca 1699
 Lys Thr Tyr Pro Asp Ala Val Val Leu Pro Ser Ala Thr Glu Leu Pro
 520 525 530

cga gca acc ggc gcg ccg ggt gtc cca acc aag gac atc ggt gga cgc 1747
 Arg Ala Thr Gly Ala Pro Gly Val Pro Thr Lys Asp Ile Gly Gly Arg
 535 540 545

ctg gcc cca atc aag aag gca atg tgg ctg gct aag ggc ctg aag cac 1795
 Leu Ala Pro Ile Lys Lys Ala Met Trp Leu Ala Lys Gly Leu Lys His
 550 555 560 565

tcc ctg tct aag gaa gat gcc tcc cac cac gag gtg cca cag gcc aac 1843
 Ser Leu Ser Lys Glu Asp Ala Ser His His Glu Val Pro Gln Ala Asn
 570 575 580

ttc gca cca atc gaa gca cgt tgg ttc agc ctg tcc cga gtc gat ggc 1891
 Phe Ala Pro Ile Glu Ala Arg Trp Phe Ser Leu Ser Arg Val Asp Gly
 585 590 595

gca aca gtt acc acc gcg gat ggc cgc ggc gtg gtc tac cgc aag cgc 1939
 Ala Thr Val Thr Thr Ala Asp Gly Arg Gly Val Val Tyr Arg Lys Arg
 600 605 610

gac cgc gac aaa gct aaa gaa ctt ggc aaa gaa gca cgc gca ctg caa 1987
 Asp Arg Asp Lys Ala Lys Glu Leu Gly Lys Glu Ala Arg Ala Leu Gln
 615 620 625

aag caa gta gca gag cgt ttc gac gaa ctc agt cgc gcc tac cgc aac 2035
 Lys Gln Val Ala Glu Arg Phe Asp Glu Leu Ser Arg Ala Tyr Arg Asn
 630 635 640 645

gct cat cct gag ctt gtg agc cgt gaa gcc tgg gga aag gtc ttc gat 2083
 Ala His Pro Glu Leu Val Ser Arg Glu Ala Trp Gly Lys Val Phe Asp
 650 655 660

gag caa taaggaagta cagattctgg tag 2112
 Glu Gln

<210> 2818

<211> 663

<212> PRT

<213> Corynebacterium glutamicum

<400> 2818

Met Lys Gly Glu Asp Thr Ser Met Ser Ala Thr Asn Leu Ala Val Glu
 1 5 10 15

Gln Leu Gln Arg Val Leu Leu Pro Arg Arg Gly Glu Pro Ala Asp Val
 20 25 30

Arg Ser Leu Tyr Leu Leu Glu Ala Glu Ser Asn Lys Glu Arg Leu Glu
 35 40 45

Trp Glu Asp Arg Phe Ser Val Ser Val Pro Ala Gly Ala Glu Val Ser
 50 55 60

Phe Gln Thr Tyr Phe Asn Ala Phe Pro Ala Ser Tyr Trp Arg Arg Trp

65	70	75	80
Ser Gln Leu Asp	Ser Val Val Leu Lys	Leu Lys Val Ser Gly	Glu Ala
	85	90	95
Arg Val Asp Leu Tyr Arg Ser Lys	Ile Asp Gly Ala Arg	Ile Gly Ile	
	100	105	110
Thr Gly Ser Val Val Lys Asp	Asp Phe Ile Glu Phe	Glu Val Ser Leu	
	115	120	125
Ala Pro Phe Glu Asp Gly Gly Trp Ile Trp Phe	Asp Leu Thr Ala Glu		
	130	135	140
Thr Asp Ala Thr Val Glu Glu Ala Gly Trp Tyr Ala Pro His Ala Pro			
	145	150	155
Lys Ala Gln Ile Met Pro Asp Gly Ser Glu Val Gly Pro Phe Glu Ala			
	165	170	175
Arg Ala Thr Val Gly Ile Pro Thr Phe Asn Arg Pro Ala Asp Ala Val			
	180	185	190
Ala Ala Leu Glu Ala Leu Ala Ser Asp Pro Ala Val Asp Ala Val Ile			
	195	200	205
Asp Thr Val Ile Met Pro Asp Gln Gly Asn Lys His Pro Ala Asp Glu			
	210	215	220
Pro Gly Tyr Lys Ala Ala Val Glu His Phe Gly Asp Arg Phe Phe Glu			
	225	230	235
Phe Arg Gln Gly Asn Leu Gly Gly Ser Gly Gly Tyr Ser Arg Ile Met			
	245	250	255
Phe Glu Ala Leu Gly Gly Val Asp Gly Lys Gly Glu Ala Gly Ala Ala			
	260	265	270
Lys Ser Pro Tyr Ile Leu Tyr Met Asp Asp Asp Ile Ala Ile Glu Pro			
	275	280	285
Asp Ser Val Leu Arg Ala Leu Gln Val Ala Arg Tyr Ala Lys Ser Pro			
	290	295	300
Ile Leu Val Gly Gly Gln Met Leu Asn Leu Gln Glu Arg Ser His Leu			
	305	310	315
His Thr Met Gly Glu Val Val Gly Gly His Asp Phe Met Trp Thr Ala			
	325	330	335
Ala Pro His Val His Tyr Asp His Asp Phe Ser Ala His Pro Leu His			
	340	345	350
Asp Arg Gly Lys Phe Asp Asp Lys Pro Asp Ala Pro Asn Ser Arg Asp			
	355	360	365
Leu His Arg Arg Ile Asp Val Asp Phe Asn Gly Trp Trp Met Cys Met			
	370	375	380
Ile Pro Arg Val Val Ala Glu Gln Ile Gly Gln Pro Leu Pro Leu Phe			
	385	390	395
			400

Ile Lys Trp Asp Asp Ala Glu Tyr Gly Leu Arg Ala Arg Lys Ala Gly
405 410 415

Phe Pro Thr Ala Thr Trp Pro Gly Ile Ala Ile Trp His Met Ala Trp
420 425 430

Ser Asp Lys Asp Asp Ala Ile Asp Trp Gln Ala Tyr Phe His Leu Arg
435 440 445

Asn Arg Leu Val Val Ala Ala Met Tyr His Gln Gly Ser Val Asp Gly
450 455 460

Ile Val Arg Ser Met Gln Lys Ala Thr Phe Lys His Leu Leu Cys Leu
465 470 475 480

Glu Tyr Ser Thr Val Ala Ile Gln Asn Glu Ala Met Lys Asp Phe Leu
485 490 495

Ala Gly Pro Asp Gln Leu Phe Ser Ile Leu Asp Thr Ser Leu Pro Arg
500 505 510

Ile Ala Ala Ile Arg Lys Thr Tyr Pro Asp Ala Val Val Leu Pro Ser
515 520 525

Ala Thr Glu Leu Pro Arg Ala Thr Gly Ala Pro Gly Val Pro Thr Lys
530 535 540

Asp Ile Gly Gly Arg Leu Ala Pro Ile Lys Lys Ala Met Trp Leu Ala
545 550 555 560

Lys Gly Leu Lys His Ser Leu Ser Lys Glu Asp Ala Ser His His Glu
565 570 575

Val Pro Gln Ala Asn Phe Ala Pro Ile Glu Ala Arg Trp Phe Ser Leu
580 585 590

Ser Arg Val Asp Gly Ala Thr Val Thr Thr Ala Asp Gly Arg Gly Val
595 600 605

Val Tyr Arg Lys Arg Asp Arg Asp Lys Ala Lys Glu Leu Gly Lys Glu
610 615 620

Ala Arg Ala Leu Gln Lys Gln Val Ala Glu Arg Phe Asp Glu Leu Ser
625 630 635 640

Arg Ala Tyr Arg Asn Ala His Pro Glu Leu Val Ser Arg Glu Ala Trp
645 650 655

Gly Lys Val Phe Asp Glu Gln
660

<210> 2819

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

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55 60 65	
ttc tgg gca ggc tgg acc cgc aaa tgg atc agc gac gac gga ctg atc	355
Phe Trp Ala Gly Trp Thr Arg Lys Trp Ile Ser Asp Asp Gly Leu Ile	
70 75 80 85	
gtc cta cgc acc gtc cga aac ctc ctg gct gga aac ggg cca gta ttc	403
Val Leu Arg Thr Val Arg Asn Leu Leu Ala Gly Asn Gly Pro Val Phe	
90 95 100	
aac gct ggc gaa cgc gtc gaa gcc aac aca tct act ctg tgg caa tac	451
Asn Ala Gly Glu Arg Val Glu Ala Asn Thr Ser Thr Leu Trp Gln Tyr	
105 110 115	
tgc atc tat ctg gtt gcc tta gta act gac tat cgc ctc gaa gat att	499
Cys Ile Tyr Leu Val Ala Leu Val Thr Asp Tyr Arg Leu Glu Asp Ile	
120 125 130	
gct ctg tgg ctt gcg ctg ctg ttc acc acc gca gcg tcc atc atc ggt	547
Ala Leu Trp Leu Ala Leu Leu Phe Thr Thr Ala Ala Ser Ile Ile Gly	
135 140 145	
gtc ctg ggt acc gcg cat ctc cac cgc aaa cgc att gcc gta ttg ctt	595
Val Leu Gly Thr Ala His Leu His Arg Lys Arg Ile Ala Val Leu Leu	
150 155 160 165	
cct gca ggc gtg atc ggc tac ttc agc ctt tcc ccg gcg cga gac ttt	643
Pro Ala Gly Val Ile Gly Tyr Phe Ser Leu Ser Pro Ala Arg Asp Phe	
170 175 180	
gcc act tcc gga ttg gag tgg ggc cta tct ttg atg tgg att tcc atc	691
Ala Thr Ser Gly Leu Glu Trp Gly Leu Ser Leu Met Trp Ile Ser Ile	
185 190 195	
caa tgg ctg ctg ctg gtg ttg tgg gcg act tcg ggc aag acc tcg ggc	739
Gln Trp Leu Leu Leu Val Leu Trp Ala Thr Ser Gly Lys Thr Ser Gly	
200 205 210	
aag aag gct tcg ggc gca aaa act tca aat cct atc gtt aat gcc ggt	787
Lys Lys Ala Ser Gly Ala Lys Thr Ser Asn Pro Ile Val Asn Ala Gly	
215 220 225	
gca ata acc tat gct ttg gcc ttt tgg tca ggc ttg agc tgg ctg gtt	835
Ala Ile Thr Tyr Ala Leu Ala Phe Trp Ser Gly Leu Ser Trp Leu Val	
230 235 240 245	
cgc cca gaa ctg gcg atg tat ggc ggt ttg act gga gtg ttg ctg ctg	883
Arg Pro Glu Leu Ala Met Tyr Gly Gly Leu Thr Gly Val Leu Leu Leu	
250 255 260	
ctt act gcg cca cga tgg cgg gta gtt ttg ggg atc ctg gtg gcg gct	931
Leu Thr Ala Pro Arg Trp Arg Val Val Leu Gly Ile Leu Val Ala Ala	
265 270 275	
ttg cct ctt cca gct gcg tac caa atc ttc cgc atg ggt tat tac ggg	979
Leu Pro Leu Pro Ala Ala Tyr Gln Ile Phe Arg Met Gly Tyr Tyr Gly	
280 285 290	

ctg atg gtg ccg cac acg gct gta gcg aaa tca gcc tca gat gcg gtg Leu Met Val Pro His Thr Ala Val Ala Lys Ser Ala Ser Asp Ala Val 295 300 305	1027
tgg ggg act ggt tgg gaa tat gtt gag gat ttc acg ggg cct tac aac Trp Gly Thr Gly Trp Glu Tyr Val Glu Asp Phe Thr Gly Pro Tyr Asn 310 315 320 325	1075
ctg tgg ctc ggt ttg gcc ttg ctg ttg gcc gca ggc gcg ttg aca gtg Leu Trp Leu Gly Leu Ala Leu Leu Leu Ala Ala Gly Ala Leu Thr Val 330 335 340	1123
tgg aaa act gac aag cac tta gcg ata ccg aag ggg cgg ctg ggg ctg Trp Lys Thr Asp Lys His Leu Ala Ile Pro Lys Gly Arg Leu Gly Leu 345 350 355	1171
cgc act ccg ggt atg gct ata gcg ttg ctg gtt atc tgt gcg ctc gtc Arg Thr Pro Gly Met Ala Ile Ala Leu Leu Val Ile Cys Ala Leu Val 360 365 370	1219
cac ttc ctt tac gtt atc cgt gtt ggt ggc gac ttc atg cat gga cgc His Phe Leu Tyr Val Ile Arg Val Gly Gly Asp Phe Met His Gly Arg 375 380 385	1267
atg ctg ctc ctt cca ctt ttt gcc att ctg ctg cct gtt tct gtc att Met Leu Leu Leu Pro Leu Phe Ala Ile Leu Leu Pro Val Ser Val Ile 390 395 400 405	1315
ccg gtc aat gtt gtt gat cga ggt tgg cag gat ttg gtt gcg ctg gtt Pro Val Asn Val Val Asp Arg Gly Trp Gln Asp Leu Val Ala Leu Val 410 415 420	1363
ctc gtt ttc tct acg tgg gtg tgg tcc act gtg gtt ttt gtg cag ggg Leu Val Phe Ser Thr Trp Val Trp Ser Thr Val Val Phe Val Gln Gly 425 430 435	1411
cac caa tgg gaa aat acc ggc cag cat gtg gtt gat gag cgt gat ttt His Gln Trp Glu Asn Thr Gly Gln His Val Val Asp Glu Arg Asp Phe 440 445 450	1459
tgg att gat ttc acc aac cga gat gaa gat cat cct ccg ctt tat gca Trp Ile Asp Phe Thr Asn Arg Asp Glu Asp His Pro Pro Leu Tyr Ala 455 460 465	1507
gag gat ttc ctc act gtt gat tcc atg aat gat tac gca gag gtt atg Glu Asp Phe Leu Thr Val Asp Ser Met Asn Asp Tyr Ala Glu Val Met 470 475 480 485	1555
cgc gat cag acg ttg gtt aat cca aca ggc cag caa ctc aat att ctg Arg Asp Gln Thr Leu Val Asn Pro Thr Gly Gln Gln Leu Asn Ile Leu 490 495 500	1603
gcc agc agt gac ccg acc act tat tcg tgg atc acc aca cct cgc gtg Ala Ser Ser Asp Pro Thr Thr Tyr Ser Trp Ile Thr Thr Pro Arg Val 505 510 515	1651
gag ggg gtt gaa gcc ggt gat ttg gct aac ctc tcg cca act gtt ttc Glu Gly Val Glu Ala Gly Asp Leu Ala Asn Leu Ser Pro Thr Val Phe 520 525 530	1699
cat gtg aac ctc ggc atg acc tcc atg aac gca ccg ctc aac gtg cgt	1747

His Val Asn Leu Gly Met Thr Ser Met Asn Ala Pro Leu Asn Val Arg
 535 540 545
 gtg aca gac ctg att ggt ttg gca acg cca ctg gca gcc cgc cag cca 1795
 Val Thr Asp Leu Ile Gly Leu Ala Thr Pro Leu Ala Ala Arg Gln Pro
 550 555 560 565
 cgc att gaa ggt ggt cga atc ggc cac gat aaa ttg atg gac ttg gaa 1843
 Arg Ile Glu Gly Gly Arg Ile Gly His Asp Lys Leu Met Asp Leu Glu
 570 575 580
 tgg cag gtc gcg gaa tcc gcc act ccg ctg gcg tac aca ccg ggt tgg 1891
 Trp Gln Val Ala Glu Ser Ala Thr Pro Leu Ala Tyr Thr Pro Gly Trp
 585 590 595
 ttg gat act caa aag act tat gag gcc cgc cag gcg cta cgc cac cca 1939
 Leu Asp Thr Gln Lys Thr Tyr Glu Ala Arg Gln Ala Leu Arg His Pro
 600 605 610
 gaa ttg gtt cac ctt ttc cag act tac cgt gag cca atg tcc tac cac 1987
 Glu Leu Val His Leu Phe Gln Thr Tyr Arg Glu Pro Met Ser Tyr His
 615 620 625
 cgg ttt gtg gac aat att aaa tac gca ctg act acc gga aga aca ctg 2035
 Arg Phe Val Asp Asn Ile Lys Tyr Ala Leu Thr Thr Gly Arg Thr Leu
 630 635 640 645
 gaa att tca gat aat cct gaa gat ctt ttg aaa gaa ttt aac ccg acc 2083
 Glu Ile Ser Asp Asn Pro Glu Asp Leu Leu Lys Glu Phe Asn Pro Thr
 650 655 660
 cct gca gag att cag gac ggg tta gaa act att gct tgg cct ggg gaa 2131
 Pro Ala Glu Ile Gln Asp Gly Leu Glu Thr Ile Ala Trp Pro Gly Glu
 665 670 675
 att aaa ctt gat gaa cct cgc gga gaa cct tta tat agc tct cag 2176
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<210> 2822

<211> 692

<212> PRT

<213> Corynebacterium glutamicum

<400> 2822

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Phe Glu Glu Thr Ser Ser Ser Ala Pro Arg Ala Ala Ser Asn Gly Ser
 35 40 45

Ser Gly Pro Asn Tyr Thr Leu Ile Thr Thr Phe Leu Ala Ala Leu Thr
 50 55 60

Ala Gly Ile Phe Ala Phe Trp Ala Gly Trp Thr Arg Lys Trp Ile Ser

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Asp Asp Gly Leu Ile Val Leu Arg Thr Val Arg Asn Leu Leu Ala Gly						
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Asn Gly Pro Val Phe Asn Ala Gly Glu Arg Val Glu Ala Asn Thr Ser						
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Thr Leu Trp Gln Tyr Cys Ile Tyr Leu Val Ala Leu Val Thr Asp Tyr						
	115			120		125
Arg Leu Glu Asp Ile Ala Leu Trp Leu Ala Leu Leu Phe Thr Thr Ala						
	130			135		140
Ala Ser Ile Ile Gly Val Leu Gly Thr Ala His Leu His Arg Lys Arg						
	145			150		155
Ile Ala Val Leu Leu Pro Ala Gly Val Ile Gly Tyr Phe Ser Leu Ser						
	165			170		175
Pro Ala Arg Asp Phe Ala Thr Ser Gly Leu Glu Trp Gly Leu Ser Leu						
	180			185		190
Met Trp Ile Ser Ile Gln Trp Leu Leu Leu Val Leu Trp Ala Thr Ser						
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Gly Lys Thr Ser Gly Lys Lys Ala Ser Gly Ala Lys Thr Ser Asn Pro						
	210			215		220
Ile Val Asn Ala Gly Ala Ile Thr Tyr Ala Leu Ala Phe Trp Ser Gly						
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Leu Ser Trp Leu Val Arg Pro Glu Leu Ala Met Tyr Gly Gly Leu Thr						
	245			250		255
Gly Val Leu Leu Leu Leu Thr Ala Pro Arg Trp Arg Val Val Leu Gly						
	260			265		270
Ile Leu Val Ala Ala Leu Pro Leu Pro Ala Ala Tyr Gln Ile Phe Arg						
	275			280		285
Met Gly Tyr Tyr Gly Leu Met Val Pro His Thr Ala Val Ala Lys Ser						
	290			295		300
Ala Ser Asp Ala Val Trp Gly Thr Gly Trp Glu Tyr Val Glu Asp Phe						
	305			310		315
Thr Gly Pro Tyr Asn Leu Trp Leu Gly Leu Ala Leu Leu Leu Ala Ala						
	325			330		335
Gly Ala Leu Thr Val Trp Lys Thr Asp Lys His Leu Ala Ile Pro Lys						
	340			345		350
Gly Arg Leu Gly Leu Arg Thr Pro Gly Met Ala Ile Ala Leu Leu Val						
	355			360		365
Ile Cys Ala Leu Val His Phe Leu Tyr Val Ile Arg Val Gly Gly Asp						
	370			375		380
Phe Met His Gly Arg Met Leu Leu Leu Pro Leu Phe Ala Ile Leu Leu						
	385			390		395
						400

Pro Val Ser Val Ile Pro Val Asn Val Val Asp Arg Gly Trp Gln Asp
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Leu Val Ala Leu Val Leu Val Phe Ser Thr Trp Val Trp Ser Thr Val
420 425 430

Val Phe Val Gln Gly His Gln Trp Glu Asn Thr Gly Gln His Val Val
435 440 445

Asp Glu Arg Asp Phe Trp Ile Asp Phe Thr Asn Arg Asp Glu Asp His
450 455 460

Pro Pro Leu Tyr Ala Glu Asp Phe Leu Thr Val Asp Ser Met Asn Asp
465 470 475 480

Tyr Ala Glu Val Met Arg Asp Gln Thr Leu Val Asn Pro Thr Gly Gln
485 490 495

Gln Leu Asn Ile Leu Ala Ser Ser Asp Pro Thr Thr Tyr Ser Trp Ile
500 505 510

Thr Thr Pro Arg Val Glu Gly Val Glu Ala Gly Asp Leu Ala Asn Leu
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Ser Pro Thr Val Phe His Val Asn Leu Gly Met Thr Ser Met Asn Ala
530 535 540

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Ala Ala Arg Gln Pro Arg Ile Glu Gly Gly Arg Ile Gly His Asp Lys
565 570 575

Leu Met Asp Leu Glu Trp Gln Val Ala Glu Ser Ala Thr Pro Leu Ala
580 585 590

Tyr Thr Pro Gly Trp Leu Asp Thr Gln Lys Thr Tyr Glu Ala Arg Gln
595 600 605

Ala Leu Arg His Pro Glu Leu Val His Leu Phe Gln Thr Tyr Arg Glu
610 615 620

Pro Met Ser Tyr His Arg Phe Val Asp Asn Ile Lys Tyr Ala Leu Thr
625 630 635 640

Thr Gly Arg Thr Leu Glu Ile Ser Asp Asn Pro Glu Asp Leu Leu Lys
645 650 655

Glu Phe Asn Pro Thr Pro Ala Glu Ile Gln Asp Gly Leu Glu Thr Ile
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Ala Trp Pro Gly Glu Ile Lys Leu Asp Glu Pro Arg Gly Glu Pro Leu
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Tyr Ser Ser Gln
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<211> 372

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(349)

<223> RXA02609

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Val Glu Arg Ser Ala
1 5

gag gcg caa gcg ttc ctg gat gcg ctg aaa gat gaa aaa atc gac atc 163
Glu Ala Gln Ala Phe Leu Asp Ala Leu Lys Asp Glu Lys Ile Asp Ile
10 15 20

tcc ggc gtg gag gac cag ttg att gcg act gcg cga aat tac tgc agt 211
Ser Gly Val Glu Asp Gln Leu Ile Ala Thr Ala Arg Asn Tyr Cys Ser
25 30 35

tcg gaa aac aag gac caa aac gtc act gtc gat gcg gtt gca ggc cag 259
Ser Glu Asn Lys Asp Gln Asn Val Thr Val Asp Ala Val Ala Gly Gln
40 45 50

ctc atc gtg cag gga cgc acc agc gtg aag gaa gat caa gca gcg gaa 307
Leu Ile Val Gln Gly Arg Thr Ser Val Lys Glu Asp Gln Ala Ala Glu
55 60 65

att tct acg ctg ctg aag gaa tct gcg gat cgg acg tat tgt 349
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taaccgatga ggaaaaccat cac 372

<210> 2824

<211> 83

<212> PRT

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<400> 2824

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Arg Asn Tyr Cys Ser Ser Glu Asn Lys Asp Gln Asn Val Thr Val Asp
35 40 45

Ala Val Ala Gly Gln Leu Ile Val Gln Gly Arg Thr Ser Val Lys Glu
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Asp Gln Ala Ala Glu Ile Ser Thr Leu Leu Lys Glu Ser Ala Asp Arg
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Thr Tyr Cys

<210> 2826

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 2826

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Gln Leu Asn Ile Gly Gln Val Thr Gln Thr Ile Gln Arg Leu Gln Arg
 35 40 45

Asp Gly Leu Ala Glu Thr Ala Gly Thr Thr Val Ser Ser Asn Gly Arg
 50 55 60

Thr Val Asp Thr Phe Gln Pro Thr Asp Leu Gly Arg Glu Leu Val Ala
 65 70 75 80

Gln Trp Phe Glu Ser Pro Val Thr Val Thr Leu Ser Glu Arg Asp Glu
 85 90 95

Leu Val Thr Lys Ile Ala Ile Ala Glu Ser Arg Gly Leu Asn Leu Ile
 100 105 110

Pro Leu Leu Asp Ile Gln Arg Asn Thr Val Met Ala Glu Leu Arg Ala
 115 120 125

Leu Asn Lys Ser Ser Arg Asp Leu Ala Glu Thr Arg Asn Thr Gln Arg
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Leu Leu Val Glu Lys Arg Ile Phe Glu Leu Glu Ala Gln Ala Arg Trp
 145 150 155 160

Leu Asp Arg Ile Glu Ala Leu Glu Gln
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<210> 2827

<211> 1023

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1000)

<223> RXA02619

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 Met Arg Ser Val Val
 1 5

tta gaa cta cta gag aac tgg aag gaa tca ctc gtg ctt cac ccc tca 163

Leu	Glu	Leu	Leu	Glu	Asn	Trp	Lys	Glu	Ser	Leu	Val	Leu	His	Pro	Ser		
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Leu	Thr	Glu	Leu	Ala	Asp	Ala	Ala	Pro	Leu	Ala	Gln	Asp	Phe	Ala	Thr		
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gtc	cgc	ggt	gtg	ctg	aag	gaa	tcg	ctg	gat	ttg	ttg	ggc	aat	gca	ctg	259	
Val	Arg	Gly	Val	Leu	Lys	Glu	Ser	Leu	Asp	Leu	Leu	Gly	Asn	Ala	Leu		
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aac	cac	ggt	gaa	gag	ccc	gcg	gag	ctt	gca	ggg	tgg	ctg	tca	caa	gtt	307	
Asn	His	Gly	Glu	Glu	Pro	Ala	Glu	Leu	Ala	Gly	Trp	Leu	Ser	Gln	Val		
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Ile	Thr	Asp	Val	Leu	His	Ser	Pro	Gly	Leu	Asp	Ala	His	Val	Val	Leu		
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Thr	Gly	Pro	Val	Gly	Arg	Gly	Asp	Ala	Leu	Pro	Thr	Ser	Pro	Val	Arg		
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tgg	ctg	gcg	gtc	gtc	gat	agc	caa	gaa	gat	ccg	aat	gaa	aag	att	tca	451	
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Thr	Arg	Glu	Glu	Trp	Glu	Gln	Arg	Ala	Arg	Ala	Gly	Glu	Asp	Pro	Glu		
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Glu	Thr	Tyr	Glu	Gly	Leu	Pro	Ser	Leu	Asp	Met	Val	Val	Asn	Ile	Arg		
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Glu	Asn	Leu	Met	Ile	Pro	Thr	Val	Lys	Ile	Ala	Arg	Trp	Ala	Ala	His		
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aag	gct	ggt	tct	ttg	gcg	cct	acg	act	gcg	cag	cgc	ctc	gtg	gat	gcc	787	
Lys	Ala	Gly	Ser	Leu	Ala	Pro	Thr	Thr	Ala	Gln	Arg	Leu	Val	Asp	Ala		
	215					220					225						
cgt	ggt	gtg	ctc	acc	aat	gat	gaa	gtc	gac	gcg	ctg	aca	cag	gtg	tgg	835	
Arg	Gly	Val	Leu	Thr	Asn	Asp	Glu	Val	Asp	Ala	Leu	Thr	Gln	Val	Trp		
	230				235					240				245			
act	tcc	gca	ctg	agc	ttg	cag	tcg	aaa	cgt	tgg	atg	gat	cac	atc	cat	883	
Thr	Ser	Ala	Leu	Ser	Leu	Gln	Ser	Lys	Arg	Trp	Met	Asp	His	Ile	His		

250 255 260
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 Asp Gln Glu Thr Thr Ala Trp Glu Leu Pro Ala Leu Gln Arg Ala Thr
 265 270 275
 ttt ggc gca tcg gct cgg ttg ctt tct gag gtg ttg cgg tcc gtt gaa 979
 Phe Gly Ala Ser Ala Arg Leu Leu Ser Glu Val Leu Arg Ser Val Glu
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 <213> Corynebacterium glutamicum
 <400> 2828
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 35 40 45
 Leu Gly Asn Ala Leu Asn His Gly Glu Glu Pro Ala Glu Leu Ala Gly
 50 55 60
 Trp Leu Ser Gln Val Ile Thr Asp Val Leu His Ser Pro Gly Leu Asp
 65 70 75 80
 Ala His Val Val Leu Thr Gly Pro Val Gly Arg Gly Asp Ala Leu Pro
 85 90 95
 Thr Ser Pro Val Arg Trp Leu Ala Val Val Asp Ser Gln Glu Asp Pro
 100 105 110
 Asn Glu Lys Ile Ser Ala Leu Leu Thr Glu Val Gly Phe Ile Ala Glu
 115 120 125
 Pro Ile Gly Ala Ala Thr Arg Glu Glu Trp Glu Gln Arg Ala Arg Ala
 130 135 140
 Gly Glu Asp Pro Glu Val Tyr Leu Asp Ala Gly Thr Trp Val Ala Ala
 145 150 155 160
 Ile Ala Glu Val Asp Asp Lys Ala Leu Leu Gln Asp Ala Leu Ser Ser
 165 170 175
 Arg Pro Pro Ala Val Glu Thr Tyr Glu Gly Leu Pro Ser Leu Asp Met
 180 185 190
 Val Val Asn Ile Arg Glu Asn Leu Met Ile Pro Thr Val Lys Ile Ala
 195 200 205
 Arg Trp Ala Ala His Lys Ala Gly Ser Leu Ala Pro Thr Thr Ala Gln

210	215	220
Arg Leu Val Asp Ala	Arg Gly Val Leu Thr	Asn Asp Glu Val Asp Ala
225	230	235 240
Leu Thr Gln Val Trp Thr Ser Ala Leu Ser	Leu Gln Ser Lys Arg Trp	
	245 250	255
Met Asp His Ile His Asp Gln Glu Thr Thr Ala Trp Glu Leu Pro Ala		
	260 265	270
Leu Gln Arg Ala Thr Phe Gly Ala Ser Ala Arg Leu Leu Ser Glu Val		
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Leu Arg Ser Val Glu Ala Arg Glu Ile Asp Thr Lys		
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<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> RXA02620

<400> 2829

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                                   Val Gly Arg Pro Arg
                                   1 5
aga tca gct ccg cga cgg gca ggc aag aat cct cgc gag gag att ctt 163
Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro Arg Glu Glu Ile Leu
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gac gcc tct gct gag ctt ttc acc cgt caa ggc ttc gca aca acc tcc 211
Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly Phe Ala Thr Thr Ser
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acg cat caa atc gct gat gcc gtg gga atc cgc caa gcc tcg ctg tat 259
Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln Ala Ser Leu Tyr
                                   40 45 50
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Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu Thr Leu Leu Lys Ser
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Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu Ser Thr Leu Asp
                                   70 75 80 85
gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc tcc gaa gtg cgt 403
Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala Ser Glu Val Arg
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ccc cgc gca gaa ctc ccc ttc cac atc acc atg tcg gtg atc gaa atg Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met Ser Val Ile Glu Met 150 155 160 165			595
cgt cgc aac gac ggc aag att cca agc ccg ctt tcc gca gac agc ctc Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu Ser Ala Asp Ser Leu 170 175 180			643
ccg gag acc gca att atg ctt gcc gac gcc tcc ctc gcc gtc ctc ggc Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser Leu Ala Val Leu Gly 185 190 195			691
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Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu 50 55 60
Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp 65 70 75 80
Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val 85 90 95
Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg 100 105 110
Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His 115 120 125

Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu
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Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met
 145 150 155 160

Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu
 165 170 175

Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser
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Leu Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr
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Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys
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<210> 2831

<211> 957

<212> DNA

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<222> (101)..(934)

<223> RXA02639

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 Met Ile Ala Leu Gly
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tca gcg ccc aag ctg gtt gcc tcc gat gtt gat ggc acc ctc atc aat 163
 Ser Ala Pro Lys Leu Val Ala Ser Asp Val Asp Gly Thr Leu Ile Asn
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 Ser Ser Glu Arg Val Pro Gln Arg Leu Arg Asp Val Ile Thr Arg Met
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acc aat cag ggc gtg acc ctg gcg ctg tcc acg ggc cgc ccg ccg cgc 259
 Thr Asn Gln Gly Val Thr Leu Ala Leu Ser Thr Gly Arg Pro Pro Arg
 40 45 50

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 Trp Ile His Tyr Val Leu Asp Gln Leu Ser Val Lys Pro Ile Cys Val
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 Ala Ala Gln Thr Leu Ser Pro Glu Val Met Ala Ser Ala Val Met Ala
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Ala Arg Ala Ala Leu Glu Glu His Gly Gly Val Ser Ile Ala Val Glu
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Arg Ala Gly Lys Ser Ala Tyr Asp Pro Ala Asp Glu Leu Phe Leu Val
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Thr Pro Glu Tyr Ser His Ala Trp Pro Ser Asn Asp His Gly Thr Phe
135 140 145

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Ser Asp Tyr Leu Asp Ser Lys Gln Leu Phe Asp Ile Val Arg Ala Ser
170 175 180

gtt ccc gag gat caa gtc cac gtc acc ttc tcc atg tcc ggc gga ctc 691
Val Pro Glu Asp Gln Val His Val Thr Phe Ser Met Ser Gly Gly Leu
185 190 195

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Ile Glu Ile Ala Ala Pro Gly Val Thr Lys Ala Leu Gly Val Ser Met
200 205 210

ctg gca gag cgc cta aag att gcg caa aag gac gtt ata acg ttc ggc 787
Leu Ala Glu Arg Leu Lys Ile Ala Gln Lys Asp Val Ile Thr Phe Gly
215 220 225

gac atg ccc aac gat att gaa atg ctc cag tgg gcc ggc cgg gga gtg 835
Asp Met Pro Asn Asp Ile Glu Met Leu Gln Trp Ala Gly Arg Gly Val
230 235 240 245

gcg atg ggc aac gcc cga cca gag gtc aaa gcc gtg tca gac cac atc 883
Ala Met Gly Asn Ala Arg Pro Glu Val Lys Ala Val Ser Asp His Ile
250 255 260

acc cgc acc aac gac gac gcc ggt gta gca gat gta ttg gag tgg tgg 931
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<212> PRT

<213> Corynebacterium glutamicum

<400> 2832

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35 40 45

Gly Arg Pro Pro Arg Trp Ile His Tyr Val Leu Asp Gln Leu Ser Val
50 55 60

Lys Pro Ile Cys Val Cys Ala Asn Gly Ala Val Leu Tyr Asp Ser Ala
65 70 75 80

Ala Asp Glu Ile Leu Ala Ala Gln Thr Leu Ser Pro Glu Val Met Ala
85 90 95

Ser Ala Val Met Ala Ala Arg Ala Ala Leu Glu Glu His Gly Gly Val
100 105 110

Ser Ile Ala Val Glu Arg Ala Gly Lys Ser Ala Tyr Asp Pro Ala Asp
115 120 125

Glu Leu Phe Leu Val Thr Pro Glu Tyr Ser His Ala Trp Pro Ser Asn
130 135 140

Asp His Gly Thr Phe Glu Glu Ala Glu Val Leu Ser Glu Pro Ala Thr
145 150 155 160

Lys Leu Leu Met Arg Ser Asp Tyr Leu Asp Ser Lys Gln Leu Phe Asp
165 170 175

Ile Val Arg Ala Ser Val Pro Glu Asp Gln Val His Val Thr Phe Ser
180 185 190

Met Ser Gly Gly Leu Ile Glu Ile Ala Ala Pro Gly Val Thr Lys Ala
195 200 205

Leu Gly Val Ser Met Leu Ala Glu Arg Leu Lys Ile Ala Gln Lys Asp
210 215 220

Val Ile Thr Phe Gly Asp Met Pro Asn Asp Ile Glu Met Leu Gln Trp
225 230 235 240

Ala Gly Arg Gly Val Ala Met Gly Asn Ala Arg Pro Glu Val Lys Ala
245 250 255

Val Ser Asp His Ile Thr Arg Thr Asn Asp Asp Ala Gly Val Ala Asp
260 265 270

Val Leu Glu Trp Trp Phe
275

<210> 2833

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> RXA02647

<400> 2833

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                               Val Ala Leu Ser Val
                               1 5

ttc act cca gtt gcc cag gct cag tcc tct gac gca ctg aca cag ctc 163
Phe Thr Pro Val Ala Gln Ala Gln Ser Ser Asp Ala Leu Thr Gln Leu
                               10 15 20

tca gac aac atc acc tca tca cag atc ctt gat gat gat gga aat cca 211
Ser Asp Asn Ile Thr Ser Ser Gln Ile Leu Asp Asp Asp Gly Asn Pro
                               25 30 35

gtc gat gga aac gaa acc tgg cca ggc agc tct gaa ggc agc tca atg 259
Val Asp Gly Asn Glu Thr Trp Pro Gly Ser Ser Glu Gly Ser Ser Met
                               40 45 50

ctc agc aat ggc gac att cct gcg gcc cca agc ttg agc tcc tcc ggc 307
Leu Ser Asn Gly Asp Ile Pro Ala Ala Pro Ser Leu Ser Ser Ser Gly
                               55 60 65

aaa gac acc agc gat gat gac gat gaa atc agc gaa gag cag caa gca 355
Lys Asp Thr Ser Asp Asp Asp Asp Glu Ile Ser Glu Glu Gln Gln Ala
70 75 80 85

ctg atc gat cgg ttg tcc gaa atg cca gtg att ggt tcc att gtc tcc 403
Leu Ile Asp Arg Leu Ser Glu Met Pro Val Ile Gly Ser Ile Val Ser
90 95 100

cca cca gaa tgg ctt gcc att cct ttt gcg gta ctg cag gga ttg ctc 451
Pro Pro Glu Trp Leu Ala Ile Pro Phe Ala Val Leu Gln Gly Leu Leu
105 110 115

gca atc acc act ctt gct tcc acc gca gca tcc ttc atg gtg acc gtc 499
Ala Ile Thr Thr Leu Ala Ser Thr Ala Ala Ser Phe Met Val Thr Val
120 125 130

gac cca tcg ttc aag cag act ctg cgt gac atg ctc acc cag ttt ggc 547
Asp Pro Ser Phe Lys Gln Thr Leu Arg Asp Met Leu Thr Gln Phe Gly
135 140 145

atc aac gtc gac gct taaaagcaca ctgacataaa atg 585
Ile Asn Val Asp Ala
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<210> 2834

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 2834

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Val Ala Leu Ser Val Phe Thr Pro Val Ala Gln Ala Gln Ser Ser Asp
1 5 10 15

Ala Leu Thr Gln Leu Ser Asp Asn Ile Thr Ser Ser Gln Ile Leu Asp
20 25 30

Asp Asp Gly Asn Pro Val Asp Gly Asn Glu Thr Trp Pro Gly Ser Ser
35 40 45

Glu Gly Ser Ser Met Leu Ser Asn Gly Asp Ile Pro Ala Ala Pro Ser

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50	55	60
Leu Ser Ser Ser Gly Lys Asp Thr Ser Asp Asp Asp Asp Glu Ile Ser		
65	70	75 80
Glu Glu Gln Gln Ala Leu Ile Asp Arg Leu Ser Glu Met Pro Val Ile		
	85	90 95
Gly Ser Ile Val Ser Pro Pro Glu Trp Leu Ala Ile Pro Phe Ala Val		
	100	105 110
Leu Gln Gly Leu Leu Ala Ile Thr Thr Leu Ala Ser Thr Ala Ala Ser		
	115	120 125
Phe Met Val Thr Val Asp Pro Ser Phe Lys Gln Thr Leu Arg Asp Met		
	130	135 140
Leu Thr Gln Phe Gly Ile Asn Val Asp Ala		
145	150	

<210> 2835

<211> 1125

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1102)

<223> RXA02649

<400> 2835

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atttgttcctt tttggcgccg atgccgatag gtttaaaggc gtg cta aaa cga ttc 115
                                   Val Leu Lys Arg Phe
                                   1 5

tct cac cac tcc agc ccg caa gtt ctt tca cgg aaa gtt gtc gcg tcc 163
Ser His His Ser Ser Pro Gln Val Leu Ser Arg Lys Val Val Ala Ser
          10          15          20

gca tta gct tta aca acc gcg ctg gct tta gcc gcg tgt agt tcc tca 211
Ala Leu Ala Leu Thr Thr Ala Leu Ala Leu Ala Ala Cys Ser Ser Ser
          25          30          35

gcc gag ccg gac tcc cct gaa gtt gag cag gcg gtg ggt ctt gcg gtg 259
Ala Glu Pro Asp Ser Pro Glu Val Glu Gln Ala Val Gly Leu Ala Val
          40          45          50

gat acg cca cgt gtg gtg gtt gtg gat cca ggc act ggc gat ttg cag 307
Asp Thr Pro Arg Val Val Val Val Asp Pro Gly Thr Gly Asp Leu Gln
          55          60          65

cgc ttg caa tac aaa gac atc gcc cct gat gcc aca cag gaa cag acc 355
Arg Leu Gln Tyr Lys Asp Ile Ala Pro Asp Ala Thr Gln Glu Gln Thr
          70          75          80          85

atc aat att gct gaa ggt ttt gcc caa tcg gtg gtg aat gcg gac agc 403
Ile Asn Ile Ala Glu Gly Phe Ala Gln Ser Val Val Asn Ala Asp Ser
          90          95          100

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gtg gat ccg cag gca cca gcc ggt ggc gat gtc acc aca ttc cac ctt	451
Val Asp Pro Gln Ala Pro Ala Gly Gly Asp Val Thr Thr Phe His Leu	
105 110 115	
cct gtt aaa gcc acc acc gag gaa gcg gag ttc agc gat cag gaa atg	499
Pro Val Lys Ala Thr Thr Glu Glu Ala Glu Phe Ser Asp Gln Glu Met	
120 125 130	
gtg agc gcg act cgc gat atc tct cta ctt ttc ggt aaa cct acc tac	547
Val Ser Ala Thr Arg Asp Ile Ser Leu Leu Phe Gly Lys Pro Thr Tyr	
135 140 145	
acc gat ctt tcc caa gtt gaa gat gtg aat tcc acc gag gga ttc acg	595
Thr Asp Leu Ser Gln Val Glu Asp Val Asn Ser Thr Glu Gly Phe Thr	
150 155 160 165	
ctg gga atc cgc gca aca gat agt gga cag cac acc acc tta agt ttc	643
Leu Gly Ile Arg Ala Thr Asp Ser Gly Gln His Thr Thr Leu Ser Phe	
170 175 180	
gca gcc cct gtt gat tcc act gaa act ggt cgc atg ctc atg gag caa	691
Ala Ala Pro Val Asp Ser Thr Glu Thr Gly Arg Met Leu Met Glu Gln	
185 190 195	
tac tta ctc acg ttt acg tcc ctt ccc att gtg ttc ccc tct gac gat	739
Tyr Leu Leu Thr Phe Thr Ser Leu Pro Ile Val Phe Pro Ser Asp Asp	
200 205 210	
att ggc gtg ggc gcg aag tgg act gtg gat agc cgt gtg aca ggc gaa	787
Ile Gly Val Gly Ala Lys Trp Thr Val Asp Ser Arg Val Thr Gly Glu	
215 220 225	
tca acg ctg cta caa acc gtg acc tac acg atc aca ggg atc gac ggc	835
Ser Thr Leu Leu Gln Thr Val Thr Tyr Thr Ile Thr Gly Ile Asp Gly	
230 235 240 245	
gac aaa gta aac ctc gat gtg gaa gtc tct cag cgc ccc agc atg ggt	883
Asp Lys Val Asn Leu Asp Val Glu Val Ser Gln Arg Pro Ser Met Gly	
250 255 260	
gcg ttg gag atc acc gat gaa gaa tcg gac gag acc acc ggg cag ctc	931
Ala Leu Glu Ile Thr Asp Glu Glu Ser Asp Glu Thr Thr Gly Gln Leu	
265 270 275	
act gtc ctt aat tcc aac acc acc tcc gtg ggc acc ttg gaa gtc gat	979
Thr Val Leu Asn Ser Asn Thr Thr Ser Val Gly Thr Leu Glu Val Asp	
280 285 290	
ctg act cag cct tta ccc acg tca gga cag gtt tct tgg acc act cgc	1027
Leu Thr Gln Pro Leu Pro Thr Ser Gly Gln Val Ser Trp Thr Thr Arg	
295 300 305	
gtg att tac ggc ggt tcc aat gag cag gtg cgt gtg gtg cag gat tcc	1075
Val Ile Tyr Gly Gly Ser Asn Glu Gln Val Arg Val Val Gln Asp Ser	
310 315 320 325	
acc tct tcg gtg agc ttc gga gac cag taatttacca attagggttg	1122
Thr Ser Ser Val Ser Phe Gly Asp Gln	
330	

cca

1125

<210> 2836

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 2836

Val Leu Lys Arg Phe Ser His His Ser Ser Pro Gln Val Leu Ser Arg
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Lys Val Val Ala Ser Ala Leu Ala Leu Thr Thr Ala Leu Ala Leu Ala
20 25 30

Ala Cys Ser Ser Ser Ala Glu Pro Asp Ser Pro Glu Val Glu Gln Ala
35 40 45

Val Gly Leu Ala Val Asp Thr Pro Arg Val Val Val Val Asp Pro Gly
50 55 60

Thr Gly Asp Leu Gln Arg Leu Gln Tyr Lys Asp Ile Ala Pro Asp Ala
65 70 75 80

Thr Gln Glu Gln Thr Ile Asn Ile Ala Glu Gly Phe Ala Gln Ser Val
85 90 95

Val Asn Ala Asp Ser Val Asp Pro Gln Ala Pro Ala Gly Gly Asp Val
100 105 110

Thr Thr Phe His Leu Pro Val Lys Ala Thr Thr Glu Glu Ala Glu Phe
115 120 125

Ser Asp Gln Glu Met Val Ser Ala Thr Arg Asp Ile Ser Leu Leu Phe
130 135 140

Gly Lys Pro Thr Tyr Thr Asp Leu Ser Gln Val Glu Asp Val Asn Ser
145 150 155 160

Thr Glu Gly Phe Thr Leu Gly Ile Arg Ala Thr Asp Ser Gly Gln His
165 170 175

Thr Thr Leu Ser Phe Ala Ala Pro Val Asp Ser Thr Glu Thr Gly Arg
180 185 190

Met Leu Met Glu Gln Tyr Leu Leu Thr Phe Thr Ser Leu Pro Ile Val
195 200 205

Phe Pro Ser Asp Asp Ile Gly Val Gly Ala Lys Trp Thr Val Asp Ser
210 215 220

Arg Val Thr Gly Glu Ser Thr Leu Leu Gln Thr Val Thr Tyr Thr Ile
225 230 235 240

Thr Gly Ile Asp Gly Asp Lys Val Asn Leu Asp Val Glu Val Ser Gln
245 250 255

Arg Pro Ser Met Gly Ala Leu Glu Ile Thr Asp Glu Glu Ser Asp Glu
260 265 270

Thr Thr Gly Gln Leu Thr Val Leu Asn Ser Asn Thr Thr Ser Val Gly

275	280	285
Thr Leu Glu Val Asp Leu Thr Gln Pro Leu Pro Thr Ser Gly Gln Val		
290	295	300
Ser Trp Thr Thr Arg Val Ile Tyr Gly Gly Ser Asn Glu Gln Val Arg		
305	310	315
Val Val Gln Asp Ser Thr Ser Ser Val Ser Phe Gly Asp Gln		
325	330	

<210> 2837

<211> 702

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(679)

<223> RXA02652

<400> 2837

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ctgatctcca acacgcttta gacgttctcc gcgagcaata atg gat ggt gtc gat	115
Met Asp Gly Val Asp	
1 5	

aaa ggg cga cgc atc gtc gcc ctc cta gca att ctc gca ttg gtt gtc	163
Lys Gly Arg Arg Ile Val Ala Leu Leu Ala Ile Leu Ala Leu Val Val	
10 15 20	

gtg gtt gcg atc ttg agt ttc agc gac cgc acc gcg aaa ccc atg cag	211
Val Val Ala Ile Leu Ser Phe Ser Asp Arg Thr Ala Lys Pro Met Gln	
25 30 35	

ctc aac ggt gac atg ctc ggc caa gac aac acg gaa act tcc gtc gag	259
Leu Asn Gly Asp Met Leu Gly Gln Asp Asn Thr Glu Thr Ser Val Glu	
40 45 50	

tac cgt cag cgg gca tcg gaa tca ttg gaa aat gcc gcg gtc ggc gaa	307
Tyr Arg Gln Arg Ala Ser Glu Ser Leu Glu Asn Ala Ala Val Gly Glu	
55 60 65	

gaa gcc tat tca ctg gtg acg ttc aca cag ccg ctt tcg cct tcc gag	355
Glu Ala Tyr Ser Leu Val Thr Phe Thr Gln Pro Leu Ser Pro Ser Glu	
70 75 80 85	

gcc tct aac ctt ctt aaa gga gtc ggt cgc gtc aat gcc atg gtt atg	403
Ala Ser Asn Leu Leu Lys Gly Val Gly Arg Val Asn Ala Met Val Met	
90 95 100	

ctc tcg gct cct gcc atg gat cta ccc gaa ccc atc gca ggc gag acc	451
Leu Ser Ala Pro Ala Met Asp Leu Pro Glu Pro Ile Ala Gly Glu Thr	
105 110 115	

cgt gaa gat gtt ttt aac cgt caa ata aag ctt gtc gac gcc cag tta	499
Arg Glu Asp Val Phe Asn Arg Gln Ile Lys Leu Val Asp Ala Gln Leu	
120 125 130	

tcc ggt atc ggc aac gtc cgc gcg ccg ggc gaa ctc aac ggg gta gtg 547
 Ser Gly Ile Gly Asn Val Arg Ala Pro Gly Glu Leu Asn Gly Val Val
 135 140 145

gtt tgg gat att cct cag aaa gtt cgt gtg ttg tcc gag agc tcg ctg 595
 Val Trp Asp Ile Pro Gln Lys Val Arg Val Leu Ser Glu Ser Ser Leu
 150 155 160 165

gtt tat agt gtc gaa acc ctg cca cct gac gcg gcg tgg ggc agt ttc 643
 Val Tyr Ser Val Glu Thr Leu Pro Pro Asp Ala Ala Trp Gly Ser Phe
 170 175 180

ggg att cga cca gtc gat act tcg ggt act aat ttt tagaagaaaa 689
 Gly Ile Arg Pro Val Asp Thr Ser Gly Thr Asn Phe
 185 190

ttccagatgc ccc 702

<210> 2838

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 2838

Met Asp Gly Val Asp Lys Gly Arg Arg Ile Val Ala Leu Leu Ala Ile
 1 5 10 15

Leu Ala Leu Val Val Val Val Ala Ile Leu Ser Phe Ser Asp Arg Thr
 20 25 30

Ala Lys Pro Met Gln Leu Asn Gly Asp Met Leu Gly Gln Asp Asn Thr
 35 40 45

Glu Thr Ser Val Glu Tyr Arg Gln Arg Ala Ser Glu Ser Leu Glu Asn
 50 55 60

Ala Ala Val Gly Glu Glu Ala Tyr Ser Leu Val Thr Phe Thr Gln Pro
 65 70 75 80

Leu Ser Pro Ser Glu Ala Ser Asn Leu Leu Lys Gly Val Gly Arg Val
 85 90 95

Asn Ala Met Val Met Leu Ser Ala Pro Ala Met Asp Leu Pro Glu Pro
 100 105 110

Ile Ala Gly Glu Thr Arg Glu Asp Val Phe Asn Arg Gln Ile Lys Leu
 115 120 125

Val Asp Ala Gln Leu Ser Gly Ile Gly Asn Val Arg Ala Pro Gly Glu
 130 135 140

Leu Asn Gly Val Val Val Trp Asp Ile Pro Gln Lys Val Arg Val Leu
 145 150 155 160

Ser Glu Ser Ser Leu Val Tyr Ser Val Glu Thr Leu Pro Pro Asp Ala
 165 170 175

Ala Trp Gly Ser Phe Gly Ile Arg Pro Val Asp Thr Ser Gly Thr Asn
 180 185 190

Phe

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<210> 2839
<211> 1107
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1084)  
<223> RXA02655
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Met Ser Pro Glu Ala 5																
1																
aaa gaa gcc caa gat tct agg cgc aac gag atg ccc gag aaa aag cga 163																
Lys Glu Ala Gln Asp Ser Arg Arg Asn Glu Met Pro Glu Lys Lys Arg 20																
10 15																
gcg gtg cta cgt aaa gcg att aag ttg gaa tgg gca acg atc gca tgg 211																
Ala Val Leu Arg Lys Ala Ile Lys Leu Glu Trp Ala Thr Ile Ala Trp 35																
25 30																
gtt ctt ttt tcg atc gtt ttg gta ggt gtt gtc gct ggt caa tcg cag 259																
Val Leu Phe Ser Ile Val Leu Val Gly Val Val Ala Gly Gln Ser Gln 50																
40 45																
gcc atg cgt agt gca tgg att gaa gac atg ctt tct ttg gta cca cct 307																
Ala Met Arg Ser Ala Trp Ile Glu Asp Met Leu Ser Leu Val Pro Pro 65																
55 60																
atc gct ttt ctt tta gcc tcc cga atc agc aaa gct gtg gca acc aga 355																
Ile Ala Phe Leu Leu Ala Ser Arg Ile Ser Lys Ala Val Ala Thr Arg 85																
70 75																
aaa cat cca tac ggc aag cac cgg tcg att gct atc ggg cac caa gct 403																
Lys His Pro Tyr Gly Lys His Arg Ser Ile Ala Ile Gly His Gln Ala 100																
90 95																
gca gca ctg gcc ctg ctt atc atg gga agc ctt tta att tat gaa gcg 451																
Ala Ala Leu Ala Leu Leu Ile Met Gly Ser Leu Leu Ile Tyr Glu Ala 115																
105 110																
gta tct gca ctg atc aag gga gaa agg cct ccg ata ggt tta gct att 499																
Val Ser Ala Leu Ile Lys Gly Glu Arg Pro Pro Ile Gly Leu Ala Ile 130																
120 125																
tta ttt ggc cat gac gtg tgg tca ggt tgg tta atg atc ggg gtt atg 547																
Leu Phe Gly His Asp Val Trp Ser Gly Trp Leu Met Ile Gly Val Met 145																
135 140																
att tca gtg tcg atc ccg atg gtg att gta ggg cga gta aaa ata aac 595																
Ile Ser Val Ser Ile Pro Met Val Ile Val Gly Arg Val Lys Ile Asn 165																
150 155 160																

tta gct aaa gat ctc cac gat aaa ctc ctc tat gca gac gcg gat atg 643
 Leu Ala Lys Asp Leu His Asp Lys Leu Leu Tyr Ala Asp Ala Asp Met
 170 175 180

gcc aag gct gac tgg ggc aca gca gtc gct agc aca gta ggc gtg ctc 691
 Ala Lys Ala Asp Trp Gly Thr Ala Val Ala Ser Thr Val Gly Val Leu
 185 190 195

gga ata gga ctg ggt ttt tgg tgg gcg gat gca gtt gca gct cta gta 739
 Gly Ile Gly Leu Gly Phe Trp Trp Ala Asp Ala Val Ala Ala Leu Val
 200 205 210

ata tca gct tca att ctc aga gat ggc gtg ata aat atg aaa gct gct 787
 Ile Ser Ala Ser Ile Leu Arg Asp Gly Val Ile Asn Met Lys Ala Ala
 215 220 225

ata tct gac tta ggt gat gga cga gcc atg act tat gac aat tcc gcc 835
 Ile Ser Asp Leu Gly Asp Gly Arg Ala Met Thr Tyr Asp Asn Ser Ala
 230 235 240 245

cct cac cca tta aat gat gat gtg gaa aag gct gcc cta gag atg cat 883
 Pro His Pro Leu Asn Asp Asp Val Glu Lys Ala Ala Leu Glu Met His
 250 255 260

tgg gtc aaa cac gcc cgc gct agg ata cgc gac caa ggc cgc tgt ttc 931
 Trp Val Lys His Ala Arg Ala Arg Ile Arg Asp Gln Gly Arg Cys Phe
 265 270 275

cac aca gag tta ttt gtc gaa cca gta gaa gga tac aca cct gct ccg 979
 His Thr Glu Leu Phe Val Glu Pro Val Glu Gly Tyr Thr Pro Ala Pro
 280 285 290

gaa gaa ata act tct cta gtt aag cga atc caa aac ctt gac tgg aag 1027
 Glu Glu Ile Thr Ser Leu Val Lys Arg Ile Gln Asn Leu Asp Trp Lys
 295 300 305

ctg caa gat gtc gta gct tcc gtc gtc gaa aaa atc gac cgg ttt cag 1075
 Leu Gln Asp Val Val Ala Ser Val Val Glu Lys Ile Asp Arg Phe Gln
 310 315 320 325

gcc cct tcg taaaacttaa ctgagaaagt gat 1107
 Ala Pro Ser

<210> 2840

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 2840

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Pro Glu Lys Lys Arg Ala Val Leu Arg Lys Ala Ile Lys Leu Glu Trp
20 25 30

Ala Thr Ile Ala Trp Val Leu Phe Ser Ile Val Leu Val Gly Val Val
35 40 45

Ala Gly Gln Ser Gln Ala Met Arg Ser Ala Trp Ile Glu Asp Met Leu

50					55					60					
Ser	Leu	Val	Pro	Pro	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Arg	Ile	Ser	Lys
65					70					75					80
Ala	Val	Ala	Thr	Arg	Lys	His	Pro	Tyr	Gly	Lys	His	Arg	Ser	Ile	Ala
				85					90					95	
Ile	Gly	His	Gln	Ala	Ala	Ala	Leu	Ala	Leu	Leu	Ile	Met	Gly	Ser	Leu
			100					105					110		
Leu	Ile	Tyr	Glu	Ala	Val	Ser	Ala	Leu	Ile	Lys	Gly	Glu	Arg	Pro	Pro
		115					120					125			
Ile	Gly	Leu	Ala	Ile	Leu	Phe	Gly	His	Asp	Val	Trp	Ser	Gly	Trp	Leu
	130					135					140				
Met	Ile	Gly	Val	Met	Ile	Ser	Val	Ser	Ile	Pro	Met	Val	Ile	Val	Gly
145					150					155					160
Arg	Val	Lys	Ile	Asn	Leu	Ala	Lys	Asp	Leu	His	Asp	Lys	Leu	Leu	Tyr
				165					170					175	
Ala	Asp	Ala	Asp	Met	Ala	Lys	Ala	Asp	Trp	Gly	Thr	Ala	Val	Ala	Ser
			180					185					190		
Thr	Val	Gly	Val	Leu	Gly	Ile	Gly	Leu	Gly	Phe	Trp	Trp	Ala	Asp	Ala
		195					200						205		
Val	Ala	Ala	Leu	Val	Ile	Ser	Ala	Ser	Ile	Leu	Arg	Asp	Gly	Val	Ile
	210						215					220			
Asn	Met	Lys	Ala	Ala	Ile	Ser	Asp	Leu	Gly	Asp	Gly	Arg	Ala	Met	Thr
225					230					235					240
Tyr	Asp	Asn	Ser	Ala	Pro	His	Pro	Leu	Asn	Asp	Asp	Val	Glu	Lys	Ala
				245					250					255	
Ala	Leu	Glu	Met	His	Trp	Val	Lys	His	Ala	Arg	Ala	Arg	Ile	Arg	Asp
			260					265					270		
Gln	Gly	Arg	Cys	Phe	His	Thr	Glu	Leu	Phe	Val	Glu	Pro	Val	Glu	Gly
		275					280					285			
Tyr	Thr	Pro	Ala	Pro	Glu	Glu	Ile	Thr	Ser	Leu	Val	Lys	Arg	Ile	Gln
	290						295					300			
Asn	Leu	Asp	Trp	Lys	Leu	Gln	Asp	Val	Val	Ala	Ser	Val	Val	Glu	Lys
305					310					315					320
Ile	Asp	Arg	Phe	Gln	Ala	Pro	Ser								
				325											

<210> 2841

<211> 387

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(364)

<223> RXA02662

<400> 2841

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gctctacgtc ctggtcaatc cacgtattag gagcatctag atg cgc cgt aaa cta 115
                                         Met Arg Arg Lys Leu
                                         1 5
acc acc aca tta gaa aac aag ccc ggt gca cga ctt ggt ggc ttc cgc 163
Thr Thr Thr Leu Glu Asn Lys Pro Gly Ala Arg Leu Gly Gly Phe Arg
          10          15          20
gca ctt gca cca act tca aaa atc gcg ctg gtt ttc ctt ctc ctg atc 211
Ala Leu Ala Pro Thr Ser Lys Ile Ala Leu Val Phe Leu Leu Leu Ile
          25          30          35
ttc ctc ctc gcg atc ttt gcc cca ctg att gct aaa tac gat cca ctg 259
Phe Leu Leu Ala Ile Phe Ala Pro Leu Ile Ala Lys Tyr Asp Pro Leu
          40          45          50
gcc tcc gga act cca gtc cag cct cca agc ggt gag cac tgg ttt ggt 307
Ala Ser Gly Thr Pro Val Gln Pro Pro Ser Gly Glu His Trp Phe Gly
          55          60          65
acc gac gcc atc ggc cgc gat att ttc tcc cgc gta gcc acg gcg cca 355
Thr Asp Ala Ile Gly Arg Asp Ile Phe Ser Arg Val Ala Thr Ala Pro
          70          75          80          85
gag cct ccc tgatcattgg tcttttcgct acg 387
Glu Pro Pro

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<210> 2842

<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 2842

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Met Arg Arg Lys Leu Thr Thr Thr Leu Glu Asn Lys Pro Gly Ala Arg
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Leu Gly Gly Phe Arg Ala Leu Ala Pro Thr Ser Lys Ile Ala Leu Val
          20          25          30
Phe Leu Leu Leu Ile Phe Leu Leu Ala Ile Phe Ala Pro Leu Ile Ala
          35          40          45
Lys Tyr Asp Pro Leu Ala Ser Gly Thr Pro Val Gln Pro Pro Ser Gly
          50          55          60
Glu His Trp Phe Gly Thr Asp Ala Ile Gly Arg Asp Ile Phe Ser Arg
          65          70          75          80
Val Ala Thr Ala Pro Glu Pro Pro
          85

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<210> 2843

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<220>  
<221> CDS  
<222> (101)..(580)  
<223> RXA02665
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ggc 603

<210>	2844
<211>	160

<212> PRT

<213> Corynebacterium glutamicum

<400> 2844

Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His
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 Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu
 20 25 30
 Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
 35 40 45
 Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
 50 55 60
 Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
 65 70 75 80
 Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
 85 90 95
 Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
 100 105 110
 Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
 115 120 125
 Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly
 130 135 140
 Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
 145 150 155 160

<210> 2845

<211> 705

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(682)

<223> RXA02670

<400> 2845

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 ccagatTTTT ctggataaat cctggaattt cttaaaacca atg gag gac gaa tcc 115
 Met Glu Asp Glu Ser
 1 5
 gtg aag tcc ctg aac ttg gct gcc cgt cgt ggc gcg ctc gtg acc gtg 163
 Val Lys Ser Leu Asn Leu Ala Ala Arg Arg Gly Ala Leu Val Thr Val
 10 15 20
 gct gct gcg tca gct ctt gcg ctt gca tcc tgc agt gcc gga cag atc 211
 Ala Ala Ala Ser Ala Leu Ala Leu Ala Ser Cys Ser Ala Gly Gln Ile
 25 30 35
 acc cag acc tca agc cag gtt gca gca gtt gat ggc aac cag gca ggc 259

Thr Gln Thr Ser Ser Gln Val Ala Ala Val Asp Gly Asn Gln Ala Gly
 40 45 50
 tcc gcg aac gac cca gtt ctg gtg cgt gat gta acc gtg cac ctc acc 307
 Ser Ala Asn Asp Pro Val Leu Val Arg Asp Val Thr Val His Leu Thr
 55 60 65
 acc gac ggc gaa gct gga gta aag ttc acc gcc atc aac cag gac acc 355
 Thr Asp Gly Glu Ala Gln Val Lys Phe Thr Ala Ile Asn Gln Asp Thr
 70 75 80 85
 tct cac act tct cac acc ctt gag tcc gtc acc gtt gac ggc gaa gag 403
 Ser His Thr Ser His Thr Leu Glu Ser Val Thr Val Asp Gly Glu Glu
 90 95 100
 gtt gag ctt gat gat gca gag cca atc gag cgc aac tgc tcc ctc gtt 451
 Val Glu Leu Asp Asp Ala Glu Pro Ile Glu Arg Asn Cys Ser Leu Val
 105 110 115
 gca gac atc cag tcc gaa ctg gat ctg atc gag gag cca gaa gtt ggc 499
 Ala Asp Ile Gln Ser Glu Leu Asp Leu Ile Glu Glu Pro Glu Val Gly
 120 125 130
 tgc atc cag cac gta gca act tct ctg gag aac cca ggt ttc gca tac 547
 Cys Ile Gln His Val Ala Thr Ser Leu Glu Asn Pro Gly Phe Ala Tyr
 135 140 145
 ggc gga gtc gtg cca gtt gag ttc gtc ttc gac acc ggt gcg atc acc 595
 Gly Gly Val Val Pro Val Glu Phe Val Phe Asp Thr Gly Ala Ile Thr
 150 155 160 165
 atc gat gcc acc gtt tcc gca cct gtc ctc gag tca ggc gta gaa aac 643
 Ile Asp Ala Thr Val Ser Ala Pro Val Leu Glu Ser Gly Val Glu Asn
 170 175 180
 cgc gag gtc ggc gga gac act gca gag gca agc cac cac taagcctctc 692
 Arg Glu Val Gly Gly Asp Thr Ala Glu Ala Ser His His
 185 190
 aaagctgctt gaa 705

<210> 2846

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 2846

Met Glu Asp Glu Ser Val Lys Ser Leu Asn Leu Ala Ala Arg Arg Gly
 1 5 10 15
 Ala Leu Val Thr Val Ala Ala Ala Ser Ala Leu Ala Leu Ala Ser Cys
 20 25 30
 Ser Ala Gly Gln Ile Thr Gln Thr Ser Ser Gln Val Ala Ala Val Asp
 35 40 45
 Gly Asn Gln Ala Gly Ser Ala Asn Asp Pro Val Leu Val Arg Asp Val
 50 55 60
 Thr Val His Leu Thr Thr Asp Gly Glu Ala Gly Val Lys Phe Thr Ala

65		70		75		80
Ile Asn Gln Asp Thr Ser His Thr Ser His Thr Leu Glu Ser Val Thr						
	85			90		95
Val Asp Gly Glu Glu Val Glu Leu Asp Asp Ala Glu Pro Ile Glu Arg						
	100		105			110
Asn Cys Ser Leu Val Ala Asp Ile Gln Ser Glu Leu Asp Leu Ile Glu						
	115		120			125
Glu Pro Glu Val Gly Cys Ile Gln His Val Ala Thr Ser Leu Glu Asn						
	130		135		140	
Pro Gly Phe Ala Tyr Gly Gly Val Val Pro Val Glu Phe Val Phe Asp						
145		150		155		160
Thr Gly Ala Ile Thr Ile Asp Ala Thr Val Ser Ala Pro Val Leu Glu						
	165		170			175
Ser Gly Val Glu Asn Arg Glu Val Gly Gly Asp Thr Ala Glu Ala Ser						
	180		185			190

His His

<210> 2847
 <211> 1221
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1198)
 <223> RXA02672

<400> 2847
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 aacacttgcc gaagcacttg cagcagtaag cttataaagc atg aca cca aca acc 115
 Met Thr Pro Thr Thr
 1 5
 act cct gta tca aac cca gat gcc ctt tcc act gga act cag gat gtg 163
 Thr Pro Val Ser Asn Pro Asp Ala Leu Ser Thr Gly Thr Gln Asp Val
 10 15 20
 cac acc ctc aaa gga acg ttg cag cgc ctc gcc cca ggc aca cca ctt 211
 His Thr Leu Lys Gly Thr Leu Gln Arg Leu Ala Pro Gly Thr Pro Leu
 25 30 35
 cgc gat ggc tta gac cgc atc gtc cga gga cac acc ggc gcg tta atc 259
 Arg Asp Gly Leu Asp Arg Ile Val Arg Gly His Thr Gly Ala Leu Ile
 40 45 50
 gtc att ggt gat gat gaa aac gtc tcc tcg atc tgc gac ggc ggc ttt 307
 Val Ile Gly Asp Asp Glu Asn Val Ser Ser Ile Cys Asp Gly Gly Phe
 55 60 65
 gaa ttc gac gtt tcg ttt gct gca acc cga ctc cgc gag ctg tgc aag 355

Glu Phe Asp Val Ser Phe Ala Ala Thr Arg Leu Arg Glu Leu Cys Lys	
70 75 80 85	
atg gat ggc gct gtc atc ttg tct tcc gac ctt gag cgt atc aaa cgc	403
Met Asp Gly Ala Val Ile Leu Ser Ser Asp Leu Glu Arg Ile Lys Arg	
90 95 100	
gcc aat gtt cag ctg ctg cct tca cca acc tgg cca acc cag gag tcc	451
Ala Asn Val Gln Leu Leu Pro Ser Pro Thr Trp Pro Thr Gln Glu Ser	
105 110 115	
ggc acc cgc cac cgt tct gca gaa cgc acc gcg ctt cac acc ggt gtg	499
Gly Thr Arg His Arg Ser Ala Glu Arg Thr Ala Leu His Thr Gly Val	
120 125 130	
cca gtg att gcg gta tcc gaa tca caa aac acc atc act ctc tac gtc	547
Pro Val Ile Ala Val Ser Glu Ser Gln Asn Thr Ile Thr Leu Tyr Val	
135 140 145	
gag ggc aaa tcc cac atg ttg gag cag cca gct gcc ctg ctt aac cgc	595
Glu Gly Lys Ser His Met Leu Glu Gln Pro Ala Ala Leu Leu Asn Arg	
150 155 160 165	
gcc aac caa gct ttg gga aca atg gag cgc tac cgc gat cgt ctc gat	643
Ala Asn Gln Ala Leu Gly Thr Met Glu Arg Tyr Arg Asp Arg Leu Asp	
170 175 180	
cag gtc aat aac cgc ctt cac ctg gct gaa ctc cac agc tat gtc acc	691
Gln Val Asn Asn Arg Leu His Leu Ala Glu Leu His Ser Tyr Val Thr	
185 190 195	
gtg att gat gtt gtt tct gtc att cag cgc gag gaa atg ctg cgc cga	739
Val Ile Asp Val Val Ser Val Ile Gln Arg Glu Glu Met Leu Arg Arg	
200 205 210	
gtg ggt gaa atc att gat ggc gat gtt ctt gaa cta ggc aaa gac gcc	787
Val Gly Glu Ile Ile Asp Gly Asp Val Leu Glu Leu Gly Lys Asp Ala	
215 220 225	
aag gag att cag atc cag ctc agc gaa tta cgt ggc gat aat gac cga	835
Lys Glu Ile Gln Ile Gln Leu Ser Glu Leu Arg Gly Asp Asn Asp Arg	
230 235 240 245	
gaa cgt gaa tca atc att gct gat tac ctt gtc acc gac ggt att cct	883
Glu Arg Glu Ser Ile Ile Ala Asp Tyr Leu Val Thr Asp Gly Ile Pro	
250 255 260	
gca gat gag gaa atc cac gca gcc ctc gaa gcg atc tca cat tta gat	931
Ala Asp Glu Glu Ile His Ala Ala Leu Glu Ala Ile Ser His Leu Asp	
265 270 275	
gat aag gct ctg ctg aat cct gcg aac atc gcg cgt gtt ctt gga ctg	979
Asp Lys Ala Leu Leu Asn Pro Ala Asn Ile Ala Arg Val Leu Gly Leu	
280 285 290	
cca ccg acc gag gaa gca ctt gat gag cca gtc act cct cgc ggc tac	1027
Pro Pro Thr Glu Glu Ala Leu Asp Glu Pro Val Thr Pro Arg Gly Tyr	
295 300 305	
cgc acg ctc aac aga att cct cga gtg caa aaa ttc ctc atg gat aaa	1075
Arg Thr Leu Asn Arg Ile Pro Arg Val Gln Lys Phe Leu Met Asp Lys	

310	315	320	325	
ctc atc gtg gaa ttc ggc aac ttg gat gca ctg ctc aat gcg tca gta				1123
Leu Ile Val Glu Phe Gly Asn Leu Asp Ala Leu Leu Asn Ala Ser Val				
330		335	340	
gag gat cta agt gca gtc gat ggt gtg ggc tca ctg tgg gca cgc cac				1171
Glu Asp Leu Ser Ala Val Asp Gly Val Gly Ser Leu Trp Ala Arg His				
345		350	355	
atc acc gac gga ctt ggc cgt tta agt taggttaaag gtcaccgctg				1218
Ile Thr Asp Gly Leu Gly Arg Leu Ser				
360		365		
gtg				1221

<210> 2848

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 2848

Met Thr Pro Thr Thr Thr Pro Val Ser Asn Pro Asp Ala Leu Ser Thr				
1	5	10	15	
Gly Thr Gln Asp Val His Thr Leu Lys Gly Thr Leu Gln Arg Leu Ala				
20	25	30		
Pro Gly Thr Pro Leu Arg Asp Gly Leu Asp Arg Ile Val Arg Gly His				
35	40	45		
Thr Gly Ala Leu Ile Val Ile Gly Asp Asp Glu Asn Val Ser Ser Ile				
50	55	60		
Cys Asp Gly Gly Phe Glu Phe Asp Val Ser Phe Ala Ala Thr Arg Leu				
65	70	75	80	
Arg Glu Leu Cys Lys Met Asp Gly Ala Val Ile Leu Ser Ser Asp Leu				
85	90	95		
Glu Arg Ile Lys Arg Ala Asn Val Gln Leu Leu Pro Ser Pro Thr Trp				
100	105	110		
Pro Thr Gln Glu Ser Gly Thr Arg His Arg Ser Ala Glu Arg Thr Ala				
115	120	125		
Leu His Thr Gly Val Pro Val Ile Ala Val Ser Glu Ser Gln Asn Thr				
130	135	140		
Ile Thr Leu Tyr Val Glu Gly Lys Ser His Met Leu Glu Gln Pro Ala				
145	150	155	160	
Ala Leu Leu Asn Arg Ala Asn Gln Ala Leu Gly Thr Met Glu Arg Tyr				
165	170	175		
Arg Asp Arg Leu Asp Gln Val Asn Asn Arg Leu His Leu Ala Glu Leu				
180	185	190		
His Ser Tyr Val Thr Val Ile Asp Val Val Ser Val Ile Gln Arg Glu				
195	200	205		

Glu Met Leu Arg Arg Val Gly Glu Ile Ile Asp Gly Asp Val Leu Glu
 210 215 220
 Leu Gly Lys Asp Ala Lys Glu Ile Gln Ile Gln Leu Ser Glu Leu Arg
 225 230 235 240
 Gly Asp Asn Asp Arg Glu Arg Glu Ser Ile Ile Ala Asp Tyr Leu Val
 245 250 255
 Thr Asp Gly Ile Pro Ala Asp Glu Glu Ile His Ala Ala Leu Glu Ala
 260 265 270
 Ile Ser His Leu Asp Asp Lys Ala Leu Leu Asn Pro Ala Asn Ile Ala
 275 280 285
 Arg Val Leu Gly Leu Pro Pro Thr Glu Glu Ala Leu Asp Glu Pro Val
 290 295 300
 Thr Pro Arg Gly Tyr Arg Thr Leu Asn Arg Ile Pro Arg Val Gln Lys
 305 310 315 320
 Phe Leu Met Asp Lys Leu Ile Val Glu Phe Gly Asn Leu Asp Ala Leu
 325 330 335
 Leu Asn Ala Ser Val Glu Asp Leu Ser Ala Val Asp Gly Val Gly Ser
 340 345 350
 Leu Trp Ala Arg His Ile Thr Asp Gly Leu Gly Arg Leu Ser
 355 360 365

<210> 2849

<211> 1041

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1018)

<223> RXA02678

<400> 2849

ctgtgggagcgc gcgaacaggg cgctcgacatg ctcgccacca attatccgga ccgtgcggcgc 60

gagcttttga acgcacatcc caagcccgcc atgtacgcta atg cgc atg gca aag 115
 Met Arg Met Ala Lys
 1 5

aag act aag aag aat gaa cag ctg ccg gag ggc atg agc cgt cgt cag 163
 Lys Thr Lys Lys Asn Glu Gln Leu Pro Glu Gly Met Ser Arg Arg Gln
 10 15 20

gca aaa ctt gca gcc cgc gcg gct gaa cgt gca gca ctt gag cgt gaa 211
 Ala Lys Leu Ala Ala Arg Ala Ala Glu Arg Ala Ala Leu Glu Arg Glu
 25 30 35

cct cgc cca ttc gag ggc ctg gca atg gag tca cag ctc gtt gca ctg 259
 Pro Arg Pro Phe Glu Gly Leu Ala Met Glu Ser Gln Leu Val Ala Leu
 40 45 50

cag gaa ttc att cca tct gca acc gca ccc atc acc gtt gca ggc acc	307
Gln Glu Phe Ile Pro Ser Ala Thr Ala Pro Ile Thr Val Ala Gly Thr	
55 60 65	
gat cgc aag atc acc ctc tgt acc gtg ctt cca ggc gca gct gcg gca	355
Asp Arg Lys Ile Thr Leu Cys Thr Val Leu Pro Gly Ala Ala Ala Ala	
70 75 80 85	
ctt gtc cgc gaa gaa gca ttc ggc ggc gaa gcg ttt gtt gca atg cag	403
Leu Val Arg Glu Glu Ala Phe Gly Gly Glu Ala Phe Val Ala Met Gln	
90 95 100	
cag gcc atc cgc tcc aac aac cca agc aag gac ctc gcg ttc gcg ctg	451
Gln Ala Ile Arg Ser Asn Asn Pro Ser Lys Asp Leu Ala Phe Ala Leu	
105 110 115	
aac tgg gtc atc aac gca aaa gcc ggc gag tca ctg gcc acc gcc aca	499
Asn Trp Val Ile Asn Ala Lys Ala Gly Glu Ser Leu Ala Thr Ala Thr	
120 125 130	
gcg gac ggc acc cag cca gag cta aag agc ttg ctt aac gac gcc gac	547
Ala Asp Gly Thr Gln Pro Glu Leu Lys Ser Leu Leu Asn Asp Ala Asp	
135 140 145	
acc ctc gaa atc acc act cac cag gac ttc aac tgg tgg ctg gcg gaa	595
Thr Leu Glu Ile Thr His Gln Asp Phe Asn Trp Trp Leu Ala Glu	
150 155 160 165	
aac gac aac ctc tcc cca gaa gtt gcg cag cac atg cag gca gcc aat	643
Asn Asp Asn Leu Ser Pro Glu Val Ala Gln His Met Gln Ala Ala Asn	
170 175 180	
gac tcc atc ctg cct tca cac gaa gtc gaa gca gac gtc cca ggc gct	691
Asp Ser Ile Leu Pro Ser His Glu Val Glu Ala Asp Val Pro Gly Ala	
185 190 195	
gtt tgg tgg gtc aac cca ggc gga aaa gcg cac atc cgt tgg gtc cgc	739
Val Trp Trp Val Asn Pro Gly Gly Lys Ala His Ile Arg Trp Val Arg	
200 205 210	
acc gaa aac gaa acc gca ctg ttc aac gct ttg gca cgc atc gca gca	787
Thr Glu Asn Glu Thr Ala Leu Phe Asn Ala Leu Ala Arg Ile Ala Ala	
215 220 225	
cgt ggc gag ctg aat ctc ggc gaa gaa act aag ttc gct ggt gct ttc	835
Arg Gly Glu Leu Asn Leu Gly Glu Glu Thr Lys Phe Ala Gly Ala Phe	
230 235 240 245	
cgc acc cac ggc atc gtc gtc cca gtg tgg gat ctc gat cct gag cgt	883
Arg Thr His Gly Ile Val Val Pro Val Trp Asp Leu Asp Pro Glu Arg	
250 255 260	
cca tcc acc gat tac gcc gat gtt ttg gtt gca ctc aac gag aag atc	931
Pro Ser Thr Asp Tyr Ala Asp Val Leu Val Ala Leu Asn Glu Lys Ile	
265 270 275	
gtc gct gaa ctg gat aac gat gca cag ctc aac gcc gac gag cgc cgt	979
Val Ala Glu Leu Asp Asn Asp Ala Gln Leu Asn Ala Asp Glu Arg Arg	
280 285 290	
cag ctg gag aac atc aag tcc cgc cag gtg acc atc cgc taaaatctct	1028

Gln Leu Glu Asn Ile Lys Ser Arg Gln Val Thr Ile Arg
 295 300 305

taaaaacact tca

1041

<210> 2850

<211> 306

<212> PRT

<213> Corynebacterium glutamicum

<400> 2850

Met Arg Met Ala Lys Lys Thr Lys Lys Asn Glu Gln Leu Pro Glu Gly
 1 5 10 15

Met Ser Arg Arg Gln Ala Lys Leu Ala Ala Arg Ala Ala Glu Arg Ala
 20 25 30

Ala Leu Glu Arg Glu Pro Arg Pro Phe Glu Gly Leu Ala Met Glu Ser
 35 40 45

Gln Leu Val Ala Leu Gln Glu Phe Ile Pro Ser Ala Thr Ala Pro Ile
 50 55 60

Thr Val Ala Gly Thr Asp Arg Lys Ile Thr Leu Cys Thr Val Leu Pro
 65 70 75 80

Gly Ala Ala Ala Ala Leu Val Arg Glu Glu Ala Phe Gly Gly Glu Ala
 85 90 95

Phe Val Ala Met Gln Gln Ala Ile Arg Ser Asn Asn Pro Ser Lys Asp
 100 105 110

Leu Ala Phe Ala Leu Asn Trp Val Ile Asn Ala Lys Ala Gly Glu Ser
 115 120 125

Leu Ala Thr Ala Thr Ala Asp Gly Thr Gln Pro Glu Leu Lys Ser Leu
 130 135 140

Leu Asn Asp Ala Asp Thr Leu Glu Ile Thr Thr His Gln Asp Phe Asn
 145 150 155 160

Trp Trp Leu Ala Glu Asn Asp Asn Leu Ser Pro Glu Val Ala Gln His
 165 170 175

Met Gln Ala Ala Asn Asp Ser Ile Leu Pro Ser His Glu Val Glu Ala
 180 185 190

Asp Val Pro Gly Ala Val Trp Trp Val Asn Pro Gly Gly Lys Ala His
 195 200 205

Ile Arg Trp Val Arg Thr Glu Asn Glu Thr Ala Leu Phe Asn Ala Leu
 210 215 220

Ala Arg Ile Ala Ala Arg Gly Glu Leu Asn Leu Gly Glu Glu Thr Lys
 225 230 235 240

Phe Ala Gly Ala Phe Arg Thr His Gly Ile Val Val Pro Val Trp Asp
 245 250 255

Leu Asp Pro Glu Arg Pro Ser Thr Asp Tyr Ala Asp Val Leu Val Ala

gaa atg ctt ctg gac ttg gtc tcc aac tcg atc ggc ctg gca gat act 547
 Glu Met Leu Leu Asp Leu Val Ser Asn Ser Ile Gly Leu Ala Asp Thr
 135 140 145

gaa acc act gcg act gca att agt aaa atc cga gca acg ctt tcc gag 595
 Glu Thr Thr Ala Thr Ala Ile Ser Lys Ile Arg Ala Thr Leu Ser Glu
 150 155 160 165

acc tac ctg ttc gga acc ccc gac gga tta acc ttg gcg ctt agt ggc 643
 Thr Tyr Leu Phe Gly Thr Pro Asp Gly Leu Thr Leu Ala Leu Ser Gly
 170 175 180

cca cac gtt gat ttc gaa gtc tcc cac cag ggc agc acc gcg aaa att 691
 Pro His Val Asp Phe Glu Val Ser His Gln Gly Ser Thr Ala Lys Ile
 185 190 195

act tac cgc gat cca agc acc gac acc tta acc gcc gaa gat cgg gta 739
 Thr Tyr Arg Asp Pro Ser Thr Asp Thr Leu Thr Ala Glu Asp Arg Val
 200 205 210

gat acc gca agt gtg gct gct gct ccg ccg gag gtt gtt taggcgtttg 788
 Asp Thr Ala Ser Val Ala Ala Ala Pro Pro Glu Val Val
 215 220 225

ccgagaaatt ttc 801

<210> 2852

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 2852

Met Thr Leu Leu Glu Asn Ser Ser Gly Asp Pro Gly Ser Asp Ser Gly
 1 5 10 15

Gly Ala Arg Tyr Ser Leu Asn Ser Leu Lys Val Ser Glu Gln Ala Ala
 20 25 30

Ala Asn Ala Val Leu Lys Ala Val Leu Asn Asp Val Ser Tyr Gln Glu
 35 40 45

Phe Ala Asp Ser Ser Tyr Leu Glu Ile Thr Gly Thr Pro Ser Ala Asp
 50 55 60

Gly Thr Trp Gly Ile Ser Phe Gly Gly Pro Ser Glu Ser Ala Ser Val
 65 70 75 80

Glu Phe Ser Asp Gly Ser Ile Ser Phe Ser Pro Val Asp Met Thr Val
 85 90 95

Pro Ala Thr Arg Leu Pro Gln Met Gly Ala Phe Tyr Glu Thr Leu Thr
 100 105 110

Glu Glu Gln Leu Gly Met Leu Glu Thr Gly Leu Ala Val Ser Thr Val
 115 120 125

Asp Ser Ser Gln Gln Glu Met Leu Leu Asp Leu Val Ser Asn Ser Ile
 130 135 140

Gly Leu Ala Asp Thr Glu Thr Thr Ala Thr Ala Ile Ser Lys Ile Arg

145		150		155		160
Ala Thr Leu Ser Glu Thr Tyr Leu Phe Gly Thr Pro Asp Gly Leu Thr						
	165			170		175
Leu Ala Leu Ser Gly Pro His Val Asp Phe Glu Val Ser His Gln Gly						
	180		185		190	
Ser Thr Ala Lys Ile Thr Tyr Arg Asp Pro Ser Thr Asp Thr Leu Thr						
	195		200		205	
Ala Glu Asp Arg Val Asp Thr Ala Ser Val Ala Ala Ala Pro Pro Glu						
	210		215		220	
Val Val						
225						

<210> 2853
 <211> 780
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(757)
 <223> RXA02685

<400> 2853
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 Met Ser Gly Leu Arg
 1 5
 tca atc ctg cgc ctc atc gac gat ctc ctc gca ccg gtt gcg ctc aac 163
 Ser Ile Leu Arg Leu Ile Asp Asp Leu Leu Ala Pro Val Ala Leu Asn
 10 15 20
 gac cag caa gtt gca ctg aat gcc tca atg gca aac tcc gca tgg ctg 211
 Asp Gln Gln Val Ala Leu Asn Ala Ser Met Ala Asn Ser Ala Trp Leu
 25 30 35
 gat ctc acc ttg caa ttg tgt tcc gcc gga gtg ctg ttt tcc tgg gga 259
 Asp Leu Thr Leu Gln Leu Cys Ser Ala Gly Val Leu Phe Ser Trp Gly
 40 45 50
 gca cta gcg atc tac ctg cta ggt gaa cgt ttt cag tgg att aaa ccc 307
 Ala Leu Ala Ile Tyr Leu Leu Gly Glu Arg Phe Gln Trp Ile Lys Pro
 55 60 65
 aaa gac tgg gca tgg ggt gca ggc ctt gca gca ctc att ggt att cca 355
 Lys Asp Trp Ala Trp Gly Ala Gly Leu Ala Ala Leu Ile Gly Ile Pro
 70 75 80 85
 ggg tta atc ttc tac gcc agt gct gtt cat ttg ggg ctg tcc aaa cag 403
 Gly Leu Ile Phe Tyr Ala Ser Ala Val His Leu Gly Leu Ser Lys Gln
 90 95 100
 gtt gtg ccc acc acg ttg gaa acc tgg tgg gaa atc cca gta ctt ctt 451
 Val Val Pro Thr Thr Leu Glu Thr Trp Trp Glu Ile Pro Val Leu Leu

105	110	115	
atc tgg tca gct gcc aac gcc ttt ggt gaa gag atc gtg gta gtc atg			499
Ile Trp Ser Ala Ala Asn Ala Phe Gly Glu Glu Ile Val Val Val Met			
120	125	130	
tgg ttt ttc acc agg ctg cgc cag ctg aag tgg agt gtg cct gca gtt			547
Trp Phe Phe Thr Arg Leu Arg Gln Leu Lys Trp Ser Val Pro Ala Val			
135	140	145	
atc gtg aca tct tca gta cta cgc ggt tcc tat cac ctc tac cag gga			595
Ile Val Thr Ser Ser Val Leu Arg Gly Ser Tyr His Leu Tyr Gln Gly			
150	155	160	165
atc tct gca ggc ttg ggc aac atc atc atg gga gta gcg ttc gcg tac			643
Ile Ser Ala Gly Leu Gly Asn Ile Ile Met Gly Val Ala Phe Ala Tyr			
170	175	180	
ttc tat cac cgc acg ggc aaa atc tgg cca ctg gta atc gct cac ttc			691
Phe Tyr His Arg Thr Gly Lys Ile Trp Pro Leu Val Ile Ala His Phe			
185	190	195	
ttg att gat gcg gtg gct ttt gtg ggc tac tcc gca att ggc ggg aat			739
Leu Ile Asp Ala Val Ala Phe Val Gly Tyr Ser Ala Ile Gly Gly Asn			
200	205	210	
tta agt tgg tta ggg ctt taaactgaag ttcctatttt att			780
Leu Ser Trp Leu Gly Leu			
215			

<210> 2854

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 2854

Met Ser Gly Leu Arg Ser Ile Leu Arg Leu Ile Asp Asp Leu Leu Ala	
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Pro Val Ala Leu Asn Asp Gln Gln Val Ala Leu Asn Ala Ser Met Ala	
20 25 30	
Asn Ser Ala Trp Leu Asp Leu Thr Leu Gln Leu Cys Ser Ala Gly Val	
35 40 45	
Leu Phe Ser Trp Gly Ala Leu Ala Ile Tyr Leu Leu Gly Glu Arg Phe	
50 55 60	
Gln Trp Ile Lys Pro Lys Asp Trp Ala Trp Gly Ala Gly Leu Ala Ala	
65 70 75 80	
Leu Ile Gly Ile Pro Gly Leu Ile Phe Tyr Ala Ser Ala Val His Leu	
85 90 95	
Gly Leu Ser Lys Gln Val Val Pro Thr Thr Leu Glu Thr Trp Trp Glu	
100 105 110	
Ile Pro Val Leu Leu Ile Trp Ser Ala Ala Asn Ala Phe Gly Glu Glu	
115 120 125	

Ile Val Val Val Met Trp Phe Phe Thr Arg Leu Arg Gln Leu Lys Trp
 130 135 140

Ser Val Pro Ala Val Ile Val Thr Ser Ser Val Leu Arg Gly Ser Tyr
 145 150 155 160

His Leu Tyr Gln Gly Ile Ser Ala Gly Leu Gly Asn Ile Ile Met Gly
 165 170 175

Val Ala Phe Ala Tyr Phe Tyr His Arg Thr Gly Lys Ile Trp Pro Leu
 180 185 190

Val Ile Ala His Phe Leu Ile Asp Ala Val Ala Phe Val Gly Tyr Ser
 195 200 205

Ala Ile Gly Gly Asn Leu Ser Trp Leu Gly Leu
 210 215

<210> 2855

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXA02688

<400> 2855

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gggttcgcgc agcaagcgaa ggaaggaac ttaactagcc atg gcc ggc cgg att 115
 Met Ala Gly Arg Ile
 1 5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163
 Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
 10 15 20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa 211
 Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
 25 30 35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259
 Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
 40 45 50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307
 Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
 55 60 65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg 355
 Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
 70 75 80 85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac 403
 Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
 90 95 100

ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451

Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
 105 110 115
 ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt 499
 Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
 120 125 130
 gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga 547
 Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg
 135 140 145
 atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc 595
 Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
 150 155 160 165
 agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg 643
 Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
 170 175 180
 gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg 691
 Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
 185 190 195
 gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc 739
 Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
 200 205 210
 tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg 789
 Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
 215 220
 gat 792

<210> 2856

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 2856

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 Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
 20 25 30
 Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
 35 40 45
 Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
 50 55 60
 Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
 65 70 75 80
 Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
 85 90 95
 Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
 100 105 110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
115 120 125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
130 135 140

Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
145 150 155 160

Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr
165 170 175

His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly
180 185 190

Asn Cys Arg Phe Val Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln
195 200 205

Trp Asp Val Val Arg Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
210 215 220

<210> 2857

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(442)

<223> RXA02689

<400> 2857

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catccgcgga ggtcggagta cctgtagagg agaacgctcc atg att gaa gtc agc 115
Met Ile Glu Val Ser
1 5

gac gaa cgc ttc gag gaa ctg gtc gaa cta gcc ttc gac caa gtt ccc 163
Asp Glu Arg Phe Glu Glu Leu Val Glu Leu Ala Phe Asp Gln Val Pro
10 15 20

cag caa ttc ctg gat cat atg cgc aac gtg gtt tta ctc att gag gat 211
Gln Gln Phe Leu Asp His Met Arg Asn Val Val Leu Leu Ile Glu Asp
25 30 35

ttc aac cca gat tcg cct tat atc ttg ggt tta tac cac ggc gtt gct 259
Phe Asn Pro Asp Ser Pro Tyr Ile Leu Gly Leu Tyr His Gly Val Ala
40 45 50

ctc aca gag cgc aca ttc aac cac ggt ggc ctg ccg gat tcc atc acc 307
Leu Thr Glu Arg Thr Phe Asn His Gly Gly Leu Pro Asp Ser Ile Thr
55 60 65

att tat aaa ggt gcg ttg caa aat tac tgc aat tca gag gaa caa cta 355
Ile Tyr Lys Gly Ala Leu Gln Asn Tyr Cys Asn Ser Glu Glu Gln Leu
70 75 80 85

gtg gag cag gtg cgg gtg acc gtg ctg cat gag att ggg cat tat ttt 403
Val Glu Gln Val Arg Val Thr Val Leu His Glu Ile Gly His Tyr Phe

90								95				100				
ggc	ctc	ggc	gaa	gag	gac	ctg	cac	agg	ctc	gga	tac	gcc	taaaacgcct	452		
Gly	Leu	Gly	Glu	Glu	Asp	Leu	His	Arg	Leu	Gly	Tyr	Ala				
			105				110									

cattaggtgc aca 465

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<210> 2858
<211> 114
<212> PRT
<213> Corynebacterium glutamicum
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Phe Asp Gln Val Pro Gln Gln Phe Leu Asp His Met Arg Asn Val Val
      20             25             30
Leu Leu Ile Glu Asp Phe Asn Pro Asp Ser Pro Tyr Ile Leu Gly Leu
      35             40             45
Tyr His Gly Val Ala Leu Thr Glu Arg Thr Phe Asn His Gly Gly Leu
      50             55             60
Pro Asp Ser Ile Thr Ile Tyr Lys Gly Ala Leu Gln Asn Tyr Cys Asn
      65             70             75             80
Ser Glu Glu Gln Leu Val Glu Gln Val Arg Val Thr Val Leu His Glu
      85             90             95
Ile Gly His Tyr Phe Gly Leu Gly Glu Glu Asp Leu His Arg Leu Gly
      100             105             110
Tyr Ala

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<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1198)
<223> RXA02690
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tctgacgtga acccattttg gtggcatgat ggtgtcaatt atg agt aca aac ttt 115
Met Ser Thr Asn Phe
1 5
gac act tcg acg tct cca gag ggt gaa acc aag aag aac tct tct ttc 163
Asp Thr Ser Thr Ser Pro Glu Gly Glu Thr Lys Lys Asn Ser Ser Phe
10 15 20

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cgc act gcg gcc tct gtg cag acc atg ctt gtt gca gct ttg gca gca	211
Arg Thr Ala Ala Ser Val Gln Thr Met Leu Val Ala Ala Leu Ala Ala	
25 30 35	
acg gct gct gtt ggc gtg tac tcc tac aac acg gac aat tca gca aac	259
Thr Ala Ala Val Gly Val Tyr Ser Tyr Asn Thr Asp Asn Ser Ala Asn	
40 45 50	
ggc ggc gaa tcc ccc aca gga cct gag caa agt aca gtg tcc acc acc	307
Gly Gly Glu Ser Pro Thr Gly Pro Glu Gln Ser Thr Val Ser Thr Thr	
55 60 65	
gca act att gcc tca ttt acc act gct gac gtg ggc caa tgt gca acc	355
Ala Thr Ile Ala Ser Phe Thr Thr Ala Asp Val Gly Gln Cys Ala Thr	
70 75 80 85	
tgg gat gtt aac aat gaa ggt cta gtg tct ggt ttt gaa caa acc agc	403
Trp Asp Val Asn Asn Glu Gly Leu Val Ser Gly Phe Glu Gln Thr Ser	
90 95 100	
tgc gat caa gag cac cgc ttt gaa att tct gct cgg gaa aac ttg gca	451
Cys Asp Gln Glu His Arg Phe Glu Ile Ser Ala Arg Glu Asn Leu Ala	
105 110 115	
act tac cca agt tcg gaa ttc ggt ccg gac gca gct cca cca aac ctc	499
Thr Tyr Pro Ser Ser Glu Phe Gly Pro Asp Ala Ala Pro Pro Asn Leu	
120 125 130	
acc cgt cag gcg cag ctg cgt gaa gag ctc tgc caa tct cct acc ttg	547
Thr Arg Gln Ala Gln Leu Arg Glu Glu Leu Cys Gln Ser Pro Thr Leu	
135 140 145	
gcg tat ttg aat aac cgt ttc gat cca tcg ggg cgc tac acc atc gcc	595
Ala Tyr Leu Asn Asn Arg Phe Asp Pro Ser Gly Arg Tyr Thr Ile Ala	
150 155 160 165	
ccg atc ctg cca cct gcg gaa gcg tgg gct gcg gga gat cgc acc atg	643
Pro Ile Leu Pro Pro Ala Glu Ala Trp Ala Ala Gly Asp Arg Thr Met	
170 175 180	
ctc tgt gga ctt cag gca acc gac gct tca ggc act cca caa ctc acc	691
Leu Cys Gly Leu Gln Ala Thr Asp Ala Ser Gly Thr Pro Gln Leu Thr	
185 190 195	
gtc gga ccg ata gca gcc aat gac cag gca cgc gtt ttt gaa acc ggc	739
Val Gly Pro Ile Ala Ala Asn Asp Gln Ala Arg Val Phe Glu Thr Gly	
200 205 210	
gcc tgc gtg aag gtg gaa tcc tcc gca gag ttc cgc caa gtt gat tgc	787
Ala Cys Val Lys Val Glu Ser Ser Ala Glu Phe Arg Gln Val Asp Cys	
215 220 225	
acg gaa gat cac cac ctc gaa tca att ttg aca gtc aac ctt ggt gtc	835
Thr Glu Asp His His Leu Glu Ser Ile Leu Thr Val Asn Leu Gly Val	
230 235 240 245	
ccc ttc cca cag ggc gcg ccc agc acg gat gag cag aac aat ttc ctc	883
Pro Phe Pro Gln Gly Ala Pro Ser Thr Asp Glu Gln Asn Asn Phe Leu	
250 255 260	
gga aac acc tgc acc caa gca tcc att gat tac cta ggc tcc gaa gaa	931

Gly Asn Thr Cys Thr Gln Ala Ser Ile Asp Tyr Leu Gly Ser Glu Glu
 265 270 275

aac gtc tac caa tcc acc ctg cag acc ttc tgg cca acg att acc tcc 979
 Asn Val Tyr Gln Ser Thr Leu Gln Thr Phe Trp Pro Thr Ile Thr Ser
 280 285 290

aac tcc tgg ttg ggc ggt tca cac agc gtg aac tgc ttc ctc atg tca 1027
 Asn Ser Trp Leu Gly Gly Ser His Ser Val Asn Cys Phe Leu Met Ser
 295 300 305

cca tcc acc gag ggt gct gca aca ttt aac acc ctc aac ggt tca gcg 1075
 Pro Ser Thr Glu Gly Ala Ala Thr Phe Asn Thr Leu Asn Gly Ser Ala
 310 315 320 325

act ggc aca ttc acc atc aac ggt gaa gtt ccc cca cct cag cca gag 1123
 Thr Gly Thr Phe Thr Ile Asn Gly Glu Val Pro Pro Pro Gln Pro Glu
 330 335 340

cgc gat ccg ctc cgt gac act gca gga acg aca gca tcc gcg gag gtc 1171
 Arg Asp Pro Leu Arg Asp Thr Ala Gly Thr Thr Ala Ser Ala Glu Val
 345 350 355

gga gta cct gta gag gag aac gct cca tgattgaagt cagcgacgaa 1218
 Gly Val Pro Val Glu Glu Asn Ala Pro
 360 365

cgc 1221

<210> 2860 .

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 2860

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Lys Asn Ser Ser Phe Arg Thr Ala Ala Ser Val Gln Thr Met Leu Val
 20 25 30

Ala Ala Leu Ala Ala Thr Ala Ala Val Gly Val Tyr Ser Tyr Asn Thr
 35 40 45

Asp Asn Ser Ala Asn Gly Gly Glu Ser Pro Thr Gly Pro Glu Gln Ser
 50 55 60

Thr Val Ser Thr Thr Ala Thr Ile Ala Ser Phe Thr Thr Ala Asp Val
 65 70 75 80

Gly Gln Cys Ala Thr Trp Asp Val Asn Asn Glu Gly Leu Val Ser Gly
 85 90 95

Phe Glu Gln Thr Ser Cys Asp Gln Glu His Arg Phe Glu Ile Ser Ala
 100 105 110

Arg Glu Asn Leu Ala Thr Tyr Pro Ser Ser Glu Phe Gly Pro Asp Ala
 115 120 125

Ala Pro Pro Asn Leu Thr Arg Gln Ala Gln Leu Arg Glu Glu Leu Cys

130	135	140
Gln Ser Pro Thr Leu Ala Tyr Leu Asn Asn Arg Phe Asp Pro Ser Gly 145 150 155 160		
Arg Tyr Thr Ile Ala Pro Ile Leu Pro Pro Ala Glu Ala Trp Ala Ala 165 170 175		
Gly Asp Arg Thr Met Leu Cys Gly Leu Gln Ala Thr Asp Ala Ser Gly 180 185 190		
Thr Pro Gln Leu Thr Val Gly Pro Ile Ala Ala Asn Asp Gln Ala Arg 195 200 205		
Val Phe Glu Thr Gly Ala Cys Val Lys Val Glu Ser Ser Ala Glu Phe 210 215 220		
Arg Gln Val Asp Cys Thr Glu Asp His His Leu Glu Ser Ile Leu Thr 225 230 235 240		
Val Asn Leu Gly Val Pro Phe Pro Gln Gly Ala Pro Ser Thr Asp Glu 245 250 255		
Gln Asn Asn Phe Leu Gly Asn Thr Cys Thr Gln Ala Ser Ile Asp Tyr 260 265 270		
Leu Gly Ser Glu Glu Asn Val Tyr Gln Ser Thr Leu Gln Thr Phe Trp 275 280 285		
Pro Thr Ile Thr Ser Asn Ser Trp Leu Gly Gly Ser His Ser Val Asn 290 295 300		
Cys Phe Leu Met Ser Pro Ser Thr Glu Gly Ala Ala Thr Phe Asn Thr 305 310 315 320		
Leu Asn Gly Ser Ala Thr Gly Thr Phe Thr Ile Asn Gly Glu Val Pro 325 330 335		
Pro Pro Gln Pro Glu Arg Asp Pro Leu Arg Asp Thr Ala Gly Thr Thr 340 345 350		
Ala Ser Ala Glu Val Gly Val Pro Val Glu Glu Asn Ala Pro 355 360 365		

<210> 2861

<211> 1359

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1336)

<223> RXA02700

<400> 2861

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aagtctcggt agggggagaa gttacagtaa gggcgtttta gtg gtt ccc tcg ttg 115

Val Val Pro Ser Leu

1

5

cag caa tgg cga aaa cct gct ctc atc ctg gcc att ttg acg gtg cta Gln Gln Trp Arg Lys Pro Ala Leu Ile Leu Ala Ile Leu Thr Val Leu 10 15 20	163
ggc gta ctc ctg acc cat tgg ttc gcc tgg cca ctc acc tgg ccg ctg Gly Val Leu Leu Thr His Trp Phe Ala Trp Pro Leu Thr Trp Pro Leu 25 30 35	211
ggg ctg cgt ctt ccc gtt gat gta gag gtg tac tgg cag ggt gcg cgc Gly Leu Arg Leu Pro Val Asp Val Glu Val Tyr Trp Gln Gly Ala Arg 40 45 50	259
gag ttt tgg ctc gcc gat gat ctc tac gac atc agg tat gac acc act Glu Phe Trp Leu Ala Asp Asp Leu Tyr Asp Ile Arg Tyr Asp Thr Thr 55 60 65	307
ttc gac aac ttg ccg ttc acc tat ccc cct ttc ggt gcg ttg gtg ttc Phe Asp Asn Leu Pro Phe Thr Tyr Pro Pro Phe Gly Ala Leu Val Phe 70 75 80 85	355
acc cca ttg tgg tgg att cat gac ctc ttt ggt ctt ctc gtc acc gaa Thr Pro Leu Trp Trp Ile His Asp Leu Phe Gly Leu Leu Val Thr Glu 90 95 100	403
cgt gtc ttc gcg cta atc acg ctg ctc acc acc tac gct gtg gca gtt Arg Val Phe Ala Leu Ile Thr Leu Thr Thr Tyr Ala Val Ala Val 105 110 115	451
ttc ctg ctc cgc ctg gcc ggc gtg cgc gat cgt gtg tgg gaa ttc gtc Phe Leu Leu Arg Leu Ala Gly Val Arg Asp Arg Val Trp Glu Phe Val 120 125 130	499
gca ttc gca gcc ctg ctc gtg tcc gcg ccg gtg tat ttc aca ctc aat Ala Phe Ala Ala Leu Leu Val Ser Ala Pro Val Tyr Phe Thr Leu Asn 135 140 145	547
att ggg caa ata aac gtc atg ctc atg gct tta acg ctt ttc gac gtc Ile Gly Gln Ile Asn Val Met Leu Met Ala Leu Thr Leu Phe Asp Val 150 155 160 165	595
gcc ctc ccc cgc agc acg cgc cat tca ggc gtg ctc aaa tac gtg cca Ala Leu Pro Arg Ser Thr Arg His Ser Gly Val Leu Lys Tyr Val Pro 170 175 180	643
ctc ggc gta ctc acc ggc att gcc gct gcg atc aaa cta acc cca cta Leu Gly Val Leu Thr Gly Ile Ala Ala Ala Ile Lys Leu Thr Pro Leu 185 190 195	691
gtg ttc ggg ctg tat ttc ctc atc ctg tgg gtc gtg act aaa tca cca Val Phe Gly Leu Tyr Phe Leu Ile Leu Trp Val Val Thr Lys Ser Pro 200 205 210	739
cgc gga ctg ttt gga atg att ggt ggc ttc ctc ggg gca tcc ggg ctt Arg Gly Leu Phe Gly Met Ile Gly Gly Phe Leu Gly Ala Ser Gly Leu 215 220 225	787
gca att att ttc cga cca tcc att agc atc caa tat ttc acc gac gtg Ala Ile Ile Phe Arg Pro Ser Ile Ser Ile Gln Tyr Phe Thr Asp Val 230 235 240 245	835

ctg ttt acc gca gaa cgc atc ggc gac ctc cac ttc gca cgc aat gtc 883
 Leu Phe Thr Ala Glu Arg Ile Gly Asp Leu His Phe Ala Arg Asn Val
 250 255 260

tcc atc cgt gcg gtt ttg gaa cga ctc ccc gaa ctt ggt tcc gca gca 931
 Ser Ile Arg Ala Val Leu Glu Arg Leu Pro Glu Leu Gly Ser Ala Ala
 265 270 275

tct atc atg tgg ctt gtt gct gtg gcg cta gtg atc atc gca gtc gca 979
 Ser Ile Met Trp Leu Val Ala Val Ala Leu Val Ile Ile Ala Val Ala
 280 285 290

gtt gct gct tac cga atc ctg cgg acg gat ctc tcc gcg cac aat cgt 1027
 Val Ala Ala Tyr Arg Ile Leu Arg Thr Asp Leu Ser Ala His Asn Arg
 295 300 305

ctg ctg gct gtt tcc ctc gtg tcg ctc gtt gca ctg ttg tgc tcc ccc 1075
 Leu Leu Ala Val Ser Leu Val Ser Leu Val Ala Leu Leu Cys Ser Pro
 310 315 320 325

gtc agt tgg tac cac cac tgg gtg tgg ctt ggt ccg tta atc gtc gct 1123
 Val Ser Trp Tyr His His Trp Val Trp Leu Gly Pro Leu Ile Val Ala
 330 335 340

ctc tgg cta act caa cac cgc tgg ctg gct cta tgg ggc gca ttc gcc 1171
 Leu Trp Leu Thr Gln His Arg Trp Leu Ala Leu Trp Gly Ala Phe Ala
 345 350 355

gtg aca ttc gga tca ttc cac aat ttc cta ccc tca gaa aac aat atg 1219
 Val Thr Phe Gly Ser Phe His Asn Phe Leu Pro Ser Glu Asn Asn Met
 360 365 370

gag ctc acc tgg ccg tgg tgg atg cat gtc ctc gca gca cat tat ttg 1267
 Glu Leu Thr Trp Pro Trp Trp Met His Val Leu Ala Ala His Tyr Leu
 375 380 385

atc ttc tcc gca gtg gtt act gcc gta ttt agt tgt ggg aaa atg ccc 1315
 Ile Phe Ser Ala Val Val Thr Ala Val Phe Ser Cys Gly Lys Met Pro
 390 395 400 405

caa aaa aca gag ctt tcc cac taatcgatca ggagtatcac atc 1359
 Gln Lys Thr Glu Leu Ser His
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<210> 2862

<211> 412

<212> PRT

<213> Corynebacterium glutamicum

<400> 2862

Val Val Pro Ser Leu Gln Gln Trp Arg Lys Pro Ala Leu Ile Leu Ala
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Ile Leu Thr Val Leu Gly Val Leu Leu Thr His Trp Phe Ala Trp Pro
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Leu Thr Trp Pro Leu Gly Leu Arg Leu Pro Val Asp Val Glu Val Tyr
 35 40 45

Trp Gln Gly Ala Arg Glu Phe Trp Leu Ala Asp Asp Leu Tyr Asp Ile

50					55					60					
Arg	Tyr	Asp	Thr	Thr	Phe	Asp	Asn	Leu	Pro	Phe	Thr	Tyr	Pro	Pro	Phe
65					70					75					80
Gly	Ala	Leu	Val	Phe	Thr	Pro	Leu	Trp	Trp	Ile	His	Asp	Leu	Phe	Gly
				85					90					95	
Leu	Leu	Val	Thr	Glu	Arg	Val	Phe	Ala	Leu	Ile	Thr	Leu	Leu	Thr	Thr
			100					105					110		
Tyr	Ala	Val	Ala	Val	Phe	Leu	Leu	Arg	Leu	Ala	Gly	Val	Arg	Asp	Arg
		115					120					125			
Val	Trp	Glu	Phe	Val	Ala	Phe	Ala	Ala	Leu	Leu	Val	Ser	Ala	Pro	Val
	130					135					140				
Tyr	Phe	Thr	Leu	Asn	Ile	Gly	Gln	Ile	Asn	Val	Met	Leu	Met	Ala	Leu
145				150					155						160
Thr	Leu	Phe	Asp	Val	Ala	Leu	Pro	Arg	Ser	Thr	Arg	His	Ser	Gly	Val
			165					170						175	
Leu	Lys	Tyr	Val	Pro	Leu	Gly	Val	Leu	Thr	Gly	Ile	Ala	Ala	Ala	Ile
			180					185					190		
Lys	Leu	Thr	Pro	Leu	Val	Phe	Gly	Leu	Tyr	Phe	Leu	Ile	Leu	Trp	Val
		195					200					205			
Val	Thr	Lys	Ser	Pro	Arg	Gly	Leu	Phe	Gly	Met	Ile	Gly	Gly	Phe	Leu
	210					215					220				
Gly	Ala	Ser	Gly	Leu	Ala	Ile	Ile	Phe	Arg	Pro	Ser	Ile	Ser	Ile	Gln
225				230					235						240
Tyr	Phe	Thr	Asp	Val	Leu	Phe	Thr	Ala	Glu	Arg	Ile	Gly	Asp	Leu	His
			245						250					255	
Phe	Ala	Arg	Asn	Val	Ser	Ile	Arg	Ala	Val	Leu	Glu	Arg	Leu	Pro	Glu
			260					265					270		
Leu	Gly	Ser	Ala	Ala	Ser	Ile	Met	Trp	Leu	Val	Ala	Val	Ala	Leu	Val
		275					280					285			
Ile	Ile	Ala	Val	Ala	Val	Ala	Ala	Tyr	Arg	Ile	Leu	Arg	Thr	Asp	Leu
	290					295					300				
Ser	Ala	His	Asn	Arg	Leu	Leu	Ala	Val	Ser	Leu	Val	Ser	Leu	Val	Ala
305				310					315					320	
Leu	Leu	Cys	Ser	Pro	Val	Ser	Trp	Tyr	His	His	Trp	Val	Trp	Leu	Gly
			325					330						335	
Pro	Leu	Ile	Val	Ala	Leu	Trp	Leu	Thr	Gln	His	Arg	Trp	Leu	Ala	Leu
			340					345					350		
Trp	Gly	Ala	Phe	Ala	Val	Thr	Phe	Gly	Ser	Phe	His	Asn	Phe	Leu	Pro
		355					360					365			
Ser	Glu	Asn	Asn	Met	Glu	Leu	Thr	Trp	Pro	Trp	Trp	Met	His	Val	Leu
	370					375					380				

Ala Ala His Tyr Leu Ile Phe Ser Ala Val Val Thr Ala Val Phe Ser
 385 390 395 400

Cys Gly Lys Met Pro Gln Lys Thr Glu Leu Ser His
 405 410

<210> 2863

<211> 1423

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1408)

<223> RXA02701

<400> 2863

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acgaacggtg ttttcatggt taagaaaagg actcctggtt ttg acg aac ccc cag 115
 Leu Thr Asn Pro Gln
 1 5

aca gca cat gct gcc gcg tct gac tcc gca tcc cag aag gag gct cct 163
 Thr Ala His Ala Ala Ser Asp Ser Ala Ser Gln Lys Glu Ala Pro
 10 15 20

aat cct tca ctc tcc atc act gta ggt att aaa gat ctg ctg ggg ctg 211
 Asn Pro Ser Leu Ser Ile Thr Val Gly Ile Lys Asp Leu Leu Gly Leu
 25 30 35

ctt tca gtt ctt ggc att gca gcg ggg ctg ata gcc aac aag att ctc 259
 Leu Ser Val Leu Gly Ile Ala Ala Gly Leu Ile Ala Asn Lys Ile Leu
 40 45 50

atc gaa cgc tac aac tgg cgc atc gat gcc gca gtt tac cgc gaa ggc 307
 Ile Glu Arg Tyr Asn Trp Arg Ile Asp Ala Ala Val Tyr Arg Glu Gly
 55 60 65

gcg tta gcg ctg gtc aac ggg gaa tca ctg tac gcg cag ccg ttt gat 355
 Ala Leu Ala Leu Val Asn Gly Glu Ser Leu Tyr Ala Gln Pro Phe Asp
 70 75 80 85

atg ggt gat att tca cta ccc ttt atc tac cca ccg att ggt gcc atc 403
 Met Gly Asp Ile Ser Leu Pro Phe Ile Tyr Pro Pro Ile Gly Ala Ile
 90 95 100

ctg ttt gcg cct tgg ggg tac ttt gat ttc atc aca gtt gaa ctt gcg 451
 Leu Phe Ala Pro Trp Gly Tyr Phe Asp Phe Ile Thr Val Glu Leu Ala
 105 110 115

gga aac ctt gtt gtc ata ggc tca tcc ctg ctg tta tta ctg tgc ctg 499
 Gly Asn Leu Val Val Ile Gly Ser Ser Leu Leu Leu Leu Leu Cys Leu
 120 125 130

tat ctt gtc acc aac gct gtt ctt agc ggt cga gac aag ctg ttg gcc 547
 Tyr Leu Val Thr Asn Ala Val Leu Ser Gly Arg Asp Lys Leu Leu Ala
 135 140 145

ttc acc atc gct gcg att tcc tgg ccg atc gct ctc ttt gca gag cca	595
Phe Thr Ile Ala Ala Ile Ser Trp Pro Ile Ala Leu Phe Ala Glu Pro	
150 155 160 165	
gtg ttt ttg aac gct gac ttg ggc caa atc aac att ttg atc atg gct	643
Val Phe Leu Asn Ala Asp Leu Gly Gln Ile Asn Ile Leu Ile Met Ala	
170 175 180	
ttg gtt gtc atg gac ctg ctt ccg att aag cgc aga atc ccc cga ggt	691
Leu Val Val Met Asp Leu Leu Pro Ile Lys Arg Arg Ile Pro Arg Gly	
185 190 195	
gtc ctg att ggc ctt gca gcc gcc atc aaa atc act ccg ctg gcc atg	739
Val Leu Ile Gly Leu Ala Ala Ala Ile Lys Ile Thr Pro Leu Ala Met	
200 205 210	
ctg ttg tat ttc ctg gtg aag aag gat ttc cgc gga atc atc aat gcg	787
Leu Leu Tyr Phe Leu Val Lys Lys Asp Phe Arg Gly Ile Ile Asn Ala	
215 220 225	
gtg atc tca cta ctt gcc ttc act gct atc ggt gct gtg ctc gca tgg	835
Val Ile Ser Leu Leu Ala Phe Thr Ala Ile Gly Ala Val Leu Ala Trp	
230 235 240 245	
gaa aac acc aaa gag ttc ttc tct tca acc ctt ctc aac tta agt gct	883
Glu Asn Thr Lys Glu Phe Phe Ser Ser Thr Leu Leu Asn Leu Ser Ala	
250 255 260	
gaa ggc gat tca ggc gta gac acc acg ttc caa tcc aac agc tcg att	931
Glu Gly Asp Ser Gly Val Asp Thr Thr Phe Gln Ser Asn Ser Ser Ile	
265 270 275	
cag gcc atg ctg tat cgc tgg tgg acc tca aag gca gat gcc gaa gca	979
Gln Ala Met Leu Tyr Arg Trp Trp Thr Ser Lys Ala Asp Ala Glu Ala	
280 285 290	
tcc tca ctg ccc acc atc ttg tgg atc gta ctg tcc ctg att gct gtg	1027
Ser Ser Leu Pro Thr Ile Leu Trp Ile Val Leu Ser Leu Ile Ala Val	
295 300 305	
gcg gcc gtt gcc tac cta atg cac caa ctc ttc tcc aga gga ttg cac	1075
Ala Ala Val Ala Tyr Leu Met His Gln Leu Phe Ser Arg Gly Leu His	
310 315 320 325	
gtt gag gca gtc atg gtt aac gcc atg ctc atg cta ctt atc tcc ccc	1123
Val Glu Ala Val Met Val Asn Ala Met Leu Met Leu Leu Ile Ser Pro	
330 335 340	
atc tca tgg tct cac cac tgg gtg tgg cta ccg ctg tgg gct gtg gtg	1171
Ile Ser Trp Ser His His Trp Val Trp Leu Pro Leu Trp Ala Val Val	
345 350 355	
ttc ttc gtt cga tac cgc cag cac cgc tct cac ccg aag ttc ttg ttg	1219
Phe Phe Val Arg Tyr Arg Gln His Arg Ser His Pro Lys Phe Leu Leu	
360 365 370	
tgg agc gga gtt atc ttg agc gtc atg ctg ctg atg ctg cca cca aaa	1267
Trp Ser Gly Val Ile Leu Ser Val Met Leu Leu Met Leu Pro Pro Lys	
375 380 385	
tgg tgg ttt ggc cgc gat ggc gtc aac gtc ttc gaa ctg aat ttc tgg	1315

Trp Trp Phe Gly Arg Asp Gly Val Asn Val Phe Glu Leu Asn Phe Trp
 390 395 400 405

gag aaa cta ctc atc tct gac tgg acg tgg ctc tcc atc ggg ctc atg 1363
 Glu Lys Leu Leu Ile Ser Asp Trp Thr Trp Leu Ser Ile Gly Leu Met
 410 415 420

atc acc ttg ggt ctt ggg ctg aaa gca ttt ccc aaa ata tcc aaa 1408
 Ile Thr Leu Gly Leu Gly Leu Lys Ala Phe Pro Lys Ile Ser Lys
 425 430 435

tagataaagg tgtgg 1423

<210> 2864
 <211> 436
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2864
 Leu Thr Asn Pro Gln Thr Ala His Ala Ala Ala Ser Asp Ser Ala Ser
 1 5 10 15

Gln Lys Glu Ala Pro Asn Pro Ser Leu Ser Ile Thr Val Gly Ile Lys
 20 25 30

Asp Leu Leu Gly Leu Leu Ser Val Leu Gly Ile Ala Ala Gly Leu Ile
 35 40 45

Ala Asn Lys Ile Leu Ile Glu Arg Tyr Asn Trp Arg Ile Asp Ala Ala
 50 55 60

Val Tyr Arg Glu Gly Ala Leu Ala Leu Val Asn Gly Glu Ser Leu Tyr
 65 70 75 80

Ala Gln Pro Phe Asp Met Gly Asp Ile Ser Leu Pro Phe Ile Tyr Pro
 85 90 95

Pro Ile Gly Ala Ile Leu Phe Ala Pro Trp Gly Tyr Phe Asp Phe Ile
 100 105 110

Thr Val Glu Leu Ala Gly Asn Leu Val Val Ile Gly Ser Ser Leu Leu
 115 120 125

Leu Leu Leu Cys Leu Tyr Leu Val Thr Asn Ala Val Leu Ser Gly Arg
 130 135 140

Asp Lys Leu Leu Ala Phe Thr Ile Ala Ala Ile Ser Trp Pro Ile Ala
 145 150 155 160

Leu Phe Ala Glu Pro Val Phe Leu Asn Ala Asp Leu Gly Gln Ile Asn
 165 170 175

Ile Leu Ile Met Ala Leu Val Val Met Asp Leu Leu Pro Ile Lys Arg
 180 185 190

Arg Ile Pro Arg Gly Val Leu Ile Gly Leu Ala Ala Ala Ile Lys Ile
 195 200 205

Thr Pro Leu Ala Met Leu Leu Tyr Phe Leu Val Lys Lys Asp Phe Arg
 210 215 220

Gly Ile Ile Asn Ala Val Ile Ser Leu Leu Ala Phe Thr Ala Ile Gly
 225 230 235 240
 Ala Val Leu Ala Trp Glu Asn Thr Lys Glu Phe Phe Ser Ser Thr Leu
 245 250 255
 Leu Asn Leu Ser Ala Glu Gly Asp Ser Gly Val Asp Thr Thr Phe Gln
 260 265 270
 Ser Asn Ser Ser Ile Gln Ala Met Leu Tyr Arg Trp Trp Thr Ser Lys
 275 280 285
 Ala Asp Ala Glu Ala Ser Ser Leu Pro Thr Ile Leu Trp Ile Val Leu
 290 295 300
 Ser Leu Ile Ala Val Ala Ala Val Ala Tyr Leu Met His Gln Leu Phe
 305 310 315 320
 Ser Arg Gly Leu His Val Glu Ala Val Met Val Asn Ala Met Leu Met
 325 330 335
 Leu Leu Ile Ser Pro Ile Ser Trp Ser His His Trp Val Trp Leu Pro
 340 345 350
 Leu Trp Ala Val Val Phe Phe Val Arg Tyr Arg Gln His Arg Ser His
 355 360 365
 Pro Lys Phe Leu Leu Trp Ser Gly Val Ile Leu Ser Val Met Leu Leu
 370 375 380
 Met Leu Pro Pro Lys Trp Trp Phe Gly Arg Asp Gly Val Asn Val Phe
 385 390 395 400
 Glu Leu Asn Phe Trp Glu Lys Leu Leu Ile Ser Asp Trp Thr Trp Leu
 405 410 415
 Ser Ile Gly Leu Met Ile Thr Leu Gly Leu Gly Leu Lys Ala Phe Pro
 420 425 430
 Lys Ile Ser Lys
 435

<210> 2865

<211> 918

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(895)

<223> RXA02712

<400> 2865

ctgaaacggc ttcggaagct gaaattgaag aaaaccacg tgccgcacct gtgaaggtgc 60

gcgcaatcga aagaatcggc aacaactcag gagacctctc atg acc atg aca aat 115

Met Thr Met Thr Asn

1

5

ggc tcc cgc aca gag tcg gga aag att cgc gat cga cgt gtc gct gac	163
Gly Ser Arg Thr Glu Ser Gly Lys Ile Arg Asp Arg Arg Val Ala Asp	
10 15 20	
gct gat cca cgg tat ggc cgt cgc gtc tcg gtg agt agg gat ttc tcc	211
Ala Asp Pro Arg Tyr Gly Arg Arg Val Ser Val Ser Arg Asp Phe Ser	
25 30 35	
aca gcg gaa gct tcg ggg agg ggc gcg tcg ata agc acg caa cct cgt	259
Thr Ala Glu Ala Ser Gly Arg Gly Ala Ser Ile Ser Thr Gln Pro Arg	
40 45 50	
cgt gac atg gcg ccg gaa agg cgc cac aca acc cgg gcc cta gtg aac	307
Arg Asp Met Ala Pro Glu Arg Arg His Thr Thr Arg Ala Leu Val Asn	
55 60 65	
cct ggc gtg caa cca acg cgt aag cgt ttg atg cag cac aag ctg ggc	355
Pro Gly Val Gln Pro Thr Arg Lys Arg Leu Met Gln His Lys Leu Gly	
70 75 80 85	
tct cag cag gtt atg tcg gtg cgt ggt cgc cgc gtt gag gca aaa cgt	403
Ser Gln Gln Val Met Ser Val Arg Gly Arg Arg Val Glu Ala Lys Arg	
90 95 100	
gct gat cct aag gtg atc cag ctg tct gtg ctg gtg gtt atc ctg ctg	451
Ala Asp Pro Lys Val Ile Gln Leu Ser Val Leu Val Val Ile Leu Leu	
105 110 115	
tgc gtt ggt gtt ggc gcg acc atg ggt ctg tcc gga acg tct aca cag	499
Cys Val Gly Val Gly Ala Thr Met Gly Leu Ser Gly Thr Ser Thr Gln	
120 125 130	
cag act ttc cag ttg cag gaa ctt cag gca act gaa acg gat ttg agc	547
Gln Thr Phe Gln Leu Gln Glu Leu Gln Ala Thr Glu Thr Asp Leu Ser	
135 140 145	
aat cgc att gag tcg ctc aac cga gat gtg gaa gat gct cgc tca gca	595
Asn Arg Ile Glu Ser Leu Asn Arg Asp Val Glu Asp Ala Arg Ser Ala	
150 155 160 165	
gca acc ttg gca gcg aat gct acg gag atg ggc ttg gta tcc cca gtg	643
Ala Thr Leu Ala Ala Asn Ala Thr Glu Met Gly Leu Val Ser Pro Val	
170 175 180	
gaa cct ggc gtg ctc gca gtg cag gaa aac ggt gat gtt gtg gag gag	691
Glu Pro Gly Val Leu Ala Val Gln Glu Asn Gly Asp Val Val Glu Glu	
185 190 195	
cgc gaa gca aat cca gag aca cgc cct ata gtt gac atc aat gga caa	739
Arg Glu Ala Asn Pro Glu Thr Arg Pro Ile Val Asp Ile Asn Gly Gln	
200 205 210	
cag acc cga cca aat cgg gca tca agc aac cct gac gag act aac gca	787
Gln Thr Arg Pro Asn Arg Ala Ser Ser Asn Pro Asp Glu Thr Asn Ala	
215 220 225	
gtg act gaa aac ctc cag gcg att cca caa gaa gca gca gct ccg ccg	835
Val Thr Glu Asn Leu Gln Ala Ile Pro Gln Glu Ala Ala Ala Pro Pro	
230 235 240 245	
tat cag acc aac act gtt cct tat gct gca acc acc gga caa gca ggt	883

Tyr Gln Thr Asn Thr Val Pro Tyr Ala Ala Thr Thr Gly Gln Ala Gly
 250 255 260

ggc gca ggg cag tgactttccc cagcaatggc aga
 Gly Ala Gly Gln
 265

918

<210> 2866

<211> 265

<212> PRT

<213> Corynebacterium glutamicum

<400> 2866

Met Thr Met Thr Asn Gly Ser Arg Thr Glu Ser Gly Lys Ile Arg Asp
 1 5 10 15

Arg Arg Val Ala Asp Ala Asp Pro Arg Tyr Gly Arg Arg Val Ser Val
 20 25 30

Ser Arg Asp Phe Ser Thr Ala Glu Ala Ser Gly Arg Gly Ala Ser Ile
 35 40 45

Ser Thr Gln Pro Arg Arg Asp Met Ala Pro Glu Arg Arg His Thr Thr
 50 55 60

Arg Ala Leu Val Asn Pro Gly Val Gln Pro Thr Arg Lys Arg Leu Met
 65 70 75 80

Gln His Lys Leu Gly Ser Gln Gln Val Met Ser Val Arg Gly Arg Arg
 85 90 95

Val Glu Ala Lys Arg Ala Asp Pro Lys Val Ile Gln Leu Ser Val Leu
 100 105 110

Val Val Ile Leu Leu Cys Val Gly Val Gly Ala Thr Met Gly Leu Ser
 115 120 125

Gly Thr Ser Thr Gln Gln Thr Phe Gln Leu Gln Glu Leu Gln Ala Thr
 130 135 140

Glu Thr Asp Leu Ser Asn Arg Ile Glu Ser Leu Asn Arg Asp Val Glu
 145 150 155 160

Asp Ala Arg Ser Ala Ala Thr Leu Ala Ala Asn Ala Thr Glu Met Gly
 165 170 175

Leu Val Ser Pro Val Glu Pro Gly Val Leu Ala Val Gln Glu Asn Gly
 180 185 190

Asp Val Val Glu Glu Arg Glu Ala Asn Pro Glu Thr Arg Pro Ile Val
 195 200 205

Asp Ile Asn Gly Gln Gln Thr Arg Pro Asn Arg Ala Ser Ser Asn Pro
 210 215 220

Asp Glu Thr Asn Ala Val Thr Glu Asn Leu Gln Ala Ile Pro Gln Glu
 225 230 235 240

Ala Ala Ala Pro Pro Tyr Gln Thr Asn Thr Val Pro Tyr Ala Ala Thr
 245 250 255

Thr Gly Gln Ala Gly Gly Ala Gly Gln
260 265

<210> 2867

<211> 552

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(529)

<223> RXA02714

<400> 2867

cgcggtggtc ttgcatgaga ggccactacg caccctcaga gacaaactga atgggttggtt 60

ctgtttatgc cactgagttg ctgggaaggg gacttcaagg atg ttc ctt ggt acc 115
Met Phe Leu Gly Thr
1 5

tat acc ccg aaa ctc gat gac aaa ggc agg ctg act ctt cca gca aag 163
Tyr Thr Pro Lys Leu Asp Asp Lys Gly Arg Leu Thr Leu Pro Ala Lys
10 15 20

ttc cgt gag gac ctt gcg ggg gga ttg atg gtc act aaa ggt caa gac 211
Phe Arg Glu Asp Leu Ala Gly Gly Leu Met Val Thr Lys Gly Gln Asp
25 30 35

cac agt ctc gcg gtt tat ccg aag gaa gaa ttt gca gca agg gct cgc 259
His Ser Leu Ala Val Tyr Pro Lys Glu Glu Phe Ala Ala Arg Ala Arg
40 45 50

aag gca gct gca gtt tct agg aca aac cct gag gct cgt gcg ttt atc 307
Lys Ala Ala Ala Val Ser Arg Thr Asn Pro Glu Ala Arg Ala Phe Ile
55 60 65

cga aac ctt gca gca agc gcg gat gaa caa cga ccc gac ggc cag ggg 355
Arg Asn Leu Ala Ala Ser Ala Asp Glu Gln Arg Pro Asp Gly Gln Gly
70 75 80 85

cgc atc acc ctt tcg gca gcg cac cgc aca tat gcg ggg ctg aca aaa 403
Arg Ile Thr Leu Ser Ala Ala His Arg Thr Tyr Ala Gly Leu Thr Lys
90 95 100

gag tgt gtc gtt atc ggt tcg gtg gat ttt ctg gag att tgg gac gct 451
Glu Cys Val Val Ile Gly Ser Val Asp Phe Leu Glu Ile Trp Asp Ala
105 110 115

caa gcc tgg gcc gcg tat cag gaa gag acg gag gct gcc ttc tca gca 499
Gln Ala Trp Ala Ala Tyr Gln Glu Thr Glu Ala Ala Phe Ser Ala
120 125 130

gct gaa gat gac gtc ctt gga gga ttg ctc tgatagttgg gcaatgcttc 549
Ala Glu Asp Asp Val Leu Gly Gly Leu Leu
135 140

gaa 552

<210> 2868

<211> 143

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 2868

Met Phe Leu Gly Thr Tyr Thr Pro Lys Leu Asp Asp Lys Gly Arg Leu
 1 5 10 15

Thr Leu Pro Ala Lys Phe Arg Glu Asp Leu Ala Gly Gly Leu Met Val
 20 25 30

Thr Lys Gly Gln Asp His Ser Leu Ala Val Tyr Pro Lys Glu Glu Phe
 35 40 45

Ala Ala Arg Ala Arg Lys Ala Ala Ala Val Ser Arg Thr Asn Pro Glu
 50 55 60

Ala Arg Ala Phe Ile Arg Asn Leu Ala Ala Ser Ala Asp Glu Gln Arg
 65 70 75 80

Pro Asp Gly Gln Gly Arg Ile Thr Leu Ser Ala Ala His Arg Thr Tyr
 85 90 95

Ala Gly Leu Thr Lys Glu Cys Val Val Ile Gly Ser Val Asp Phe Leu
 100 105 110

Glu Ile Trp Asp Ala Gln Ala Trp Ala Ala Tyr Gln Glu Glu Thr Glu
 115 120 125

Ala Ala Phe Ser Ala Ala Glu Asp Asp Val Leu Gly Gly Leu Leu
 130 135 140

<210> 2869

<211> 513

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(490)

<223> RXA02715

<400> 2869

gtttttgtcg ttattggcat aacggggaac attctggata ttctgggcgt taataaggca 60

tagaagaaaa aatgtctcta ctaaccaccg ggaggacatc gtg tcg ctt tca gag 115
 Val Ser Leu Ser Glu
 1 5

cag gag caa cgc gca ctg cgc gaa att gag caa gcg ctc atg gca gat 163
 Gln Glu Gln Arg Ala Leu Arg Glu Ile Glu Gln Ala Leu Met Ala Asp
 10 15 20

gat ccg aaa ttt gga aaa gcg gtt gca agt aac aat ggc cta gca ggc 211
 Asp Pro Lys Phe Gly Lys Ala Val Ala Ser Asn Asn Gly Leu Ala Gly
 25 30 35

ggg ggg ttt acc ctt cgg gga atc gca ctt ttc gta ctc gga ctt gtc 259
 Gly Gly Phe Thr Leu Arg Gly Ile Ala Leu Phe Val Leu Gly Leu Val

40	45	50	
ctt ctt gtt gcc ggc gtc gca tta agc cag caa aca ttg tgg ttc gtt			307
Leu Leu Val Ala Gly Val Ala Leu Ser Gln Gln Thr Leu Trp Phe Val			
55	60	65	
gcg ctc gga att atc gga ttc tta gtc atg ttc gga tcg gga gtg tgg			355
Ala Leu Gly Ile Ile Gly Phe Leu Val Met Phe Gly Ser Gly Val Trp			
70	75	80	85
atg ctg cgc ggg ggc ggc tcc aac aaa atc tcc gtc aca tcc cgc act			403
Met Leu Arg Gly Gly Gly Ser Asn Lys Ile Ser Val Thr Ser Arg Thr			
	90	95	100
tcc aat gcg aag aat cgc caa cag ggc aat tcc acc att ggg gac aaa			451
Ser Asn Ala Lys Asn Arg Gln Gln Gly Asn Ser Thr Ile Gly Asp Lys			
	105	110	115
atg gaa gaa aac ttc cgt cga cga ttc gag ggc aat aag taagaagtaa			500
Met Glu Glu Asn Phe Arg Arg Arg Phe Glu Gly Asn Lys			
	120	125	130
ctgaataagt ctt			513

<210> 2870

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 2870

Val Ser Leu Ser Glu Gln Glu Gln Arg Ala Leu Arg Glu Ile Glu Gln
1 5 10 15

Ala Leu Met Ala Asp Asp Pro Lys Phe Gly Lys Ala Val Ala Ser Asn
20 25 30

Asn Gly Leu Ala Gly Gly Gly Phe Thr Leu Arg Gly Ile Ala Leu Phe
35 40 45

Val Leu Gly Leu Val Leu Leu Val Ala Gly Val Ala Leu Ser Gln Gln
50 55 60

Thr Leu Trp Phe Val Ala Leu Gly Ile Ile Gly Phe Leu Val Met Phe
65 70 75 80

Gly Ser Gly Val Trp Met Leu Arg Gly Gly Gly Ser Asn Lys Ile Ser
85 90 95

Val Thr Ser Arg Thr Ser Asn Ala Lys Asn Arg Gln Gln Gly Asn Ser
100 105 110

Thr Ile Gly Asp Lys Met Glu Glu Asn Phe Arg Arg Arg Phe Glu Gly
115 120 125

Asn Lys
130

<210> 2871

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXA02721

<400> 2871

ccgtgatgat cgctcgtgacg atcgccgcga tgaccgcgga gacgacctgg atgtacccag 60

cttcctccag taattaagaa ggagaataga cttatccact atg gat agt ctt gac 115
Met Asp Ser Leu Asp
1 5

ccc cgc aac cgc ccc gtc cgc aag gtc ttc acg acc cgt gcc ggc ggg 163
Pro Arg Asn Arg Pro Val Arg Lys Val Phe Thr Thr Arg Ala Gly Gly
10 15 20

gtt tcg cag tcc ccg tat gct tcc ttc aac ctt ggt gat cac gtc ggc 211
Val Ser Gln Ser Pro Tyr Ala Ser Phe Asn Leu Gly Asp His Val Gly
25 30 35

gac gat cct caa gct gtg gca tcc aac cgc aat cgc ttg gct gac atc 259
Asp Asp Pro Gln Ala Val Ala Ser Asn Arg Asn Arg Leu Ala Asp Ile
40 45 50

atc ggt ttg tcc cca gac aag gtg gtg tac atg gag caa att cat tcc 307
Ile Gly Leu Ser Pro Asp Lys Val Val Tyr Met Glu Gln Ile His Ser
55 60 65

aat acc gtc aca gtc att gat gaa gcc cca gcg gat ggc cag gct gta 355
Asn Thr Val Thr Val Ile Asp Glu Ala Pro Ala Asp Gly Gln Ala Val
70 75 80 85

gag gcc acc gat gcg cta gtg acc acg caa cga ggg cta gcg ctg gcc 403
Glu Ala Thr Asp Ala Leu Val Thr Thr Gln Arg Gly Leu Ala Leu Ala
90 95 100

gtt ttg gtt gct gat tgc gtg cca gtg ctg ctg tca gac acc gac gct 451
Val Leu Val Ala Asp Cys Val Pro Val Leu Leu Ser Asp Thr Asp Ala
105 110 115

ggc gtg att gcg gca gtg cat gca ggc cgc atg gga gcc cgc aat ggc 499
Gly Val Ile Ala Ala Val His Ala Gly Arg Met Gly Ala Arg Asn Gly
120 125 130

atc gta gct aaa acc att gcg aag atg gag gag ctc ggc gcg aaa ccc 547
Ile Val Ala Lys Thr Ile Ala Lys Met Glu Glu Leu Gly Ala Lys Pro
135 140 145

agc cgc att cat gcg ctc atg ggt gca gcg gca tcg ggt gcg aac tac 595
Ser Arg Ile His Ala Leu Met Gly Ala Ala Ser Gly Ala Asn Tyr
150 155 160 165

gag gtc cca gag gcc atg gcg cgc gat gtg gaa gcc aaa ctt cca ggt 643
Glu Val Pro Glu Ala Met Ala Arg Asp Val Glu Ala Lys Leu Pro Gly
170 175 180

tcc att gcg cgt acg aca aaa ggc acc aca gga ctg gac atc cgc gca 691
Ser Ile Ala Arg Thr Thr Lys Gly Thr Thr Gly Leu Asp Ile Arg Ala

185	190	195	
ggg ctg ctg cgt caa atg ctc agc	ctg ggt gtg caa atg att gat tct		739
Gly Leu Leu Arg Gln Met Leu Ser	Leu Gly Val Gln Met Ile Asp Ser		
200	205	210	
gat cca cgc tgc acc atc gaa gac	gaa gat ctg ttt tct tac cgc cgc		787
Asp Pro Arg Cys Thr Ile Glu Asp	Glu Asp Leu Phe Ser Tyr Arg Arg		
215	220	225	
gaa ggc acg aca ggc cgc cag gcc	ggc gtg gtg tgg ctg cca aag gag		835
Glu Gly Thr Thr Gly Arg Gln Ala	Gly Val Val Trp Leu Pro Lys Glu		
230	235	240	245
gca taaattggag cgccgcgaag agc			861
Ala			

<210> 2872

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 2872

Met Asp Ser Leu Asp Pro Arg Asn Arg	Pro Val Arg Lys Val Phe Thr
1	5 10 15

Thr Arg Ala Gly Gly Val Ser Gln Ser	Pro Tyr Ala Ser Phe Asn Leu
20	25 30

Gly Asp His Val Gly Asp Asp Pro Gln	Ala Val Ala Ser Asn Arg Asn
35	40 45

Arg Leu Ala Asp Ile Ile Gly Leu Ser	Pro Asp Lys Val Val Tyr Met
50	55 60

Glu Gln Ile His Ser Asn Thr Val Thr	Val Ile Asp Glu Ala Pro Ala
65	70 75 80

Asp Gly Gln Ala Val Glu Ala Thr Asp	Ala Leu Val Thr Thr Gln Arg
85	90 95

Gly Leu Ala Leu Ala Val Leu Val Ala	Asp Cys Val Pro Val Leu Leu
100	105 110

Ser Asp Thr Asp Ala Gly Val Ile Ala	Ala Val His Ala Gly Arg Met
115	120 125

Gly Ala Arg Asn Gly Ile Val Ala Lys	Thr Ile Ala Lys Met Glu Glu
130	135 140

Leu Gly Ala Lys Pro Ser Arg Ile His	Ala Leu Met Gly Ala Ala Ala
145	150 155 160

Ser Gly Ala Asn Tyr Glu Val Pro Glu	Ala Met Ala Arg Asp Val Glu
165	170 175

Ala Lys Leu Pro Gly Ser Ile Ala Arg	Thr Thr Lys Gly Thr Thr Gly
180	185 190

Leu Asp Ile Arg Ala Gly Leu Leu Arg Gln Met Leu Ser Leu Gly Val
 195 200 205

Gln Met Ile Asp Ser Asp Pro Arg Cys Thr Ile Glu Asp Glu Asp Leu
 210 215 220

Phe Ser Tyr Arg Arg Glu Gly Thr Thr Gly Arg Gln Ala Gly Val Val
 225 230 235 240

Trp Leu Pro Lys Glu Ala
 245

<210> 2873

<211> 735

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(712)

<223> RXA02725

<400> 2873

gaaagcccg cgc tgcacatcgg tgtggcgggt tttctcatgc ccagatattg accttggtcac 60

tgtgtcaagg cattgaataa gtgccatgaa cataagtgcc atg gac aac ttc gaa 115
 Met Asp Asn Phe Glu
 1 5

cat tca aat gca tct atc cgt tta caa gca gcg ttg gcc gca gga act 163
 His Ser Asn Ala Ser Ile Arg Leu Gln Ala Ala Leu Ala Ala Gly Thr
 10 15 20

gct gag gac acc act gcg atc gat att ctt ttg tac cgc agt ggg gta 211
 Ala Glu Asp Thr Thr Ala Ile Asp Ile Leu Leu Tyr Arg Ser Gly Val
 25 30 35

gaa gaa gac ttc ttt gtg cgc gac atg ata acg tgg gcg ctc acc cgc 259
 Glu Glu Asp Phe Phe Val Arg Asp Met Ile Thr Trp Ala Leu Thr Arg
 40 45 50

atg cca gtt gat gac gtg ttt acc tca ctg gtc gct gat ttg gat tct 307
 Met Pro Val Asp Asp Val Phe Thr Ser Leu Val Ala Asp Leu Asp Ser
 55 60 65

gag gta cct gat cga cca ttc ggt gca agt caa gca ctc cac aca ctc 355
 Glu Val Pro Asp Arg Pro Phe Gly Ala Ser Gln Ala Leu His Thr Leu
 70 75 80 85

tcc aag tta agg gtc gcg cag tcg tgg cag gaa ttg caa gca cgg cct 403
 Ser Lys Leu Arg Val Ala Gln Ser Trp Gln Glu Leu Gln Ala Arg Pro
 90 95 100

tgg ctt ttg cac cgg gag gac acc gcc caa act gcg tgg cga acc ttt 451
 Trp Leu Leu His Arg Glu Asp Thr Ala Gln Thr Ala Trp Arg Thr Phe
 105 110 115

gtg gga ctg gtc cca gat gat cag acc gca tgg ttg gcg cac caa ttg 499
 Val Gly Leu Val Pro Asp Asp Gln Thr Ala Trp Leu Ala His Gln Leu
 120 125 130

ctc caa gaa ttg gat aaa gga acg cct gaa att cag cgg agt tta agt 547
 Leu Gln Glu Leu Asp Lys Gly Thr Pro Glu Ile Gln Arg Ser Leu Ser
 135 140 145

cgg gcg atg gcg gaa ttg gag ggg agg gag gcg tcg ata agc gtg ctt 595
 Arg Ala Met Ala Glu Leu Glu Gly Arg Glu Ala Ser Ile Ser Val Leu
 150 155 160 165

cta ggc gct tta acg agc gcg cac gcg gtg gcc acc gcc aag ctc att 643
 Leu Gly Ala Leu Thr Ser Ala His Ala Val Ala Thr Ala Lys Leu Ile
 170 175 180

gcg gat ccg gac tcc gat ttc atg gct gat ctg gag gaa gcg cgg cgc 691
 Ala Asp Pro Asp Ser Asp Phe Met Ala Asp Leu Glu Glu Ala Arg Arg
 185 190 195

gtg gat aat atg ggt gca tgc tgc tgc ggtgca ggtgtccaag ctc 735
 Val Asp Asn Met Gly Ala Cys
 200

<210> 2874

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 2874

Met Asp Asn Phe Glu His Ser Asn Ala Ser Ile Arg Leu Gln Ala Ala
 1 5 10 15

Leu Ala Ala Gly Thr Ala Glu Asp Thr Thr Ala Ile Asp Ile Leu Leu
 20 25 30

Tyr Arg Ser Gly Val Glu Glu Asp Phe Phe Val Arg Asp Met Ile Thr
 35 40 45

Trp Ala Leu Thr Arg Met Pro Val Asp Asp Val Phe Thr Ser Leu Val
 50 55 60

Ala Asp Leu Asp Ser Glu Val Pro Asp Arg Pro Phe Gly Ala Ser Gln
 65 70 75 80

Ala Leu His Thr Leu Ser Lys Leu Arg Val Ala Gln Ser Trp Gln Glu
 85 90 95

Leu Gln Ala Arg Pro Trp Leu Leu His Arg Glu Asp Thr Ala Gln Thr
 100 105 110

Ala Trp Arg Thr Phe Val Gly Leu Val Pro Asp Asp Gln Thr Ala Trp
 115 120 125

Leu Ala His Gln Leu Leu Gln Glu Leu Asp Lys Gly Thr Pro Glu Ile
 130 135 140

Gln Arg Ser Leu Ser Arg Ala Met Ala Glu Leu Glu Gly Arg Glu Ala
 145 150 155 160

Ser Ile Ser Val Leu Leu Gly Ala Leu Thr Ser Ala His Ala Val Ala
 165 170 175

Thr Ala Lys Leu Ile Ala Asp Pro Asp Ser Asp Phe Met Ala Asp Leu
 180 185 190

Glu Glu Ala Arg Arg Val Asp Asn Met Gly Ala Cys
 195 200

<210> 2875

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1012)

<223> RXA02727

<400> 2875

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ctaaagcagc aggtcgaaga gctagaggcg caggttgccg gtg gtc ctt ctt ccg 115
 Val Val Leu Leu Pro
 1 5

ctg cta gtt cct caa ctg cag gtg cag cca cag ttg cag ctt cca agt 163
 Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln Leu Gln Leu Pro Ser
 10 15 20

ctg ttg acg agg cag cgc tgc gca agg aaa tca aag aga agc tgc gct 211
 Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser Lys Arg Ser Cys Ala
 25 30 35

ccg aat acg gca tcc aag ctc gat gat gcc tcc aag gcc gct cag aag 259
 Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser Lys Ala Ala Gln Lys
 40 45 50

gct caa aac gat gcg aag tcc gct caa gat cag cta cag cgt gca caa 307
 Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln Leu Gln Arg Ala Gln
 55 60 65

gct gac gca aag gca gct cgc gac gaa gct gaa aag gcc aag gct gaa 355
 Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu Lys Ala Lys Ala Glu
 70 75 80 85

gct aag tca gca gca tcc tcc agc acc act aag gca gca gcg gtt ggc 403
 Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys Ala Ala Ala Val Gly
 90 95 100

gct gtc ggc gct ggc acc gga gca gca gtt gct aca ggt gct gca aat 451
 Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala Thr Gly Ala Ala Asn
 105 110 115

gtg gac acc cac atg cag gca gcg aag gtt ctg gga ctc gca cag gaa 499
 Val Asp Thr His Met Gln Ala Ala Lys Val Leu Gly Leu Ala Gln Glu
 120 125 130

atg gca gac cgc ctg acc tca gag gct cgc tcc gaa tcc aag tcc atg 547
 Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser Glu Ser Lys Ser Met
 135 140 145

ctg gac gag gct cgc gaa gca gca gag aag cag atc gag gaa gca aac 595

Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln Ile Glu Glu Ala Asn
 150 155 160 165
 agc acc tcc aac cgc act ctg gaa gat gct cgc gca aac gct gag aag 643
 Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg Ala Asn Ala Glu Lys
 170 175 180
 cag atc gct gaa gcg cag aac cgc gct gac act ctg gtc aac gaa gct 691
 Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr Leu Val Asn Glu Ala
 185 190 195
 gac gct aag gct aag aac ctg gtt tcc gaa gcc gag aag aag tcc gca 739
 Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala Glu Lys Lys Ser Ala
 200 205 210
 gcc acc ctg gcc gca tcc acc tct cgt gca gaa gct cag atc cgt caa 787
 Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu Ala Gln Ile Arg Gln
 215 220 225
 gcc gag gac aag gca aac gcc ctc cag gca gac gca gag cgc aag cac 835
 Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp Ala Glu Arg Lys His
 230 235 240 245
 acc gaa acc atg gct gca gtc aag gaa cag cag aat gct ctg gag acc 883
 Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln Asn Ala Leu Glu Thr
 250 255 260
 cgc atc gcg gaa ctg cag acc ttc gag cgt gag tac cgc acc cgt ctg 931
 Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu Tyr Arg Thr Arg Leu
 265 270 275
 aag tcc ctc ctc gag ggc cag ctg gaa gaa ctc cac gca cgt ggc tcc 979
 Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu His Ala Arg Gly Ser
 280 285 290
 tct gca cca acc aac aac aag cca tct ggt gag taaaaagaaa gattagttat 1032
 Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu
 295 300
 ctt 1035

<210> 2876

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 2876

Val Val Leu Leu Pro Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln
 1 5 10 15
 Leu Gln Leu Pro Ser Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser
 20 25 30
 Lys Arg Ser Cys Ala Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser
 35 40 45
 Lys Ala Ala Gln Lys Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln
 50 55 60
 Leu Gln Arg Ala Gln Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu

65	70	75	80
Lys Ala Lys Ala Glu Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys	85	90	95
Ala Ala Ala Val Gly Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala	100	105	110
Thr Gly Ala Ala Asn Val Asp Thr His Met Gln Ala Ala Lys Val Leu	115	120	125
Gly Leu Ala Gln Glu Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser	130	135	140
Glu Ser Lys Ser Met Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln	145	150	155
Ile Glu Glu Ala Asn Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg	165	170	175
Ala Asn Ala Glu Lys Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr	180	185	190
Leu Val Asn Glu Ala Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala	195	200	205
Glu Lys Lys Ser Ala Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu	210	215	220
Ala Gln Ile Arg Gln Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp	225	230	235
Ala Glu Arg Lys His Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln	245	250	255
Asn Ala Leu Glu Thr Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu	260	265	270
Tyr Arg Thr Arg Leu Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu	275	280	285
His Ala Arg Gly Ser Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu	290	295	300

<210> 2877

<211> 828

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(805)

<223> RXA02735

<400> 2877

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agcgtcaagc tggaaaccgt ctaaggagaa atacaacact atg gtt gat gta gta 115
 Met Val Asp Val Val
 1 5

cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc	163
Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln Ala Ala Ser Lys Phe	
10 15 20	
att gag gtt gtt gaa gca gca act gcc aat aat ggc acc gca cag gta	211
Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val	
25 30 35	
gtg ctc acc ggt ggt ggc gcc ggc atc aag ttg ctg gaa aag ctc agc	259
Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser	
40 45 50	
gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc	307
Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly	
55 60 65	
gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag	355
Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu Ser Asn Glu Gly Gln	
70 75 80 85	
gct cgt gag gca ctg ttg tcc aag gtt tct atc cct gaa gcc aac att	403
Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile Pro Glu Ala Asn Ile	
90 95 100	
cac gga tat ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct	451
His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala	
105 110 115	
tac gaa gct gtg ttg gat gaa ttc gca cca aac ggc ttt gat ctt cac	499
Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His	
120 125 130	
ctg ctc ggc atg ggt ggc gaa ggc cat atc aac tcc ctg ttc cct cac	547
Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn Ser Leu Phe Pro His	
135 140 145	
acc gat gca gtc aag gaa tcc tcc gca aag gtc atc gcg gtg ttt gat	595
Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val Ile Ala Val Phe Asp	
150 155 160 165	
tcc cct aag cct cct tca gag cgt gca act cta acc ctt cct gcg gtt	643
Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val	
170 175 180	
cac tcc gca aag cgc gtg tgg ttg ctg gtt tct ggt gcg gag aag gct	691
His Ser Ala Lys Arg Val Trp Leu Leu Val Ser Gly Ala Glu Lys Ala	
185 190 195	
gag gca gct gcg gcg atc gtc aac ggt gag cct gct gtt gag tgg cct	739
Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro Ala Val Glu Trp Pro	
200 205 210	
gct gct gga gct acc gga tct gag gaa acg gta ttg ttc ttg gct gat	787
Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val Leu Phe Leu Ala Asp	
215 220 225	
gat gct gca gga aat ctc taagcagcgc cagctctaac aag	828
Asp Ala Ala Gly Asn Leu	
230 235	

<210> 2878

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 2878

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1 5 10 15
Ala Ala Ser Lys Phe Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn
20 25 30
Gly Thr Ala Gln Val Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu
35 40 45
Leu Glu Lys Leu Ser Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile
50 55 60
His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
65 70 75 80
Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile
85 90 95
Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
100 105 110
Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn
115 120 125
Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn
130 135 140
Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
145 150 155 160
Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu
165 170 175
Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser
180 185 190
Gly Ala Glu Lys Ala Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro
195 200 205
Ala Val Glu Trp Pro Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val
210 215 220
Leu Phe Leu Ala Asp Asp Ala Ala Gly Asn Leu
225 230 235

<210> 2879

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXA02736

<400> 2879

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acggtcacac	ctggcgcagg	ccataatttta	ggggcaaaaa	atg atc ttt gaa ctt	115	
				Met Ile Phe Glu Leu		
				1 5		
ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt	163					
Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg						
	10 15 20					
gaa tcg ggc acc cag gtc acc acc ggc cga gtg ctc acc ctc atc gtg	211					
Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val						
	25 30 35					
gtc act gac tcc gaa agc gat gtc gct gca gtt acc gag tcc acc aat	259					
Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn						
	40 45 50					
gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc	307					
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly						
	55 60 65					
gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc	355					
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly						
	70 75 80 85					
gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc	403					
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val						
	90 95 100					
gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc	451					
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr						
	105 110 115					
ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag	499					
Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln						
	120 125 130					
gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac	547					
Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr						
	135 140 145					
gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt	595					
Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly						
	150 155 160 165					
gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt	643					
Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val						
	170 175 180					
gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg	691					
Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg						
	185 190 195					
ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg	739					
Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp						
	200 205 210					

ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct 787
 Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala
 215 220 225

ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag 835
 Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln
 230 235 240 245

cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat 883
 Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr
 250 255 260

gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca 931
 Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro
 265 270 275

tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag 979
 Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu
 280 285 290

gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc 1027
 Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser
 295 300 305

ggc ttg tcc agc gtc aag ctg gaa acc gtc taaggagaaa tacaacacta 1077
 Gly Leu Ser Ser Val Lys Leu Glu Thr Val
 310 315

tgg 1080

<210> 2880

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 2880

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 20 25 30

Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
 35 40 45

Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
 50 55 60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
 65 70 75 80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
 85 90 95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
 100 105 110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
 115 120 125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
 130 135 140
 Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu
 145 150 155 160
 Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
 165 170 175
 Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
 180 185 190
 Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
 195 200 205
 Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg
 210 215 220
 Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro
 225 230 235 240
 Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile
 245 250 255
 Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu
 260 265 270
 Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser
 275 280 285
 Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr
 290 295 300
 Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val
 305 310 315

<210> 2881

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXA02751

<400> 2881

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 Val Leu Pro Ile Ala
 1 5

 tcc ggt aac gat gac cgg aat tta atc cgt tat gtc gac ggt ggt cga 163
 Ser Gly Asn Asp Asp Arg Asn Leu Ile Arg Tyr Val Asp Gly Gly Arg
 10 15 20

 ttt gat gaa atc atg ctc acc gga gac ctc act ggc ctg agc agt ttt 211
 Phe Asp Glu Ile Met Leu Thr Gly Asp Leu Thr Gly Leu Ser Ser Phe
 25 30 35

ctt acc aac gct ggc ccg aac gcc cgg gat gat ttt gat ctc acg gtg 259
 Leu Thr Asn Ala Gly Pro Asn Ala Arg Asp Asp Phe Asp Leu Thr Val
 40 45 50

ctc atg cgc gct gcc gag gca ggc aac ctc atg gtt gtt gcc cgc ttg 307
 Leu Met Arg Ala Ala Glu Ala Gly Asn Leu Met Val Val Ala Arg Leu
 55 60 65

tta gat tta ggt gcc aat ccc cga ctc acc aat cct cgt ggt gtc acg 355
 Leu Asp Leu Gly Ala Asn Pro Arg Leu Thr Asn Pro Arg Gly Val Thr
 70 75 80 85

gcc cta cat atc gca gcg atc gcc ggg gac gat ggc att gtg gaa tgc 403
 Ala Leu His Ile Ala Ala Ile Ala Gly Asp Asp Gly Ile Val Glu Cys
 90 95 100

ctc att gat gca ggc gct gaa gtc gat gct gta gat gat caa ggt cgc 451
 Leu Ile Asp Ala Gly Ala Glu Val Asp Ala Val Asp Asp Gln Gly Arg
 105 110 115

act ccc cta tgg aac gca gcg gct cat cat ctg cct gat tct gcg gtg 499
 Thr Pro Leu Trp Asn Ala Ala Ala His His Leu Pro Asp Ser Ala Val
 120 125 130

gtg gat gtg ctg ctt cgc gca ggt gcg aat gtg aat ctg cgc gat tgc 547
 Val Asp Val Leu Leu Arg Ala Gly Ala Asn Val Asn Leu Arg Asp Cys
 135 140 145

aat gga gtc agc cca gaa gac atg ctg tagaagcatt ctttagcagg 594
 Asn Gly Val Ser Pro Glu Asp Met Leu
 150 155

att 597

<210> 2882

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 2882

Val Leu Pro Ile Ala Ser Gly Asn Asp Asp Arg Asn Leu Ile Arg Tyr
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 20 25 30

Gly Leu Ser Ser Phe Leu Thr Asn Ala Gly Pro Asn Ala Arg Asp Asp
 35 40 45

Phe Asp Leu Thr Val Leu Met Arg Ala Ala Glu Ala Gly Asn Leu Met
 50 55 60

Val Val Ala Arg Leu Leu Asp Leu Gly Ala Asn Pro Arg Leu Thr Asn
 65 70 75 80

Pro Arg Gly Val Thr Ala Leu His Ile Ala Ala Ile Ala Gly Asp Asp
 85 90 95

Gly Ile Val Glu Cys Leu Ile Asp Ala Gly Ala Glu Val Asp Ala Val

gcg acg ggt ggc acc agc ttc ttc ggg ttc atg ctg atg atc gtc ctg 547
 Ala Thr Gly Gly Thr Ser Phe Phe Gly Phe Met Leu Met Ile Val Leu
 135 140 145

gca ttc atc agt ttt gtg tac tcc ctt aac tgc tac cgc aac gcg gct 595
 Ala Phe Ile Ser Phe Val Tyr Ser Leu Asn Cys Tyr Arg Asn Ala Ala
 150 155 160 165

cga gtt gtg cgc ggt gag cag atc acc att cag agt ttc ttc aag atg 643
 Arg Val Val Arg Gly Glu Gln Ile Thr Ile Gln Ser Phe Phe Lys Met
 170 175 180

aag ggt ctt ggt aag gcg ctc ggt att tac atc ttg atc aat atc gtc 691
 Lys Gly Leu Gly Lys Ala Leu Gly Ile Tyr Ile Leu Ile Asn Ile Val
 185 190 195

atc ttc atc gga atg atc ttg ctg ctc att cct gga att atc gct gcc 739
 Ile Phe Ile Gly Met Ile Leu Leu Leu Ile Pro Gly Ile Ile Ala Ala
 200 205 210

gtg gtg ctg atc ttt gct gtt cct gtg gca ttc cag ctg cgc gac gcc 787
 Val Val Leu Ile Phe Ala Val Pro Val Ala Phe Gln Leu Arg Asp Ala
 215 220 225

tcg atc ggt gat gcg ttt tcc gca agc tgg aag gca gtg tcc aaa aac 835
 Ser Ile Gly Asp Ala Phe Ser Ala Ser Trp Lys Ala Val Ser Lys Asn
 230 235 240 245

gtt ggt cag gtc att ctc tta gaa ctg gct atc ttc gcg ttg agc ttc 883
 Val Gly Gln Val Ile Leu Leu Glu Leu Ala Ile Phe Ala Leu Ser Phe
 250 255 260

ttg ggc agc gca gtg atc atc ggt atg ttg gtg acc act ccg ctt aca 931
 Leu Gly Ser Ala Val Ile Ile Gly Met Leu Val Thr Thr Pro Leu Thr
 265 270 275

ttc ctg ctg tat gcc tac gca ttc cag acc gcc agc ggt ggt ccc atc 979
 Phe Leu Leu Tyr Ala Tyr Ala Phe Gln Thr Ala Ser Gly Gly Pro Ile
 280 285 290

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 Met Gln Arg Gln
 295

<210> 2884

<211> 297

<212> PRT

<213> Corynebacterium glutamicum

<400> 2884

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Pro Tyr Gly Ala Pro Tyr Gly Gln Pro Tyr Gly Gln Pro Phe Asp Gln
 35 40 45

Gly Phe Asn Ala Tyr Ser Ser Pro Ile Pro Pro Glu Val Pro Gln Pro

50 55 60

Ser Met Gln Glu Ala Gln Trp Arg Ser Phe Asp Leu Gly Thr Val Phe
65 70 75 80

Gly Gln Ala Trp Lys Gly Phe Thr Ala Thr Trp Gln Ala Trp Val Leu
85 90 95

Ser Ala Leu Ile Tyr Phe Ala Val Leu Leu Val Leu Met Phe Ala Trp
100 105 110

Ile Leu Pro Met Val Ser Val Leu Ala Ala Thr Ser Ser Gly Ser Asp
115 120 125

Ser Ala Ala Ile Ala Ala Thr Gly Gly Thr Ser Phe Phe Gly Phe Met
130 135 140

Leu Met Ile Val Leu Ala Phe Ile Ser Phe Val Tyr Ser Leu Asn Cys
145 150 155 160

Tyr Arg Asn Ala Ala Arg Val Val Arg Gly Glu Gln Ile Thr Ile Gln
165 170 175

Ser Phe Phe Lys Met Lys Gly Leu Gly Lys Ala Leu Gly Ile Tyr Ile
180 185 190

Leu Ile Asn Ile Val Ile Phe Ile Gly Met Ile Leu Leu Leu Ile Pro
195 200 205

Gly Ile Ile Ala Ala Val Val Leu Ile Phe Ala Val Pro Val Ala Phe
210 215 220

Gln Leu Arg Asp Ala Ser Ile Gly Asp Ala Phe Ser Ala Ser Trp Lys
225 230 235 240

Ala Val Ser Lys Asn Val Gly Gln Val Ile Leu Leu Glu Leu Ala Ile
245 250 255

Phe Ala Leu Ser Phe Leu Gly Ser Ala Val Ile Ile Gly Met Leu Val
260 265 270

Thr Thr Pro Leu Thr Phe Leu Leu Tyr Ala Tyr Ala Phe Gln Thr Ala
275 280 285

Ser Gly Gly Pro Ile Met Gln Arg Gln
290 295

<210> 2885

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXA02757

<400> 2885

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                                   1 5

ctc gac gaa cga gta tcc acc gat cct gat ttt cgg gcg gcc ttg gaa 163
Leu Asp Glu Arg Val Ser Thr Asp Pro Asp Phe Arg Ala Ala Leu Glu
                                   10 15 20

cgt tgg tac gga cac ttg att cgg aag gtg tca cgt cgc gct cgt aat 211
Arg Trp Tyr Gly His Leu Ile Arg Lys Val Ser Arg Arg Ala Arg Asn
                                   25 30 35

gcg gcg tgg gat cgg gtg caa gat tta ccc ggc gtg act gtg gaa gat 259
Ala Ala Trp Asp Arg Val Gln Asp Leu Pro Gly Val Thr Val Glu Asp
                                   40 45 50

gat gct gca aag gtt cgg gca ttt ttg ccc agc gca gtg gtg gat gtg 307
Asp Ala Ala Lys Val Arg Ala Phe Leu Pro Ser Ala Val Val Asp Val
                                   55 60 65

cct gca gat atc aaa aag ctg cag att tcc ggt acg gaa ttg cct ctc 355
Pro Ala Asp Ile Lys Lys Leu Gln Ile Ser Gly Thr Glu Leu Pro Leu
                                   70 75 80 85

gat gag ccg aat ccg atc aac gat gaa tac ccc gtt atc tac att gat 403
Asp Glu Pro Asn Pro Ile Asn Asp Glu Tyr Pro Val Ile Tyr Ile Asp
                                   90 95 100

gaa tcg ttg aag atg acg ctg gga aag gcc gct gcg cag gta gga cac 451
Glu Ser Leu Lys Met Thr Leu Gly Lys Ala Ala Ala Gln Val Gly His
                                   105 110 115

gca tcc atg ttg ctt gcc gcg cac caa ccg ttt gag tgg gtg gag cag 499
Ala Ser Met Leu Leu Ala Ala His Gln Pro Phe Glu Trp Val Glu Gln
                                   120 125 130

tgg gaa gca gcg gat ttt gcg ctg cac gtc agg gag att ccc tcg gag 547
Trp Glu Ala Ala Asp Phe Ala Leu His Val Arg Glu Ile Pro Ser Glu
                                   135 140 145

gag ttc ctg cgc ctt atc gag tct cct ggt gct gtt cca gtt cgc gat 595
Glu Phe Leu Arg Leu Ile Glu Ser Pro Gly Ala Val Pro Val Arg Asp
                                   150 155 160 165

ggc ggc ttt act gag gtt gcc ccc aac acc gtg acg gtt gtt gca att 643
Gly Gly Phe Thr Glu Val Ala Pro Asn Thr Val Thr Val Val Ala Ile
                                   170 175 180

cca taactaaacg agctttgatt aac 669
Pro

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<210> 2886

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 2886

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Val Val Lys Leu Cys Leu Asp Glu Arg Val Ser Thr Asp Pro Asp Phe
 1 5 10 15

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Arg Ala Ala Leu Glu Arg Trp Tyr Gly His Leu Ile Arg Lys Val Ser
 20 25 30
 Arg Arg Ala Arg Asn Ala Ala Trp Asp Arg Val Gln Asp Leu Pro Gly
 35 40 45
 Val Thr Val Glu Asp Asp Ala Ala Lys Val Arg Ala Phe Leu Pro Ser
 50 55 60
 Ala Val Val Asp Val Pro Ala Asp Ile Lys Lys Leu Gln Ile Ser Gly
 65 70 75 80
 Thr Glu Leu Pro Leu Asp Glu Pro Asn Pro Ile Asn Asp Glu Tyr Pro
 85 90 95
 Val Ile Tyr Ile Asp Glu Ser Leu Lys Met Thr Leu Gly Lys Ala Ala
 100 105 110
 Ala Gln Val Gly His Ala Ser Met Leu Leu Ala Ala His Gln Pro Phe
 115 120 125
 Glu Trp Val Glu Gln Trp Glu Ala Ala Asp Phe Ala Leu His Val Arg
 130 135 140
 Glu Ile Pro Ser Glu Glu Phe Leu Arg Leu Ile Glu Ser Pro Gly Ala
 145 150 155 160
 Val Pro Val Arg Asp Gly Gly Phe Thr Glu Val Ala Pro Asn Thr Val
 165 170 175
 Thr Val Val Ala Ile Pro
 180

<210> 2887

<211> 882

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02765

<400> 2887

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 ttcaaccocat ggccgtatcc tcgcggattt taggagataa atg tct aat caa tta 115
 Met Ser Asn Gln Leu
 1 5
 ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa 163
 Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu
 10 15 20
 caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg 211
 Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val
 25 30 35
 ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc 259

Phe	Ala	Lys	Val	Thr	Ala	Pro	Glu	Val	Ser	Gly	Trp	Ser	Ser	Lys	Thr		
	40						45					50					
cgc	gaa	acc	ctg	aaa	cca	gaa	ggc	gtg	cgc	gtc	gta	cga	ccg	atc	cgc	307	
Arg	Glu	Thr	Leu	Lys	Pro	Glu	Gly	Val	Arg	Val	Val	Arg	Pro	Ile	Arg		
	55					60				65							
tcc	acc	gac	ggc	cga	ttt	gtg	gtt	gcg	ggg	tgg	cgc	gca	tcg	gtg	ttc	355	
Ser	Thr	Asp	Gly	Arg	Phe	Val	Val	Ala	Gly	Trp	Arg	Ala	Ser	Val	Phe		
	70				75				80					85			
tct	acg	gga	acg	atc	agc	aag	cga	gtc	gat	gag	acg	gtc	gtt	gcg	ggc	403	
Ser	Thr	Gly	Thr	Ile	Ser	Lys	Arg	Val	Asp	Glu	Thr	Val	Val	Ala	Gly		
				90				95						100			
ctt	cgt	ttg	gca	gat	gca	tta	gtg	gat	acg	cat	gca	ccg	gaa	cct	gtg	451	
Leu	Arg	Leu	Ala	Asp	Ala	Leu	Val	Asp	Thr	His	Ala	Pro	Glu	Pro	Val		
			105					110					115				
gac	aat	gtg	ttt	aac	cgt	gct	gat	gtg	cag	gcc	tgg	gaa	gag	cag	ccc	499	
Asp	Asn	Val	Phe	Asn	Arg	Ala	Asp	Val	Gln	Ala	Trp	Glu	Glu	Gln	Pro		
		120					125					130					
ggt	cga	atc	ggt	gaa	ttg	ttg	gag	ccg	att	aat	cgc	gtg	aac	cag	gtt	547	
Gly	Arg	Ile	Gly	Glu	Leu	Leu	Glu	Pro	Ile	Asn	Arg	Val	Asn	Gln	Val		
	135					140					145						
ggt	cat	gcg	gat	atg	ttg	gcg	aca	acg	ctg	tat	gcg	gga	act	cag	cca	595	
Gly	His	Ala	Asp	Met	Leu	Ala	Thr	Thr	Leu	Tyr	Ala	Gly	Thr	Gln	Pro		
	150				155				160						165		
cct	gca	gtg	acg	gat	ttg	gtg	cca	gtg	ctg	cgt	ccg	cat	ggt	ttc	act	643	
Pro	Ala	Val	Thr	Asp	Leu	Val	Pro	Val	Leu	Arg	Pro	His	Gly	Phe	Thr		
				170				175						180			
gcg	gca	ttg	gtg	atc	gtt	gat	ggg	ttg	ctg	ctg	ggt	gcg	gtt	gat	gag	691	
Ala	Ala	Leu	Val	Ile	Val	Asp	Gly	Leu	Leu	Leu	Gly	Ala	Val	Asp	Glu		
			185				190						195				
gga	att	ctg	cgg	agg	ttt	tcg	cat	ttg	ccg	gaa	att	gag	cag	ctg	gtt	739	
Gly	Ile	Leu	Arg	Arg	Phe	Ser	His	Leu	Pro	Glu	Ile	Glu	Gln	Leu	Val		
		200					205					210					
ttg	agg	gca	ttt	ttg	ttc	cgt	cga	aac	ttg	cag	gag	ttc	tct	gag	aac	787	
Leu	Arg	Ala	Phe	Leu	Phe	Arg	Arg	Asn	Leu	Gln	Glu	Phe	Ser	Glu	Asn		
	215					220					225						
aac	gat	cgg	aat	gtt	att	tcg	aac	cta	aac	agg	gtg	gaa	tcg	aca	ctc	835	
Asn	Asp	Pro	Asn	Val	Ile	Ser	Asn	Leu	Asn	Arg	Val	Glu	Ser	Thr	Leu		
	230				235				240						245		
gtg	tcg	tat	gtt	tct	gac	aag	att	tgaggtatgt	cggaatacaa	acc						882	
Val	Ser	Tyr	Val	Ser	Asp	Lys	Ile										
				250													

<210> 2888

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 2888

Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly
1 5 10 15
Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg
20 25 30
Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly
35 40 45
Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val
50 55 60
Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp
65 70 75 80
Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu
85 90 95
Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His
100 105 110
Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala
115 120 125
Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn
130 135 140
Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr
145 150 155 160
Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg
165 170 175
Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu
180 185 190
Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu
195 200 205
Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln
210 215 220
Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg
225 230 235 240
Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile
245 250

<210> 2889

<211> 516

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(493)

<223> RXA02766

<400> 2889

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acaccttact ggcgtaaggc cagggccttag actggtaccc atg aca acc tca gaa 115
                                     Met Thr Thr Ser Glu
                                     1 5

aat ttt tat gat tct gtg ggc ggc gag gaa acg ttt tcc ctc atc gtc 163
Asn Phe Tyr Asp Ser Val Gly Gly Glu Glu Thr Phe Ser Leu Ile Val
      10      15      20

cac cgt ttt tat gaa cag gtc ccc aac gac gat att tta ggc ccg atg 211
His Arg Phe Tyr Glu Gln Val Pro Asn Asp Asp Ile Leu Gly Pro Met
      25      30      35

tat ccg ccg gat gat ttt gag ggc gcc gag cag cgt cta aag atg ttc 259
Tyr Pro Pro Asp Asp Phe Glu Gly Ala Glu Gln Arg Leu Lys Met Phe
      40      45      50

ctc agc cag tac tgg ggc ggc ccg aag gat tat cag gag cag cgt gga 307
Leu Ser Gln Tyr Trp Gly Gly Pro Lys Asp Tyr Gln Glu Gln Arg Gly
      55      60      65

cac cct cgt ctg cgc atg cgt cac gtc aat tac ccc atc ggc gtc acc 355
His Pro Arg Leu Arg Met Arg His Val Asn Tyr Pro Ile Gly Val Thr
      70      75      80      85

gca gcg gag cgt tgg ctg cag ctc atg tcc aat gca ctc gac ggc gtg 403
Ala Ala Glu Arg Trp Leu Gln Leu Met Ser Asn Ala Leu Asp Gly Val
      90      95      100

gat ttg acc gcg gag cag cgt gaa gcg att tgg gag cat atg gtg cgc 451
Asp Leu Thr Ala Glu Gln Arg Glu Ala Ile Trp Glu His Met Val Arg
      105      110      115

gcg gcc gat atg ctg atc aat tcc aac ccc gat ccg cac gct 493
Ala Ala Asp Met Leu Ile Asn Ser Asn Pro Asp Pro His Ala
      120      125      130

taacttctgc caaaaagtcg ttt 516

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<210> 2890

<211> 131

<212> PRT

<213> Corynebacterium glutamicum

<400> 2890

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Met Thr Thr Ser Glu Asn Phe Tyr Asp Ser Val Gly Gly Glu Glu Thr
  1 5 10 15

Phe Ser Leu Ile Val His Arg Phe Tyr Glu Gln Val Pro Asn Asp Asp
  20 25 30

Ile Leu Gly Pro Met Tyr Pro Pro Asp Asp Phe Glu Gly Ala Glu Gln
  35 40 45

Arg Leu Lys Met Phe Leu Ser Gln Tyr Trp Gly Gly Pro Lys Asp Tyr
  50 55 60

Gln Glu Gln Arg Gly His Pro Arg Leu Arg Met Arg His Val Asn Tyr
  65 70 75 80

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Pro Ile Gly Val Thr Ala Ala Glu Arg Trp Leu Gln Leu Met Ser Asn
85 90 95

Ala Leu Asp Gly Val Asp Leu Thr Ala Glu Gln Arg Glu Ala Ile Trp
100 105 110

Glu His Met Val Arg Ala Ala Asp Met Leu Ile Asn Ser Asn Pro Asp
115 120 125

Pro His Ala
130

<210> 2891

<211> 494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(471)

<223> RXA02774

<400> 2891

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Pro Cys Pro Pro Thr Gln Lys Leu Leu Tyr Ala Gln Met Arg Glu Ile
1 5 10 15

gca gcc gaa ctt aca gcc tgt gac gct act cgc gga ctc cat gcc gaa 96
Ala Ala Glu Leu Thr Ala Cys Asp Ala Thr Arg Gly Leu His Ala Glu
20 25 30

gtg gct gcc gaa tgg ctt agt gac gcc ata acc ggc gaa ccc acc tct 144
Val Ala Ala Glu Trp Leu Ser Asp Ala Ile Thr Gly Glu Pro Thr Ser
35 40 45

atc gag att gac ccc cac cgc aac ctg ttc tac gca ctt aat gtt gag 192
Ile Glu Ile Asp Pro His Arg Asn Leu Phe Tyr Ala Leu Asn Val Glu
50 55 60

cac ccg cga ctc cat gaa ctc ttt gcc ggt tac gct aca cgc ctt gat 240
His Pro Arg Leu His Glu Leu Phe Ala Gly Tyr Ala Thr Arg Leu Asp
65 70 75 80

gaa ctc gac cgc gca ccg cag cag tgt gag tcg cgt caa tat ttt ctt 288
Glu Leu Asp Arg Ala Pro Gln Gln Cys Glu Ser Arg Gln Tyr Phe Leu
85 90 95

gat tat gtc tgt gct gac aac cct ttt ggc tca gac aaa cca gag ggc 336
Asp Tyr Val Cys Ala Asp Asn Pro Phe Gly Ser Asp Lys Pro Glu Gly
100 105 110

att atc gtg ctg ctc gct gat cac gtg ctg gca gca gat cca gtg aca 384
Ile Ile Val Leu Leu Ala Asp His Val Leu Ala Ala Asp Pro Val Thr
115 120 125

aac aag ccg gca ctc aaa tca gag gca ttc cct act gtc aca gac tat 432
Asn Lys Pro Ala Leu Lys Ser Glu Ala Phe Pro Thr Val Thr Asp Tyr
130 135 140

tgc cgc act cac tct gct aaa cca aca gac att ctc att taaggatttt 481
 Cys Arg Thr His Ser Ala Lys Pro Thr Asp Ile Leu Ile
 145 150 155

agtcaccatg acg 494

<210> 2892

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 2892

Pro Cys Pro Pro Thr Gln Lys Leu Leu Tyr Ala Gln Met Arg Glu Ile
 1 5 10 15

Ala Ala Glu Leu Thr Ala Cys Asp Ala Thr Arg Gly Leu His Ala Glu
 20 25 30

Val Ala Ala Glu Trp Leu Ser Asp Ala Ile Thr Gly Glu Pro Thr Ser
 35 40 45

Ile Glu Ile Asp Pro His Arg Asn Leu Phe Tyr Ala Leu Asn Val Glu
 50 55 60

His Pro Arg Leu His Glu Leu Phe Ala Gly Tyr Ala Thr Arg Leu Asp
 65 70 75 80

Glu Leu Asp Arg Ala Pro Gln Gln Cys Glu Ser Arg Gln Tyr Phe Leu
 85 90 95

Asp Tyr Val Cys Ala Asp Asn Pro Phe Gly Ser Asp Lys Pro Glu Gly
 100 105 110

Ile Ile Val Leu Leu Ala Asp His Val Leu Ala Ala Asp Pro Val Thr
 115 120 125

Asn Lys Pro Ala Leu Lys Ser Glu Ala Phe Pro Thr Val Thr Asp Tyr
 130 135 140

Cys Arg Thr His Ser Ala Lys Pro Thr Asp Ile Leu Ile
 145 150 155

<210> 2893

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA02775

<400> 2893

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atacaacacc tctcacacac aaacaagaaa gggtcacccc atg acc acc gtt caa 115
 Met Thr Thr Val Gln
 1 5

gta tcc acc cgc act gtg cgc gaa cac cgt ttt act gtg cca gtg gac 163
 Val Ser Thr Arg Thr Val Arg Glu His Arg Phe Thr Val Pro Val Asp
 10 15 20

tac gct gtc ggc gcc acc att tca gaa atc tat gct gcc tgt gcc atg 211
 Tyr Ala Val Gly Ala Thr Ile Ser Glu Ile Tyr Ala Ala Cys Ala Met
 25 30 35

gcc gaa aag aaa gcc aac aac ctt ggg ctt aac act act aag gac gat 259
 Ala Glu Lys Lys Ala Asn Asn Leu Gly Leu Asn Thr Thr Lys Asp Asp
 40 45 50

tgg gca cga gtc act gtc act gat aat gct gtt gtg ttc att gtc gag 307
 Trp Ala Arg Val Thr Val Thr Asp Asn Ala Val Val Phe Ile Val Glu
 55 60 65

aat gtt atc ggg aat act tagaattgtg tgctccttaa cgg 348
 Asn Val Ile Gly Asn Thr
 70 75

<210> 2894

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 2894

Met Thr Thr Val Gln Val Ser Thr Arg Thr Val Arg Glu His Arg Phe
 1 5 10 15

Thr Val Pro Val Asp Tyr Ala Val Gly Ala Thr Ile Ser Glu Ile Tyr
 20 25 30

Ala Ala Cys Ala Met Ala Glu Lys Lys Ala Asn Asn Leu Gly Leu Asn
 35 40 45

Thr Thr Lys Asp Asp Trp Ala Arg Val Thr Val Thr Asp Asn Ala Val
 50 55 60

Val Phe Ile Val Glu Asn Val Ile Gly Asn Thr
 65 70 75

<210> 2895

<211> 465

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(442)

<223> RXA02776

<400> 2895

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caagttgtat aatccttcac tcgatgatca aacaccttcg gtg ctc tat cct gtt 115
 Val Leu Tyr Pro Val
 1 5

gaa gca gga acg gtg tct ctc gtt gat gta aag aaa gcg gct agc cgt 163

Glu Ala Gly Thr Val Ser Leu Val Asp Val Lys Lys Ala Ala Ser Arg
 10 15 20
 gcc ttt gaa cag tgg gaa aag cac aac gag tcc gct ggt gat gtc ggt 211
 Ala Phe Glu Gln Trp Glu Lys His Asn Glu Ser Ala Gly Asp Val Gly
 25 30 35
 gat gat ctt tca ctg cag agt atc gta gat ctc att gag cgt gac act 259
 Asp Asp Leu Ser Leu Gln Ser Ile Val Asp Leu Ile Glu Arg Asp Thr
 40 45 50
 ttc ccc acc gac gat gag caa gag ctc aat aat gtg gct ttg ctt atc 307
 Phe Pro Thr Asp Asp Glu Gln Glu Leu Asn Asn Val Ala Leu Leu Ile
 55 60 65
 ggc gaa ctc ctg gtg agg gag gcc ggt gga gag tgg acg tcg tac atc 355
 Gly Glu Leu Leu Val Arg Glu Ala Gly Gly Glu Trp Thr Ser Tyr Ile
 70 75 80 85
 tca aag aaa aat gat gaa gat gaa tcg ctg gag att ttc ggg gtt ttt 403
 Ser Lys Lys Asn Asp Glu Asp Glu Ser Leu Glu Ile Phe Gly Val Phe
 90 95 100
 ggc acc ggt ggc act gaa gga tta tct gta gtg ggt aat tgagttagca 452
 Gly Thr Gly Gly Thr Glu Gly Leu Ser Val Val Gly Asn
 105 110
 tggtagtgtagtga 'aaa 465

<210> 2896

<211> 114

<212> PRT

<213> Corynebacterium glutamicum

<400> 2896

Val Leu Tyr Pro Val Glu Ala Gly Thr Val Ser Leu Val Asp Val Lys
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 Lys Ala Ala Ser Arg Ala Phe Glu Gln Trp Glu Lys His Asn Glu Ser
 20 25 30
 Ala Gly Asp Val Gly Asp Asp Leu Ser Leu Gln Ser Ile Val Asp Leu
 35 40 45
 Ile Glu Arg Asp Thr Phe Pro Thr Asp Asp Glu Gln Glu Leu Asn Asn
 50 55 60
 Val Ala Leu Leu Ile Gly Glu Leu Leu Val Arg Glu Ala Gly Gly Glu
 65 70 75 80
 Trp Thr Ser Tyr Ile Ser Lys Lys Asn Asp Glu Asp Glu Ser Leu Glu
 85 90 95
 Ile Phe Gly Val Phe Gly Thr Gly Gly Thr Glu Gly Leu Ser Val Val
 100 105 110
 Gly Asn

<210> 2897
 <211> 1230
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1207)
 <223> RXA02777

<400> 2897

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gtcactgcta ccatcacaat cggttgctag taggctacaa atg aac cgc ccc ctt 115
                                         Met Asn Arg Pro Leu
                                         1 5

caa agt caa aat ttt tca ata acc agc gaa tgg gca aat gcc acg ttc 163
Gln Ser Gln Asn Phe Ser Ile Thr Ser Glu Trp Ala Asn Ala Thr Phe
                        10 15 20

aac gat atc gaa gac tct ttg gag ggg tct ttt gac atc gaa cca ggc 211
Asn Asp Ile Glu Asp Ser Leu Glu Gly Ser Phe Asp Ile Glu Pro Gly
                        25 30 35

caa tac att gga cgc gga gaa tac ttc gta gct act tct gga acg ggt 259
Gln Tyr Ile Gly Arg Gly Glu Tyr Phe Val Ala Thr Ser Gly Thr Gly
                        40 45 50

tcc aaa aag ttt atc aag gtg gtt ttg ggt gac ggt atc gat agc gaa 307
Ser Lys Lys Phe Ile Lys Val Val Leu Gly Asp Gly Ile Asp Ser Glu
                        55 60 65

cta aat cgt cgc atc gaa ggt gaa att ctt gca agt agt ctc cat ctt 355
Leu Asn Arg Arg Ile Glu Gly Glu Ile Leu Ala Ser Ser Leu His Leu
                        70 75 80 85

cca tcc aca gac cta atc tct cct gtc gta att cag tat gtg aaa gag 403
Pro Ser Thr Asp Leu Ile Ser Pro Val Val Ile Gln Tyr Val Lys Glu
                        90 95 100

tct tct aat ttt ccc ggt gac ttc tac atc gtg tcc gac ttc aaa gac 451
Ser Ser Asn Phe Pro Gly Asp Phe Tyr Ile Val Ser Asp Phe Lys Asp
                        105 110 115

gac aca gaa act tta gag cta tct aag gct tct cta ccc ctc act gac 499
Asp Thr Glu Thr Leu Glu Leu Ser Lys Ala Ser Leu Pro Leu Thr Asp
                        120 125 130

tta gcc aag atc gga gcg ttt ctc ttt cgt ttg gaa tct gta aca gtt 547
Leu Ala Lys Ile Gly Ala Phe Leu Phe Arg Leu Glu Ser Val Thr Val
                        135 140 145

ccc cct caa aat cct gca agg cga gca atg gat gtt ttg gat gga ctt 595
Pro Pro Gln Asn Pro Ala Arg Arg Ala Met Asp Val Leu Asp Gly Leu
                        150 155 160 165

tct ctt ctt gca aat aaa ggc aac att gaa aca ggc gca caa tta aca 643
Ser Leu Leu Ala Asn Lys Gly Asn Ile Glu Thr Gly Ala Gln Leu Thr
                        170 175 180

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aaa gga act ata caa gct ctt gaa atc att aat caa gaa gcg acc aac 691
 Lys Gly Thr Ile Gln Ala Leu Glu Ile Ile Asn Gln Glu Ala Thr Asn
 185 190 195

atc gag aat gca ctt gaa aaa gta act aaa gta gga tca cgg aag ttt 739
 Ile Glu Asn Ala Leu Glu Lys Val Thr Lys Val Gly Ser Arg Lys Phe
 200 205 210

ttc tcg cat gga gat ctt aaa ttt tct cag ttc tta att aat ggt gaa 787
 Phe Ser His Gly Asp Leu Lys Phe Ser Gln Phe Leu Ile Asn Gly Glu
 215 220 225

acc gga aag att ttc cta tgt gac tgg gaa gaa tgc ggt agt gca cat 835
 Thr Gly Lys Ile Phe Leu Cys Asp Trp Glu Glu Cys Gly Ser Ala His
 230 235 240 245

ttc gca aat gac cta tgt ttt ctc gca ggt gat ttg ttc tat agc aca 883
 Phe Ala Asn Asp Leu Cys Phe Leu Ala Gly Asp Leu Phe Tyr Ser Thr
 250 255 260

att cgg gaa ctg gtg gat acc aac atc aaa aac att aaa ggc tcc tcg 931
 Ile Arg Glu Leu Val Asp Thr Asn Ile Lys Asn Ile Lys Gly Ser Ser
 265 270 275

atc att cag gaa gcc tac gat aat gca acg ctt gag gct gta tca aaa 979
 Ile Ile Gln Glu Ala Tyr Asp Asn Ala Thr Leu Glu Ala Val Ser Lys
 280 285 290

gta aat gca ata tta act ggc tat tcc tca gag agg ggt tac tct ctc 1027
 Val Asn Ala Ile Leu Thr Gly Tyr Ser Ser Glu Arg Gly Tyr Ser Leu
 295 300 305

acc tcg gac gaa aaa cga atc att agt atc aga atc gga ttg gct ggt 1075
 Thr Ser Asp Glu Lys Arg Ile Ile Ser Ile Arg Ile Gly Leu Ala Gly
 310 315 320 325

cta ttt cga ctt tac act gtg agc gct aaa tct aat gag tta cgc ccg 1123
 Leu Phe Arg Leu Tyr Thr Val Ser Ala Lys Ser Asn Glu Leu Arg Pro
 330 335 340

cgc gaa tta gcc tta gcc tcc atc gga atg caa att act tta ggt caa 1171
 Arg Glu Leu Ala Leu Ala Ser Ile Gly Met Gln Ile Thr Leu Gly Gln
 345 350 355

gca ccc aat ctg gtg ttt aca gat agc aag gtg gtt taagtgagga 1217
 Ala Pro Asn Leu Val Phe Thr Asp Ser Lys Val Val
 360 365

atttgacga aac 1230

<210> 2898

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 2898

Met Asn Arg Pro Leu Gln Ser Gln Asn Phe Ser Ile Thr Ser Glu Trp
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Ala Asn Ala Thr Phe Asn Asp Ile Glu Asp Ser Leu Glu Gly Ser Phe

20							25							30						
Asp	Ile	Glu	Pro	Gly	Gln	Tyr	Ile	Gly	Arg	Gly	Glu	Tyr	Phe	Val	Ala					
		35						40				45								
Thr	Ser	Gly	Thr	Gly	Ser	Lys	Lys	Phe	Ile	Lys	Val	Val	Leu	Gly	Asp					
	50					55					60									
Gly	Ile	Asp	Ser	Glu	Leu	Asn	Arg	Arg	Ile	Glu	Gly	Glu	Ile	Leu	Ala					
65					70					75					80					
Ser	Ser	Leu	His	Leu	Pro	Ser	Thr	Asp	Leu	Ile	Ser	Pro	Val	Val	Ile					
				85					90					95						
Gln	Tyr	Val	Lys	Glu	Ser	Ser	Asn	Phe	Pro	Gly	Asp	Phe	Tyr	Ile	Val					
			100					105					110							
Ser	Asp	Phe	Lys	Asp	Asp	Thr	Glu	Thr	Leu	Glu	Leu	Ser	Lys	Ala	Ser					
		115					120					125								
Leu	Pro	Leu	Thr	Asp	Leu	Ala	Lys	Ile	Gly	Ala	Phe	Leu	Phe	Arg	Leu					
	130					135					140									
Glu	Ser	Val	Thr	Val	Pro	Pro	Gln	Asn	Pro	Ala	Arg	Arg	Ala	Met	Asp					
145					150					155					160					
Val	Leu	Asp	Gly	Leu	Ser	Leu	Leu	Ala	Asn	Lys	Gly	Asn	Ile	Glu	Thr					
				165					170					175						
Gly	Ala	Gln	Leu	Thr	Lys	Gly	Thr	Ile	Gln	Ala	Leu	Glu	Ile	Ile	Asn					
			180					185					190							
Gln	Glu	Ala	Thr	Asn	Ile	Glu	Asn	Ala	Leu	Glu	Lys	Val	Thr	Lys	Val					
		195					200					205								
Gly	Ser	Arg	Lys	Phe	Phe	Ser	His	Gly	Asp	Leu	Lys	Phe	Ser	Gln	Phe					
	210					215					220									
Leu	Ile	Asn	Gly	Glu	Thr	Gly	Lys	Ile	Phe	Leu	Cys	Asp	Trp	Glu	Glu					
225					230					235					240					
Cys	Gly	Ser	Ala	His	Phe	Ala	Asn	Asp	Leu	Cys	Phe	Leu	Ala	Gly	Asp					
				245				250						255						
Leu	Phe	Tyr	Ser	Thr	Ile	Arg	Glu	Leu	Val	Asp	Thr	Asn	Ile	Lys	Asn					
			260				265						270							
Ile	Lys	Gly	Ser	Ser	Ile	Ile	Gln	Glu	Ala	Tyr	Asp	Asn	Ala	Thr	Leu					
		275					280					285								
Glu	Ala	Val	Ser	Lys	Val	Asn	Ala	Ile	Leu	Thr	Gly	Tyr	Ser	Ser	Glu					
	290					295					300									
Arg	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Glu	Lys	Arg	Ile	Ile	Ser	Ile	Arg					
305					310					315					320					
Ile	Gly	Leu	Ala	Gly	Leu															

Ile Thr Leu Gly Gln Ala Pro Asn Leu Val Phe Thr Asp Ser Lys Val
 355 360 365

Val

<210> 2899

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXA02778

<400> 2899

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cgtttttcaa ggggttcaccg aagcaactgt tgagcacctc atg cag gtc att gag 115
                                         Met Gln Val Ile Glu
                                         1             5

acg ctt gat ccc gat cag cgc gca gcg gtg ctc gct gca gcg ata ccg 163
Thr Leu Asp Pro Asp Gln Arg Ala Ala Val Leu Ala Ala Ala Ile Pro
          10             15             20

cgc gag gct aag atc ctg ggg cga aaa gta act ctt cgc cct ggt tgg 211
Arg Glu Ala Lys Ile Leu Gly Arg Lys Val Thr Leu Arg Pro Gly Trp
          25             30             35

ggc aat atg cgc gta cac gtc gtg att gca gtt atc ttt atc aag ttt 259
Gly Asn Met Arg Val His Val Val Ile Ala Val Ile Phe Ile Lys Phe
          40             45             50

ttg caa ccg gat ctt cgc cag gcg ctg cta aca aca ggt gat gcc gta 307
Leu Gln Pro Asp Leu Arg Gln Ala Leu Leu Thr Thr Gly Asp Ala Val
          55             60             65

ctt gtc gaa gat gat acc tgaggcgcct tctggggcgt cga 348
Leu Val Glu Asp Asp Thr
          70             75
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<210> 2900

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 2900

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  1             5             10             15

Ala Ala Ala Ile Pro Arg Glu Ala Lys Ile Leu Gly Arg Lys Val Thr
          20             25             30

Leu Arg Pro Gly Trp Gly Asn Met Arg Val His Val Val Ile Ala Val
          35             40             45
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Ile Phe Ile Lys Phe Leu Gln Pro Asp Leu Arg Gln Ala Leu Leu Thr
 50 55 60

Thr Gly Asp Ala Val Leu Val Glu Asp Asp Thr
 65 70 75

<210> 2901

<211> 402

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(379)

<223> RXA02779

<400> 2901

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 gtttgaattt gccaatgca'c agtgctcaga accagaagaa atg ggc gaa tac ttc 115
 Met Gly Glu Tyr Phe
 1 5
 cag gtc gtt caa aac atc gcc atg aca ctg ggt gct ggc gaa agc gtt 163
 Gln Val Val Gln Asn Ile Ala Met Thr Leu Gly Ala Gly Glu Ser Val
 10 15 20
 gat ctt gtt gtc cgc gaa tac atc aac gat gtg gaa ggc aac ccg acc 211
 Asp Leu Val Val Arg Glu Tyr Ile Asn Asp Val Glu Gly Asn Pro Thr
 25 30 35
 atc tat cac ggt atg ccg ctg cgt act gaa tac cgc gca ttc atc gac 259
 Ile Tyr His Gly Met Pro Leu Arg Thr Glu Tyr Arg Ala Phe Ile Asp
 40 45 50
 ctt gat cac tgt gat ccg tcc gct ggt gag cct gag cct cgc tta ttg 307
 Leu Asp His Cys Asp Pro Ser Ala Gly Glu Pro Glu Pro Arg Leu Leu
 55 60 65
 ggg gtt act ccc tac tgg cac ccc tcc gtg atg gag aaa gct ctt cgc 355
 Gly Val Thr Pro Tyr Trp His Pro Ser Val Met Glu Lys Ala Leu Arg
 70 75 80 85
 ctt tgc ttc aag cga tgt tgg tgc tgaattcggg cacaatcaacg atg 402
 Leu Cys Phe Lys Arg Cys Trp Cys
 90

<210> 2902

<211> 93

<212> PRT

<213> Corynebacterium glutamicum

<400> 2902

Met Gly Glu Tyr Phe Gln Val Val Gln Asn Ile Ala Met Thr Leu Gly
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 Ala Gly Glu Ser Val Asp Leu Val Val Arg Glu Tyr Ile Asn Asp Val
 20 25 30

Glu Gly Asn Pro Thr Ile Tyr His Gly Met Pro Leu Arg Thr Glu Tyr
 35 40 45

Arg Ala Phe Ile Asp Leu Asp His Cys Asp Pro Ser Ala Gly Glu Pro
 50 55 60

Glu Pro Arg Leu Leu Gly Val Thr Pro Tyr Trp His Pro Ser Val Met
 65 70 75 80

Glu Lys Ala Leu Arg Leu Cys Phe Lys Arg Cys Trp Cys
 85 90

<210> 2903

<211> 450

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(427)

<223> RXA02780

<400> 2903

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cgatgattac cgcacctacc gtgccacaaa agacagcctc atg tcc aag ttc cat 115
 Met Ser Lys Phe His
 1 5

aca cac cgt gat gat gtc att tca cgt atc act gca cta cta ccc cag 163
 Thr His Arg Asp Asp Val Ile Ser Arg Ile Thr Ala Leu Leu Pro Gln
 10 15 20

ctt cgt gca caa gag ctg caa ggt caa tgg tct gtg gac atc atg aaa 211
 Leu Arg Ala Gln Glu Leu Gln Gly Gln Trp Ser Val Asp Ile Met Lys
 25 30 35

aac ggg gag gat ttc tac ctc att gac atg gct ctc atg tgc gag tcc 259
 Asn Gly Glu Asp Phe Tyr Leu Ile Asp Met Ala Leu Met Cys Glu Ser
 40 45 50

gca ctg tct gaa cta ctc act gtt aca gat gag tac gcc aca gtc gag 307
 Ala Leu Ser Glu Leu Leu Thr Val Thr Asp Glu Tyr Ala Thr Val Glu
 55 60 65

ccg agt gtc atc aat gac ttc gcc aac cag ctg gtc att gat tat gac 355
 Pro Ser Val Ile Asn Asp Phe Ala Asn Gln Leu Val Ile Asp Tyr Asp
 70 75 80 85

gag cac gat atg ggc ttt gat cga gac ttt cca gca ggt gtg tat aac 403
 Glu His Asp Met Gly Phe Asp Arg Asp Phe Pro Ala Gly Val Tyr Asn
 90 95 100

acc cga caa gca agt gct atc aac taaaaaatac acacatccac acc 450
 Thr Arg Gln Ala Ser Ala Ile Asn
 105

<210> 2904

<211> 109

<212> PRT

<213> Corynebacterium glutamicum

<400> 2904

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Met Ser Lys Phe His Thr His Arg Asp Asp Val Ile Ser Arg Ile Thr
 1             5             10             15
Ala Leu Leu Pro Gln Leu Arg Ala Gln Glu Leu Gln Gly Gln Trp Ser
      20             25             30
Val Asp Ile Met Lys Asn Gly Glu Asp Phe Tyr Leu Ile Asp Met Ala
      35             40             45
Leu Met Cys Glu Ser Ala Leu Ser Glu Leu Leu Thr Val Thr Asp Glu
      50             55             60
Tyr Ala Thr Val Glu Pro Ser Val Ile Asn Asp Phe Ala Asn Gln Leu
      65             70             75             80
Val Ile Asp Tyr Asp Glu His Asp Met Gly Phe Asp Arg Asp Phe Pro
      85             90             95
Ala Gly Val Tyr Asn Thr Arg Gln Ala Ser Ala Ile Asn
      100             105

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<210> 2905

<211> 672

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(649)

<223> RXA02783

<400> 2905

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gtgtggcaac caccgctttc gccgtacact cacactgtcg gtg gtc tct ggt tca 115
                               Val Val Ser Gly Ser
                               1             5
cgc gct gct gca ttc ttg aac agc aac cat att cag ggt gct gtc tcg 163
Arg Ala Ala Ala Phe Leu Asn Ser Asn His Ile Gln Gly Ala Val Ser
      10             15             20
gcc act aag cac ttt gcc ctg tgc gac aac aac gac gat att cga gca 211
Ala Thr Lys His Phe Ala Leu Cys Asp Asn Asn Asp Asp Ile Arg Ala
      25             30             35
ctc ctg tcg gtg cgc tca cca aaa aac aat gcc cgc atg tat cgc aaa 259
Leu Leu Ser Val Arg Ser Pro Lys Asn Asn Ala Arg Met Tyr Arg Lys
      40             45             50
aaa ggc aca tgg gaa atc cag cgc tat gcg aca ctc ggt aac gtc cct 307
Lys Gly Thr Trp Glu Ile Gln Arg Tyr Ala Thr Leu Gly Asn Val Pro
      55             60             65
ggc ggt ttt act agg ctg ctg aag ttt gcc gag cac aca ctc aac gaa 355
Gly Gly Phe Thr Arg Leu Leu Lys Phe Ala Glu His Thr Leu Asn Glu

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70	75	80	85	
cac agc aca gta ctc aag caa tgg atc tca ttt tct gct gct gat gtc				403
His Ser Thr Val Leu Lys Gln Trp Ile Ser Phe Ser Ala Ala Asp Val	90	95	100	
tct gac ggc agc ctg tat cga act gcc ggt ttt acc gcc gag caa cag				451
Ser Asp Gly Ser Leu Tyr Arg Thr Ala Gly Phe Thr Ala Glu Gln Gln	105	110	115	
ctt gca ccg gat tat cgc tat gtc ggt ggc gca aca ggt tgg cgc cga				499
Leu Ala Pro Asp Tyr Arg Tyr Val Gly Gly Ala Thr Gly Trp Arg Arg	120	125	130	
aca ccc aaa gaa agc ttc cag cgc aaa cgc ttt aga gac gac cca gcg				547
Thr Pro Lys Glu Ser Phe Gln Arg Lys Arg Phe Arg Asp Asp Pro Ala	135	140	145	
ttg cta tgg aac gaa tct tgg aca gag cac gaa gca gcg ctc aac aac				595
Leu Leu Trp Asn Glu Ser Trp Thr Glu His Glu Ala Ala Leu Asn Asn	150	155	160	165
gag ctc tac aga atc tac gat gcc ggc aaa acc cgg tgg gtt aaa aat				643
Glu Leu Tyr Arg Ile Tyr Asp Ala Gly Lys Thr Arg Trp Val Lys Asn	170	175	180	
gtt gct tgattctgca gattagttac tga				672
Val Ala				

<210> 2906

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 2906

Val Val Ser Gly Ser Arg Ala Ala Ala Phe Leu Asn Ser Asn His Ile	1	5	10	15
Gln Gly Ala Val Ser Ala Thr Lys His Phe Ala Leu Cys Asp Asn Asn	20	25	30	
Asp Asp Ile Arg Ala Leu Leu Ser Val Arg Ser Pro Lys Asn Asn Ala	35	40	45	
Arg Met Tyr Arg Lys Lys Gly Thr Trp Glu Ile Gln Arg Tyr Ala Thr	50	55	60	
Leu Gly Asn Val Pro Gly Gly Phe Thr Arg Leu Leu Lys Phe Ala Glu	65	70	75	80
His Thr Leu Asn Glu His Ser Thr Val Leu Lys Gln Trp Ile Ser Phe	85	90	95	
Ser Ala Ala Asp Val Ser Asp Gly Ser Leu Tyr Arg Thr Ala Gly Phe	100	105	110	
Thr Ala Glu Gln Gln Leu Ala Pro Asp Tyr Arg Tyr Val Gly Gly Ala	115	120	125	

Thr Gly Trp Arg Arg Thr Pro Lys Glu Ser Phe Gln Arg Lys Arg Phe
 130 135 140
 Arg Asp Asp Pro Ala Leu Leu Trp Asn Glu Ser Trp Thr Glu His Glu
 145 150 155 160
 Ala Ala Leu Asn Asn Glu Leu Tyr Arg Ile Tyr Asp Ala Gly Lys Thr
 165 170 175
 Arg Trp Val Lys Asn Val Ala
 180

<210> 2907
 <211> 309
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(286)
 <223> RXA02784

<400> 2907
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 tattgctaac cagctacaag atgccggtgt ctatgacgat gtg gcc ttt gcc gaa 115
 Val Ala Phe Ala Glu
 1 5
 ggc tac tac cag gaa atg gct gag gtt gta tgt gaa gca cgc gaa gag 163
 Gly Tyr Tyr Gln Glu Met Ala Glu Val Val Cys Glu Ala Arg Glu Glu
 10 15 20
 ggt atc acc cac gag gac acc ctg cat atg ctc aat gac atg atg gca 211
 Gly Ile Thr His Glu Asp Thr Leu His Met Leu Asn Asp Met Met Ala
 25 30 35
 atg aaa cga tct ggc gaa gta ctc aat acg ctc gct gat gtt ctc tat 259
 Met Lys Arg Ser Gly Glu Val Leu Asn Thr Leu Ala Asp Val Leu Tyr
 40 45 50
 gca aat gaa tgc cct gaa tat cga atc taaattgttg gtcactctgc 306
 Ala Asn Glu Cys Pro Glu Tyr Arg Ile
 55 60
 ata 309

<210> 2908
 <211> 62
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 2908
 Val Ala Phe Ala Glu Gly Tyr Tyr Gln Glu Met Ala Glu Val Val Cys
 1 5 10 15
 Glu Ala Arg Glu Gly Ile Thr His Glu Asp Thr Leu His Met Leu
 20 25 30

Asn Asp Met Met Ala Met Lys Arg Ser Gly Glu Val Leu Asn Thr Leu
 35 40 45

Ala Asp Val Leu Tyr Ala Asn Glu Cys Pro Glu Tyr Arg Ile
 50 55 60

<210> 2909

<211> 830

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(807)

<223> RXA02786

<400> 2909

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 Ile Leu Arg Asn Leu Gly Gln Ser Leu Gly Ser Leu His Ala Ala Thr
 1 5 10 15

gca gac cgc gaa gaa gac ttc aac att ctg ctc aac cgt atg ctg gcc 96
 Ala Asp Arg Glu Glu Asp Phe Asn Ile Leu Leu Asn Arg Met Leu Ala
 20 25 30

aaa tac cca gcc aca gct gag atg cag aaa aac cgc gat agg ttg ctg 144
 Lys Tyr Pro Ala Thr Ala Glu Met Gln Lys Asn Arg Asp Arg Leu Leu
 35 40 45

ccc gca gca att gag gtg ggt aaa aag ata ctt gtc gac gcc ggg gtc 192
 Pro Ala Ala Ile Glu Val Gly Lys Lys Ile Leu Val Asp Ala Gly Val
 50 55 60

acc gtt cca gaa gtc gtc gag gag ttt gcc cgc gta gct cgg cga cgc 240
 Thr Val Pro Glu Val Val Glu Glu Phe Ala Arg Val Ala Arg Arg Arg
 65 70 75 80

ctg att tcc gga cgc cac cgt gcc ttc aca cct ttt gac ttg tca ccc 288
 Leu Ile Ser Gly Arg His Arg Ala Phe Thr Pro Phe Asp Leu Ser Pro
 85 90 95

gac aac atc atc gtg gct gaa cgc acc cac ttc ctg gac tac gaa gtt 336
 Asp Asn Ile Ile Val Ala Glu Arg Thr His Phe Leu Asp Tyr Glu Val
 100 105 110

gcc ggt ttc agg gat gcc acc ttt gat gtt gct tgt gtg atc gca ggt 384
 Ala Gly Phe Arg Asp Ala Thr Phe Asp Val Ala Cys Val Ile Ala Gly
 115 120 125

ttc ccg caa ttc gtg ttc agc cgc ccc atc tct gat gat gag gta gac 432
 Phe Pro Gln Phe Val Phe Ser Arg Pro Ile Ser Asp Asp Glu Val Asp
 130 135 140

gaa ctc att gaa tcc tgg gtc caa gaa gtc cgt gga atc tgg ccc aat 480
 Glu Leu Ile Glu Ser Trp Val Gln Glu Val Arg Gly Ile Trp Pro Asn
 145 150 155 160

gtg aac aat gaa gag cgc ctc caa gca cgt atc gtg acc gct ctc atc 528
 Val Asn Asn Glu Glu Arg Leu Gln Ala Arg Ile Val Thr Ala Leu Ile
 165 170 175

ggc tgg gca cta tcg agt gtt gcc ttc atg aag ctc ggc tcc atc agc 576
 Gly Trp Ala Leu Ser Ser Val Ala Phe Met Lys Leu Gly Ser Ile Ser
 180 185 190

 ggc atg ctt aac ctg ctg cac gtc acc gaa gat gga aac acc act ttg 624
 Gly Met Leu Asn Leu Leu His Val Thr Glu Asp Gly Asn Thr Thr Leu
 195 200 205

 gat gtc tcc aac ctt gat gaa ctg ttg att cca cga tct gcc gaa gat 672
 Asp Val Ser Asn Leu Asp Glu Leu Leu Ile Pro Arg Ser Ala Glu Asp
 210 215 220

 gac gag ctg gtc cag caa gac ctc cac gac acg ttc tcc gcg ctt cag 720
 Asp Glu Leu Val Gln Gln Asp Leu His Asp Thr Phe Ser Ala Leu Gln
 225 230 235 240

 cga ttt gca gcg cgc ggg ctg gat tcc agg ttc cct gag gtg gca cga 768
 Arg Phe Ala Ala Arg Gly Leu Asp Ser Arg Phe Pro Glu Val Ala Arg
 245 250 255

 ttc gca gac gac gtg gtg cgt ttg ttc ctc aaa aat gac tagctgaaga 817
 Phe Ala Asp Asp Val Val Arg Leu Phe Leu Lys Asn Asp
 260 265

 gcaccggttg ctt 830

<210> 2910

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 2910

Ile Leu Arg Asn Leu Gly Gln Ser Leu Gly Ser Leu His Ala Ala Thr
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 Ala Asp Arg Glu Glu Asp Phe Asn Ile Leu Leu Asn Arg Met Leu Ala
 20 25 30

 Lys Tyr Pro Ala Thr Ala Glu Met Gln Lys Asn Arg Asp Arg Leu Leu
 35 40 45

 Pro Ala Ala Ile Glu Val Gly Lys Lys Ile Leu Val Asp Ala Gly Val
 50 55 60

 Thr Val Pro Glu Val Val Glu Glu Phe Ala Arg Val Ala Arg Arg Arg
 65 70 75 80

 Leu Ile Ser Gly Arg His Arg Ala Phe Thr Pro Phe Asp Leu Ser Pro
 85 90 95

 Asp Asn Ile Ile Val Ala Glu Arg Thr His Phe Leu Asp Tyr Glu Val
 100 105 110

 Ala Gly Phe Arg Asp Ala Thr Phe Asp Val Ala Cys Val Ile Ala Gly
 115 120 125

 Phe Pro Gln Phe Val Phe Ser Arg Pro Ile Ser Asp Asp Glu Val Asp
 130 135 140

Glu Leu Ile Glu Ser Trp Val Gln Glu Val Arg Gly Ile Trp Pro Asn
145 150 155 160

Val Asn Asn Glu Glu Arg Leu Gln Ala Arg Ile Val Thr Ala Leu Ile
165 170 175

Gly Trp Ala Leu Ser Ser Val Ala Phe Met Lys Leu Gly Ser Ile Ser
180 185 190

Gly Met Leu Asn Leu Leu His Val Thr Glu Asp Gly Asn Thr Thr Leu
195 200 205

Asp Val Ser Asn Leu Asp Glu Leu Leu Ile Pro Arg Ser Ala Glu Asp
210 215 220

Asp Glu Leu Val Gln Gln Asp Leu His Asp Thr Phe Ser Ala Leu Gln
225 230 235 240

Arg Phe Ala Ala Arg Gly Leu Asp Ser Arg Phe Pro Glu Val Ala Arg
245 250 255

Phe Ala Asp Asp Val Val Arg Leu Phe Leu Lys Asn Asp
260 265

<210> 2911

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXA02789

<400> 2911

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Met Lys Val Ser Ala
1 5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
10 15 20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
25 30 35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
40 45 50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
55 60 65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
70 75 80 85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
 Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
 90 95 100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
 Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
 105 110 115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
 Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
 120 125 130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
 Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
 135 140 145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
 Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
 150 155 160 165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
 Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
 170 175 180

gga tgaaccaaatt ccgaaaccgc cgg 669
 Gly

<210> 2912

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 2912

Met Lys Val Ser Ala Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly
 1 5 10 15

Arg Arg Leu Gly Leu Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala
 20 25 30

Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
 35 40 45

Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
 50 55 60

Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
 65 70 75 80

Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
 85 90 95

Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
 100 105 110

Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
 115 120 125

Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile

cgt gtt tct gaa gta tcc tcg cgg gtt act gac tcc gga aaa act gtg 547
 Arg Val Ser Glu Val Ser Ser Arg Val Thr Asp Ser Gly Lys Thr Val
 135 140 145
 gcg gtg ctc tac ccc acc atc ggc ggc gga gtc acc tac gca tac ggc 595
 Ala Val Leu Tyr Pro Thr Ile Gly Gly Gly Val Thr Tyr Ala Tyr Gly
 150 155 160 165
 cgc gga tcc atg gcc aac cca ctt gtt gcc gaa gca ggc ctg acc aac 643
 Arg Gly Ser Met Ala Asn Pro Leu Val Ala Glu Ala Gly Leu Thr Asn
 170 175 180
 gtt ttc gca gac caa tcc gaa cgc gtc ttt gag gtc acg gca gaa gaa 691
 Val Phe Ala Asp Gln Ser Glu Arg Val Phe Glu Val Thr Ala Glu Glu
 185 190 195
 ctg atc tcc gaa acc ccg act cat cat cgt ttt aca cag cga cgg ttc 739
 Leu Ile Ser Glu Thr Pro Thr His His Arg Phe Thr Gln Arg Arg Phe
 200 205 210
 ccc ttc aga cat cgt cgc aga ggt ggg caa tct cca agg gtc cag cgc 787
 Pro Phe Arg His Arg Arg Arg Gly Gly Gln Ser Pro Arg Val Gln Arg
 215 220 225
 act cac tgc tct gag tgagaacaaa gtgctgccca tac 825
 Thr His Cys Ser Glu
 230

<210> 2914

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 2914

Met Lys Ser Ala Ala Val Pro Thr Leu Asp Ala Leu Gly Val Leu Asp
 1 5 10 15
 Arg Val Val Thr Lys Ala Gly Ala Phe Pro Ala Gly Tyr Tyr Asp Ala
 20 25 30
 Asp Leu Ser Glu Arg Val Thr Asp Ile Pro Thr Leu Ser Asn Lys Ile
 35 40 45
 Asp Ala Ser Gly His Val Leu Ile Ser Lys Glu Val Val Val Ala Ala
 50 55 60
 Asn Pro Asp Ile Val Phe Gly Glu Thr Asp Thr Ile Asn Arg Ala Ser
 65 70 75 80
 Met Ala Ser Ser Asn Ile Pro Val Val Glu Glu Pro Ala Phe Cys Gly
 85 90 95
 Ser Ile Asp Gly Asp Val Ser Phe Asp Asp Val Trp Ser Gln Ile Ser
 100 105 110
 Thr Tyr Gly Thr Ile Phe Asp Arg Ser Thr Glu Ala Asp Ala Tyr Ile
 115 120 125
 Ala Thr Leu Lys Glu Arg Val Ser Glu Val Ser Ser Arg Val Thr Asp
 130 135 140

Ser Gly Lys Thr Val Ala Val Leu Tyr Pro Thr Ile Gly Gly Gly Val
 145 150 155 160

Thr Tyr Ala Tyr Gly Arg Gly Ser Met Ala Asn Pro Leu Val Ala Glu
 165 170 175

Ala Gly Leu Thr Asn Val Phe Ala Asp Gln Ser Glu Arg Val Phe Glu
 180 185 190

Val Thr Ala Glu Glu Leu Ile Ser Glu Thr Pro Thr His His Arg Phe
 195 200 205

Thr Gln Arg Arg Phe Pro Phe Arg His Arg Arg Arg Gly Gly Gln Ser
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Pro Arg Val Gln Arg Thr His Cys Ser Glu
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<211> 672

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<213> Corynebacterium glutamicum

<220>

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<223> RXA02796

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 Met Arg Leu Phe Ala
 1 5

tct atc act ccg ccg att gaa gtc acc gag cat ctg atc aac gcg ctt 163
 Ser Ile Thr Pro Pro Ile Glu Val Thr Glu His Leu Ile Asn Ala Leu
 10 15 20

cgt ccc tac aag gat gat ctg cgg tgg tct gat cca gac aat tgg cac 211
 Arg Pro Tyr Lys Asp Asp Leu Arg Trp Ser Asp Pro Asp Asn Trp His
 25 30 35

atc acg ttg gcg ttc tat gga gaa tta cct gat ggg gca gtc gaa gat 259
 Ile Thr Leu Ala Phe Tyr Gly Glu Leu Pro Asp Gly Ala Val Glu Asp
 40 45 50

ctc att gag cat ctg aca agt gca gcc cga atc aat gaa gaa ttc acc 307
 Leu Ile Glu His Leu Thr Ser Ala Ala Arg Ile Asn Glu Glu Phe Thr
 55 60 65

atc aga atc aaa ggc gca ggc tca ttt aat cgg aag aat ttg tgg atg 355
 Ile Arg Ile Lys Gly Ala Gly Ser Phe Asn Arg Lys Asn Leu Trp Met
 70 75 80 85

ggg gtt ggt ggt gac acc aaa gat ctg cgg cga ctg atg gct gat tgt 403
 Gly Val Gly Gly Asp Thr Lys Asp Leu Arg Arg Leu Met Ala Asp Cys
 90 95 100

ctg att gat cct gag gaa cgc cga cgc cag cgt gca cac ctg acc gtg 451
 Leu Ile Asp Pro Glu Glu Arg Arg Arg Gln Arg Ala His Leu Thr Val
 105 110 115

gcg aaa cca acg cag cga cag cgc agc cgc gat tgg gat cct gtc atc 499
 Ala Lys Pro Thr Gln Arg Gln Arg Ser Arg Asp Trp Asp Pro Val Ile
 120 125 130

ccc gat ctg gtc cac gct ctc tct ata tac gaa ggc ccc gaa tgg cca 547
 Pro Asp Leu Val His Ala Leu Ser Ile Tyr Glu Gly Pro Glu Trp Pro
 135 140 145

gtc gat gag att gaa ctg gtg tct tct gaa cct gga aaa ggc aga agc 595
 Val Asp Glu Ile Glu Leu Val Ser Ser Glu Pro Gly Lys Gly Arg Ser
 150 155 160 165

ggt ggg cca ctg tat aca acc gtg gcc acc att gcg ttg tca tct gcg 643
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ctg gtt taaaggctca accgcggaac ggc 672
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<210> 2916

<211> 183

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<400> 2916

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 20 25 30

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 35 40 45

Gly Ala Val Glu Asp Leu Ile Glu His Leu Thr Ser Ala Ala Arg Ile
 50 55 60

Asn Glu Glu Phe Thr Ile Arg Ile Lys Gly Ala Gly Ser Phe Asn Arg
 65 70 75 80

Lys Asn Leu Trp Met Gly Val Gly Gly Asp Thr Lys Asp Leu Arg Arg
 85 90 95

Leu Met Ala Asp Cys Leu Ile Asp Pro Glu Glu Arg Arg Arg Gln Arg
 100 105 110

Ala His Leu Thr Val Ala Lys Pro Thr Gln Arg Gln Arg Ser Arg Asp
 115 120 125

Trp Asp Pro Val Ile Pro Asp Leu Val His Ala Leu Ser Ile Tyr Glu
 130 135 140

Gly Pro Glu Trp Pro Val Asp Glu Ile Glu Leu Val Ser Ser Glu Pro
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Gly Lys Gly Arg Ser Gly Gly Pro Leu Tyr Thr Thr Val Ala Thr Ile
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Ala Leu Ser Ser Ala Leu Val
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<211> 1548

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<220>

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<222> (101)..(1525)

<223> RXA02798

<400> 2917

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                                   Met Arg Ser Val Leu
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gac tac tgg atc atg act ctt gca cct tcc acc aat gcg gtt tcg cag      163
Asp Tyr Trp Ile Met Thr Leu Ala Pro Ser Thr Asn Ala Val Ser Gln
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Gln Thr Arg Arg Asn Pro Ser Gln Ala Pro Arg Leu Leu His Arg Leu
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His Phe Phe Ala Gly Ile Ile Cys Ala Pro Leu Ile Phe Ile Ala Ala
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ctc acc gga ctg gtg tat gcg ttc tcc ccc acc att gaa agc atc tct      307
Leu Thr Gly Leu Val Tyr Ala Phe Ser Pro Thr Ile Glu Ser Ile Ser
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Asn Gln Glu Met Leu Thr Val Ser Lys Ser Ala Ser Asp Thr Ala Leu
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Pro Val Arg Glu Gln Val Ser Ile Ala Gln Glu Leu His Pro Asp Leu
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gat ctc tca ggt gtc cgg ctt ggc gat gat tcc tcc acc acc cgc gtc      451
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ctc ttc gcc gac gag acg ctt gct gaa tcc aca gtc cgc gcc gtg ttt      499
Leu Phe Ala Asp Glu Thr Leu Ala Glu Ser Thr Val Arg Ala Val Phe
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gtt gat ccc tac acc ggc gag atc acc ggt gat acc acc caa tac gga      547
Val Asp Pro Tyr Thr Gly Glu Ile Thr Gly Asp Thr Thr Gln Tyr Gly
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agc tca gct gca ctg ccg ttt cgg caa tgg gtc tcg caa ggt cac cgc      595

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Ser 150	Ser	Ala	Ala	Leu	Pro 155	Phe	Arg	Gln	Trp	Val 160	Ser	Gln	Gly	His	Arg 165	
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Ser	Trp	Leu	Gly 185	Val	Leu	Ala	Val	Gly 190	Gly	Phe	Ala	Leu	Leu	Trp	Leu 195	
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Arg	Gly 215	Arg	Val	Lys	Thr	Tyr 220	Arg	Arg	His	Ala	Ala 225	Leu	Gly	Thr	Val	
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Thr	Tyr	Ala	Gly	Ser 250	Asn	Ile	Thr	Asp	Leu	Arg	Thr	Gln	Leu	Asn 260	Trp	
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Ile	Ala	Val	Asp 345	Gly	Asp	Thr	Gly	Met	Leu	Thr	Asn	Arg	Leu	Asn	Ser 355	
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Thr	Asp	Trp	Pro	Leu	Ala	Ala	Gln	Ala	Ser	Ala	Trp	Leu	Ile	Gln	Leu 370	
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cac	atg	ggc	acc	ctg	ttt	ggc	ctt	ccc	aac	cag	gtt	gta	ctt	ggg	ctg	1267
His	Met	Gly	Thr	Leu	Phe	Gly	Leu	Pro	Asn	Gln	Val	Val	Leu	Gly	Leu 385	
375						380										
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390 395 400 405
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 410 415 420
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 Gly Phe Glu Lys Pro Thr Trp Gly Thr Ile Ala Leu Gly Val Val Val
 425 430 435
 atc gcg tat ggg ctt ctc gcg cca ctt ttt gca gtt tca ctg ctc gtg 1459
 Ile Ala Tyr Gly Leu Leu Ala Pro Leu Phe Ala Val Ser Leu Leu Val
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 ttt att gga tta agc ctt gga gtg cgg ttt att tct cgt atg tcc ggg 1507
 Phe Ile Gly Leu Ser Leu Gly Val Arg Phe Ile Ser Arg Met Ser Gly
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 <213> Corynebacterium glutamicum

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 35 40 45
 Ile Phe Ile Ala Ala Leu Thr Gly Leu Val Tyr Ala Phe Ser Pro Thr
 50 55 60
 Ile Glu Ser Ile Ser Asn Gln Glu Met Leu Thr Val Ser Lys Ser Ala
 65 70 75 80
 Ser Asp Thr Ala Leu Pro Val Arg Glu Gln Val Ser Ile Ala Gln Glu
 85 90 95
 Leu His Pro Asp Leu Asp Leu Ser Gly Val Arg Leu Gly Asp Asp Ser
 100 105 110
 Ser Thr Thr Arg Val Leu Phe Ala Asp Glu Thr Leu Ala Glu Ser Thr
 115 120 125
 Val Arg Ala Val Phe Val Asp Pro Tyr Thr Gly Glu Ile Thr Gly Asp
 130 135 140
 Thr Thr Gln Tyr Gly Ser Ser Ala Ala Leu Pro Phe Arg Gln Trp Val
 145 150 155 160
 Ser Gln Gly His Arg Met Leu Trp Leu Gly Glu Pro Gly Arg Ile Tyr
 165 170 175

Ser Glu Leu Ala Ala Ser Trp Leu Gly Val Leu Ala Val Gly Gly Phe
180 185 190

Ala Leu Leu Trp Leu Arg Asn Lys Lys Pro Gly Arg Leu Arg Lys Met
195 200 205

Val Arg Thr Gly Gly Arg Gly Arg Val Lys Thr Tyr Arg Arg His Ala
210 215 220

Ala Leu Gly Thr Val Ala Gly Leu Gly Phe Val Phe Leu Thr Phe Thr
225 230 235 240

Gly Leu Thr Trp Ser Thr Tyr Ala Gly Ser Asn Ile Thr Asp Leu Arg
245 250 255

Thr Gln Leu Asn Trp Thr Gln Pro Ser Val Asn Ala Ser Leu Thr Ala
260 265 270

Ala Pro Gln Val Asp Met His Asp Glu His Ala Gly His His Met His
275 280 285

Met Glu Ser Ala Thr Ser Gly Ser Gly Ser Ile Asp Leu Val Ala Ala
290 295 300

Thr Ala Ile Ser Glu Leu Arg Thr Pro Leu Thr Ile Thr Pro Pro Ala
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Gln Asp Gly Leu Ala Trp Thr Ala Thr Glu Asn Arg Asp Ala Tyr Arg
325 330 335

Phe Thr Thr Asp Thr Ile Ala Val Asp Gly Asp Thr Gly Met Leu Thr
340 345 350

Asn Arg Leu Asn Ser Thr Asp Trp Pro Leu Ala Ala Gln Ala Ser Ala
355 360 365

Trp Leu Ile Gln Leu His Met Gly Thr Leu Phe Gly Leu Pro Asn Gln
370 375 380

Val Val Leu Gly Leu Leu Ala Ala Ser Ile Ile Val Met Ile Gly Leu
385 390 395 400

Gly Tyr Trp Met Leu Trp Gln His Arg Pro Arg Glu Gly Trp Pro Ser
405 410 415

Ala Pro Lys Arg Ala Gly Phe Glu Lys Pro Thr Trp Gly Thr Ile Ala
420 425 430

Leu Gly Val Val Val Ile Ala Tyr Gly Leu Leu Ala Pro Leu Phe Ala
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<223> RXA02799

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1 5
gaa gac atc cag cgc gat att gag cgc acc cgc cgt cag ttg gct tcc 163
Glu Asp Ile Gln Arg Asp Ile Glu Arg Thr Arg Arg Gln Leu Ala Ser
10 15 20
acc ctc gac gag ctg gca gac cgc agc aag cct tcc aac ttg gtc gat 211
Thr Leu Asp Glu Leu Ala Asp Arg Ser Lys Pro Ser Asn Leu Val Asp
25 30 35
gac gcc aag aac cag gca acc gcg aag ctg cag gaa tca aac gta cag 259
Asp Ala Lys Asn Gln Ala Thr Ala Lys Leu Gln Glu Ser Asn Val Gln
40 45 50
aag gtg ctc ctg ggc gtc gct gct gtc gtc gtc ggt gct gtt gta ttc 307
Lys Val Leu Leu Gly Val Ala Ala Val Val Val Gly Ala Val Val Phe
55 60 65
agc gtt gtg cgt ggc cgt aag aag gca aac gat ctg aag gaa atc cag 355
Ser Val Val Arg Gly Arg Lys Lys Ala Asn Asp Leu Lys Glu Ile Gln
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Arg Leu Leu Ser Glu Arg
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<212> PRT

<213> Corynebacterium glutamicum

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20 25 30
Ser Asn Leu Val Asp Asp Ala Lys Asn Gln Ala Thr Ala Lys Leu Gln
35 40 45
Glu Ser Asn Val Gln Lys Val Leu Leu Gly Val Ala Ala Val Val Val
50 55 60
Gly Ala Val Val Phe Ser Val Val Arg Gly Arg Lys Lys Ala Asn Asp
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<212> DNA

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<223> RXA02815

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ttc gaa gta atc gca acg gtt gcc tct gaa ttc gca ggc gac gac ggc	96
Phe Glu Val Ile Ala Thr Val Ala Ser Glu Phe Ala Gly Asp Asp Gly	
20 25 30	
aac tac tcc aac gaa ttc ccc gtg gaa gat cta gtc gga tac gtt gac	144
Asn Tyr Ser Asn Glu Phe Pro Val Glu Asp Leu Val Gly Tyr Val Asp	
35 40 45	
gcc atc acc gaa gcc ggc gga tac gca gtc ctg gat ctt caa ccc gga	192
Ala Ile Thr Glu Ala Gly Gly Tyr Ala Val Leu Asp Leu Gln Pro Gly	
50 55 60	
cgc gcc aac ttc ctc gac caa gcc aaa atg tat gaa gaa ctc ctc aaa	240
Arg Ala Asn Phe Leu Asp Gln Ala Lys Met Tyr Glu Glu Leu Leu Lys	
65 70 75 80	
cga cca aac gtt gga ttg gcg cta gat ccc gag tgg aaa atc gga ccc	288
Arg Pro Asn Val Gly Leu Ala Leu Asp Pro Glu Trp Lys Ile Gly Pro	
85 90 95	
gat gag caa ccc atg aca cga gtg ggc tct gca gat gcc gcc gaa atc	336
Asp Glu Gln Pro Met Thr Arg Val Gly Ser Ala Asp Ala Ala Glu Ile	
100 105 110	
aac gaa gta tcc cag tgg ctc gcc gac ctg acc gcc gag aac gat ctt	384
Asn Glu Val Ser Gln Trp Leu Ala Asp Leu Thr Ala Glu Asn Asp Leu	
115 120 125	
cca caa aag gca ttt gta ctg cac caa ttc caa ttg gaa atg ctc acc	432
Pro Gln Lys Ala Phe Val Leu His Gln Phe Gln Leu Glu Met Leu Thr	
130 135 140	
aat cgg gat caa atc aat acc gat cac ctg gaa ctg gct gtc gtg ttg	480
Asn Arg Asp Gln Ile Asn Thr Asp His Leu Glu Leu Ala Val Val Leu	
145 150 155 160	
cac gca gat gga cac gga aac gca ggg gat aag tac gca act tgg aac	528
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<400> 2922

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20 25 30

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35 40 45

Ala Ile Thr Glu Ala Gly Gly Tyr Ala Val Leu Asp Leu Gln Pro Gly
50 55 60

Arg Ala Asn Phe Leu Asp Gln Ala Lys Met Tyr Glu Glu Leu Leu Lys
65 70 75 80

Arg Pro Asn Val Gly Leu Ala Leu Asp Pro Glu Trp Lys Ile Gly Pro
85 90 95

Asp Glu Gln Pro Met Thr Arg Val Gly Ser Ala Asp Ala Ala Glu Ile
100 105 110

Asn Glu Val Ser Gln Trp Leu Ala Asp Leu Thr Ala Glu Asn Asp Leu
115 120 125

Pro Gln Lys Ala Phe Val Leu His Gln Phe Gln Leu Glu Met Leu Thr
130 135 140

Asn Arg Asp Gln Ile Asn Thr Asp His Leu Glu Leu Ala Val Val Leu
145 150 155 160

His Ala Asp Gly His Gly Asn Ala Gly Asp Lys Tyr Ala Thr Trp Asn
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Met Leu Arg Glu Gly Leu Ser Pro
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<223> Xaa = Phe, Ser, Tyr, or Cys

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<223> Xaa = Leu, Pro, His, or Arg

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<222> (102, 135)

<223> Xaa = His or Gln

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 Met Tyr Glu Gln Gln
 1 5

aag atc ctt aac gaa gtc agt gaa aaa cgt ctt cag gca atc aaa gat 163
 Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu Gln Ala Ile Lys Asp
 10 15 20

ttt aca gaa ctg gga tct gga ttc aag att gcg atg cgg gat ctt tcc 211
 Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala Met Arg Asp Leu Ser
 25 30 35

att cgc ggt gca ggt aat ctc tta ggt gct cag cag cat gga ttt att 259
 Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln Gln His Gly Phe Ile
 40 45 50

gat gca gtc ggt ttc gat atg tat tct caa atg cta agc gaa gct gtt 307
 Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met Leu Ser Glu Ala Val
 55 60 65

tnt cgt aaa caa gga aag aat agt caa gtg gag aag ncc nct gtt gag 355
 Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu Lys Xaa Xaa Val Glu
 70 75 80 85

atc gac cnc ggt gtc gat gcg tat cta cct gaa aca tac gtg gca gat 403
 Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu Thr Tyr Val Ala Asp
 90 95 100

can cgg cag aaa atc gag atc tat aaa cga att cgt gaa ctt gat tcg 451
 Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile Arg Glu Leu Asp Ser
 105 110 115

caa gaa atg cta gat gaa cta gaa gat gat ctg ctc gac cgt ttt gga 499
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gaa can cca gaa gaa gta gca cat 523
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 20 25 30

Met Arg Asp Leu Ser Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln
 35 40 45

Gln His Gly Phe Ile Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met
 50 55 60

Leu Ser Glu Ala Val Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu
 65 70 75 80

Lys Xaa Xaa Val Glu Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu
 85 90 95

Thr Tyr Val Ala Asp Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile
 100 105 110

Arg Glu Leu Asp Ser Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu
 115 120 125

Leu Asp Arg Phe Gly Glu Xaa Pro Glu Glu Val Ala His
 130 135 140

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 <212> DNA
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 <223> RXA02842

<220>
 <221> misc_feature
 <222> (299)
 <223> n = a, t, c, or g

<220>
 <221> VARIANT
 <222> (100)
 <223> Xaa = Leu, Pro, His, or Arg

<400> 2927
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 Asp Ala Gly Phe Val Tyr Phe Gly Glu Ile Asp Asp Ala Gly His Ile
 1 5 10 15

ttc ggc ctg gca ggc gac gaa tac cga ggg ggg att cgc agg gtc gac 96
 Phe Gly Leu Ala Gly Asp Glu Tyr Arg Gly Gly Ile Arg Arg Val Asp
 20 25 30

acc cac gtg aag aaa gtt ctt tct gaa gtg tca cga cgc tcc gac gag 144
 Thr His Val Lys Lys Val Leu Ser Glu Val Ser Arg Arg Ser Asp Glu
 35 40 45

ctc ggg gag gac tgg ctg gta gtg atc aca act gat cat ggt cac ctt 192
 Leu Gly Glu Asp Trp Leu Val Val Ile Thr Thr Asp His Gly His Leu
 50 55 60

gat gag ggc ggg cac ggc ggc acc acc gat cgg gag cga gaa tcc tgg 240
 Asp Glu Gly Gly His Gly Gly Thr Thr Asp Arg Glu Arg Glu Ser Trp
 65 70 75 80

atc atc acg tgg agc ccg cac cgg gaa ctg cca cag tgg cct gaa gaa 288
 Ile Ile Thr Trp Ser Pro His Arg Glu Leu Pro Gln Trp Pro Glu Glu
 85 90 95

att gcg ccg cnt gag ctg gca gaa ctg atg ctt gtg gag cgc cga acc 336
 Ile Ala Pro Xaa Glu Leu Ala Glu Leu Met Leu Val Glu Arg Arg Thr
 100 105 110

ttg agg tgattgtcac taaa 356
 Leu Arg

<210> 2928
 <211> 114
 <212> PRT
 <213> Corynebacterium glutamicum

<220>
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 <223> Xaa = Leu, Pro, His, or Arg

<400> 2928
 Asp Ala Gly Phe Val Tyr Phe Gly Glu Ile Asp Asp Ala Gly His Ile
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 Phe Gly Leu Ala Gly Asp Glu Tyr Arg Gly Gly Ile Arg Arg Val Asp
 20 25 30
 Thr His Val Lys Lys Val Leu Ser Glu Val Ser Arg Arg Ser Asp Glu
 35 40 45
 Leu Gly Glu Asp Trp Leu Val Val Ile Thr Thr Asp His Gly His Leu
 50 55 60
 Asp Glu Gly Gly His Gly Gly Thr Thr Asp Arg Glu Arg Glu Ser Trp
 65 70 75 80
 Ile Ile Thr Trp Ser Pro His Arg Glu Leu Pro Gln Trp Pro Glu Glu
 85 90 95
 Ile Ala Pro Xaa Glu Leu Ala Glu Leu Met Leu Val Glu Arg Arg Thr
 100 105 110
 Leu Arg

<210> 2929
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(615)
 <223> RXA02845

<400> 2929
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 1 5 10 15
 cat gac cgc gat ccg gct cgc ttc cca ggc cag ggc gac ggt tcc tac 96
 His Asp Arg Asp Pro Ala Arg Phe Pro Gly Gln Gly Asp Gly Ser Tyr
 20 25 30
 ccg gat ctt ttt tgg ctg tac aaa aac gcc ctc aac ctg gtc att agc 144
 Pro Asp Leu Phe Trp Leu Tyr Lys Asn Ala Leu Asn Leu Val Ile Ser
 35 40 45
 tca gtg ttg ttc acc cgt gag cag atg gac aac atg ctc gat cag atg 192
 Ser Val Leu Phe Thr Arg Glu Gln Met Asp Asn Met Leu Asp Gln Met

50	55	60	
gat gaa cac ttc acg cgc gcg ggt atc ccg cgc atc gcg att aat att			240
Asp Glu His Phe Thr Arg Ala Gly Ile Pro Arg Ile Ala Ile Asn Ile			
65	70	75	80
gag cgc cgc gac gac gcc ctg atg aac ggc tcc ctc gag cgt gcg cta			288
Glu Arg Arg Asp Asp Ala Leu Met Asn Gly Ser Leu Glu Arg Ala Leu			
	85	90	95
gag ctg caa gag ctt atc gac gcc tcc cag cac gac gat ccc ttc gac			336
Glu Leu Gln Glu Leu Ile Asp Ala Ser Gln His Asp Asp Pro Phe Asp			
	100	105	110
gac tgc cca acc tgc caa att gca gga aaa gcg gca ctc gca atg gca			384
Asp Cys Pro Thr Cys Gln Ile Ala Gly Lys Ala Ala Leu Ala Met Ala			
	115	120	125
gca gat gat tac gac gaa acc caa aac ctc gtc tcc caa atc atc agc			432
Ala Asp Asp Tyr Asp Glu Thr Gln Asn Leu Val Ser Gln Ile Ile Ser			
	130	135	140
tac gga tcc atc ggc tgc gtc atg gaa cca gag acc acc ctc gct gcg			480
Tyr Gly Ser Ile Gly Cys Val Met Glu Pro Glu Thr Thr Leu Ala Ala			
	145	150	155
ttc atg ctg cgt gtg ctt aag tcc ggc gat gct gat tat gcc cgc tac			528
Phe Met Leu Arg Val Leu Lys Ser Gly Asp Ala Asp Tyr Ala Arg Tyr			
	165	170	175
ctg caa gat gtc agt gcg aag gca aac cca gaa ttc cag tcc ctt gat			576
Leu Gln Asp Val Ser Ala Lys Ala Asn Pro Glu Phe Gln Ser Leu Asp			
	180	185	190
tcc gtt gga cgc cac cta gaa ttc ctc ggc atc act gga			615
Ser Val Gly Arg His Leu Glu Phe Leu Gly Ile Thr Gly			
	195	200	205
<210> 2930			
<211> 205			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 2930			
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His Asp Arg Asp Pro Ala Arg Phe Pro Gly Gln Gly Asp Gly Ser Tyr			
	20	25	30
Pro Asp Leu Phe Trp Leu Tyr Lys Asn Ala Leu Asn Leu Val Ile Ser			
	35	40	45
Ser Val Leu Phe Thr Arg Glu Gln Met Asp Asn Met Leu Asp Gln Met			
	50	55	60
Asp Glu His Phe Thr Arg Ala Gly Ile Pro Arg Ile Ala Ile Asn Ile			
65	70	75	80
Glu Arg Arg Asp Asp Ala Leu Met Asn Gly Ser Leu Glu Arg Ala Leu			

85										90					95				
Glu	Leu	Gln	Glu	Leu	Ile	Asp	Ala	Ser	Gln	His	Asp	Asp	Pro	Phe	Asp				
			100					105					110						
Asp	Cys	Pro	Thr	Cys	Gln	Ile	Ala	Gly	Lys	Ala	Ala	Leu	Ala	Met	Ala				
		115					120					125							
Ala	Asp	Asp	Tyr	Asp	Glu	Thr	Gln	Asn	Leu	Val	Ser	Gln	Ile	Ile	Ser				
		130				135					140								
Tyr	Gly	Ser	Ile	Gly	Cys	Val	Met	Glu	Pro	Glu	Thr	Thr	Leu	Ala	Ala				
145					150					155					160				
Phe	Met	Leu	Arg	Val	Leu	Lys	Ser	Gly	Asp	Ala	Asp	Tyr	Ala	Arg	Tyr				
				165				170						175					
Leu	Gln	Asp	Val	Ser	Ala	Lys	Ala	Asn	Pro	Glu	Phe	Gln	Ser	Leu	Asp				
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Ser	Val	Gly	Arg	His	Leu	Glu	Phe	Leu	Gly	Ile	Thr	Gly							
		195					200					205							

<210> 2931

<211> 499

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(499)

<223> RXA02848

<400> 2931

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                                         Met Gln Ile Val Leu
                                         1 5

gct tcg cag tcc ccg tcc cgc cga aga atc ctc aat tcg gcg ggc gtc 163
Ala Ser Gln Ser Pro Ser Arg Arg Arg Ile Leu Asn Ser Ala Gly Val
          10          15          20

gag ccc ctc atc cac cca gct gat gtt gat gag gac gcg ctc ctt cac 211
Glu Pro Leu Ile His Pro Ala Asp Val Asp Glu Asp Ala Leu Leu His
          25          30          35

tcc ctc aac ggc tct gcg ccg gag gag atc gtc cgc cag ctt gcg ctg 259
Ser Leu Asn Gly Ser Ala Pro Glu Glu Ile Val Arg Gln Leu Ala Leu
          40          45          50

gct aaa gca cag gtg gtt gcg ccg tcc tat ccg ggc gac gtc gtc atc 307
Ala Lys Ala Gln Val Val Ala Pro Ser Tyr Pro Gly Asp Val Val Ile
          55          60          65

ggt ggc gat tcc atg ctg ctt atc gac gcc acc ctc caa ggc aag ccg 355
Gly Gly Asp Ser Met Leu Leu Ile Asp Ala Thr Leu Gln Gly Lys Pro
          70          75          80          85

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cac acc cgc gaa gcc acc atc gaa aga tgg aaa caa caa cgc ggc aac 403
 His Thr Arg Glu Ala Thr Ile Glu Arg Trp Lys Gln Gln Arg Gly Asn
 90 95 100

aag gcc aca ctg atc acc ggc cac gcc atc atc ttt ggc gat gaa gtg 451
 Lys Ala Thr Leu Ile Thr Gly His Ala Ile Ile Phe Gly Asp Glu Val
 105 110 115

atc gtg gag tcc tcc tcc acc aac att cat ttc gcc gag gcc agc gat 499
 Ile Val Glu Ser Ser Ser Thr Asn Ile His Phe Ala Glu Ala Ser Asp
 120 125 130

<210> 2932

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 2932

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Asn Ser Ala Gly Val Glu Pro Leu Ile His Pro Ala Asp Val Asp Glu
 20 25 30

Asp Ala Leu Leu His Ser Leu Asn Gly Ser Ala Pro Glu Glu Ile Val
 35 40 45

Arg Gln Leu Ala Leu Ala Lys Ala Gln Val Val Ala Pro Ser Tyr Pro
 50 55 60

Gly Asp Val Val Ile Gly Gly Asp Ser Met Leu Leu Ile Asp Ala Thr
 65 70 75 80

Leu Gln Gly Lys Pro His Thr Arg Glu Ala Thr Ile Glu Arg Trp Lys
 85 90 95

Gln Gln Arg Gly Asn Lys Ala Thr Leu Ile Thr Gly His Ala Ile Ile
 100 105 110

Phe Gly Asp Glu Val Ile Val Glu Ser Ser Ser Thr Asn Ile His Phe
 115 120 125

Ala Glu Ala Ser Asp
 130

<210> 2933

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2933

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18

<210> 2934

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2934

gtaaaacgac ggccagt